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(54) Abstract Title

**Human genome-derived single exon nucleic acid probes**

(57) A spatially addressable set of such probes is provided for measuring gene expression in a sample derived from human heart, the probes comprising any one of the nucleotide sequences set out in SEQ ID NOS: 1-5202 or 5203-10283 or a complementary sequence. The set may comprise 50-20,000 probes of average length 200-500 bp and may be addressably disposed upon a substrate. At least 50% of the probes lack prokaryotic and bacteriophage vector sequence and at least 50% lack homopolymeric stretches of A or T. Each of the probes may be amplifiable using at least one common primer. Also claimed are said nucleotide sequences and peptides encoded thereby.

At least one drawing originally filed was informal and the print reproduced here is taken from a later filed formal copy.  
 This print takes account of replacement documents submitted after the date of filing to enable the application to comply with the formal requirements of the Patents Rules 1995  
 The specification as filed includes sequence listings which are not reproduced here; they may be inspected in accordance with Section 118 of the Patents Act 1977.

Fig. 1.

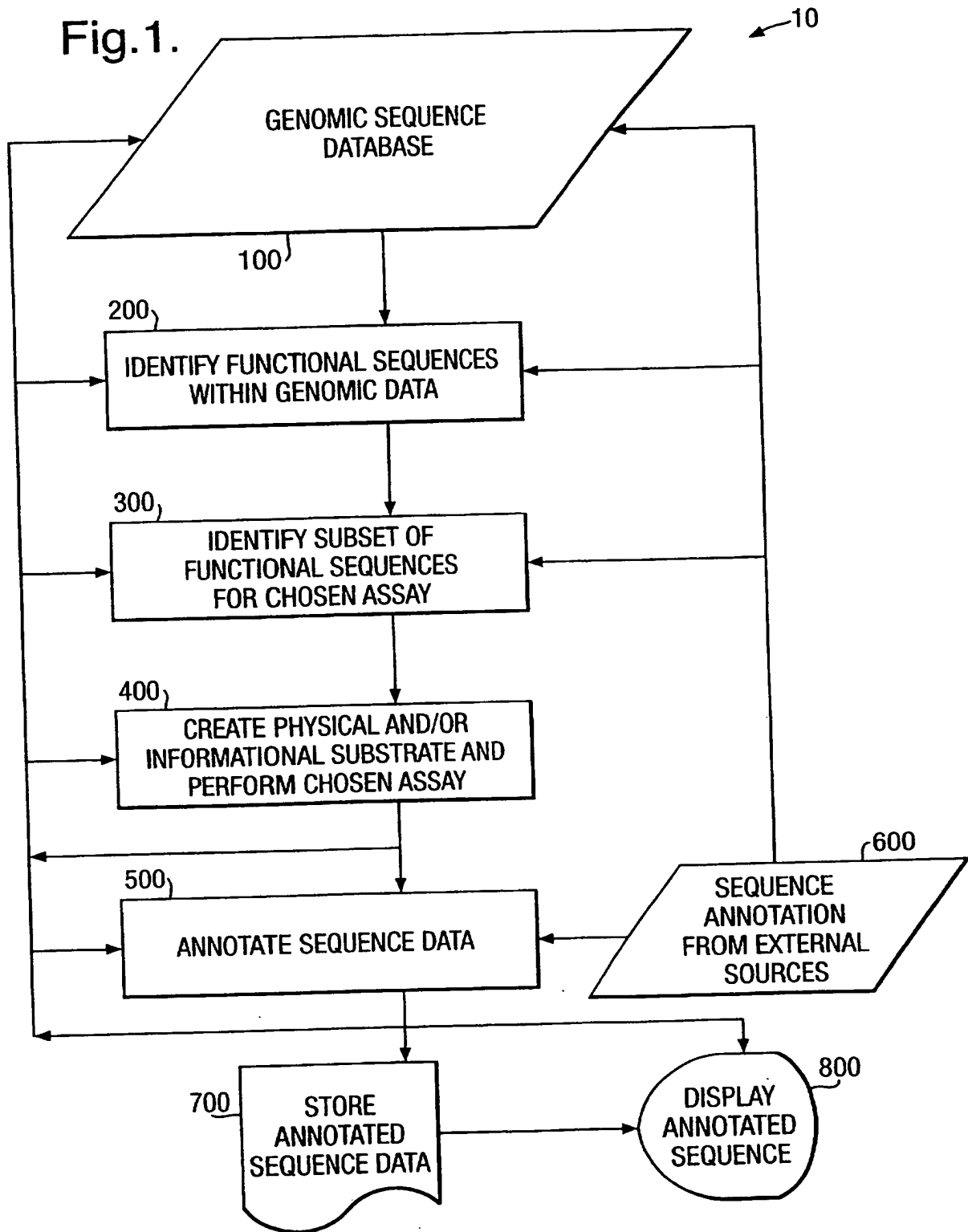


Fig.2.

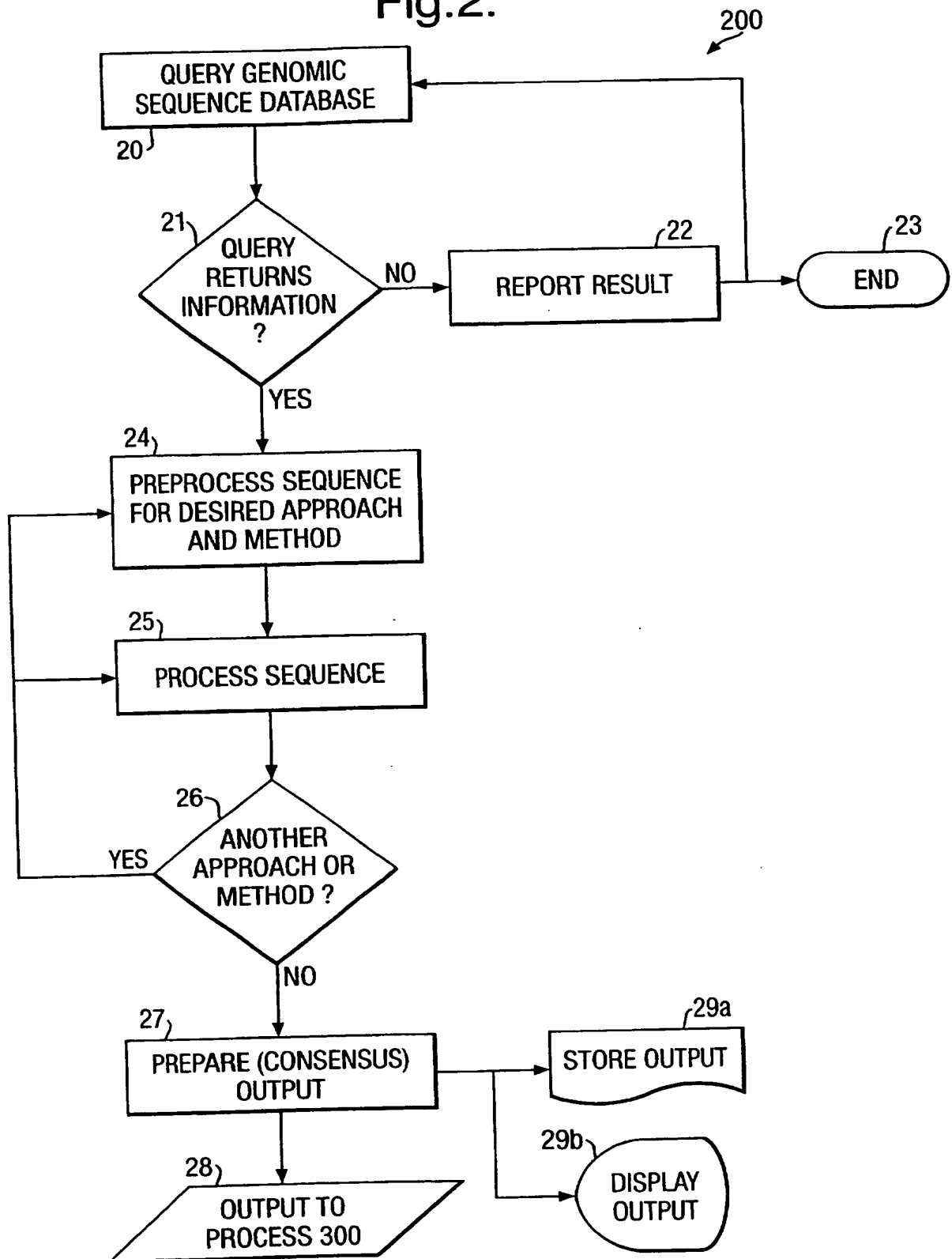


Fig.3.

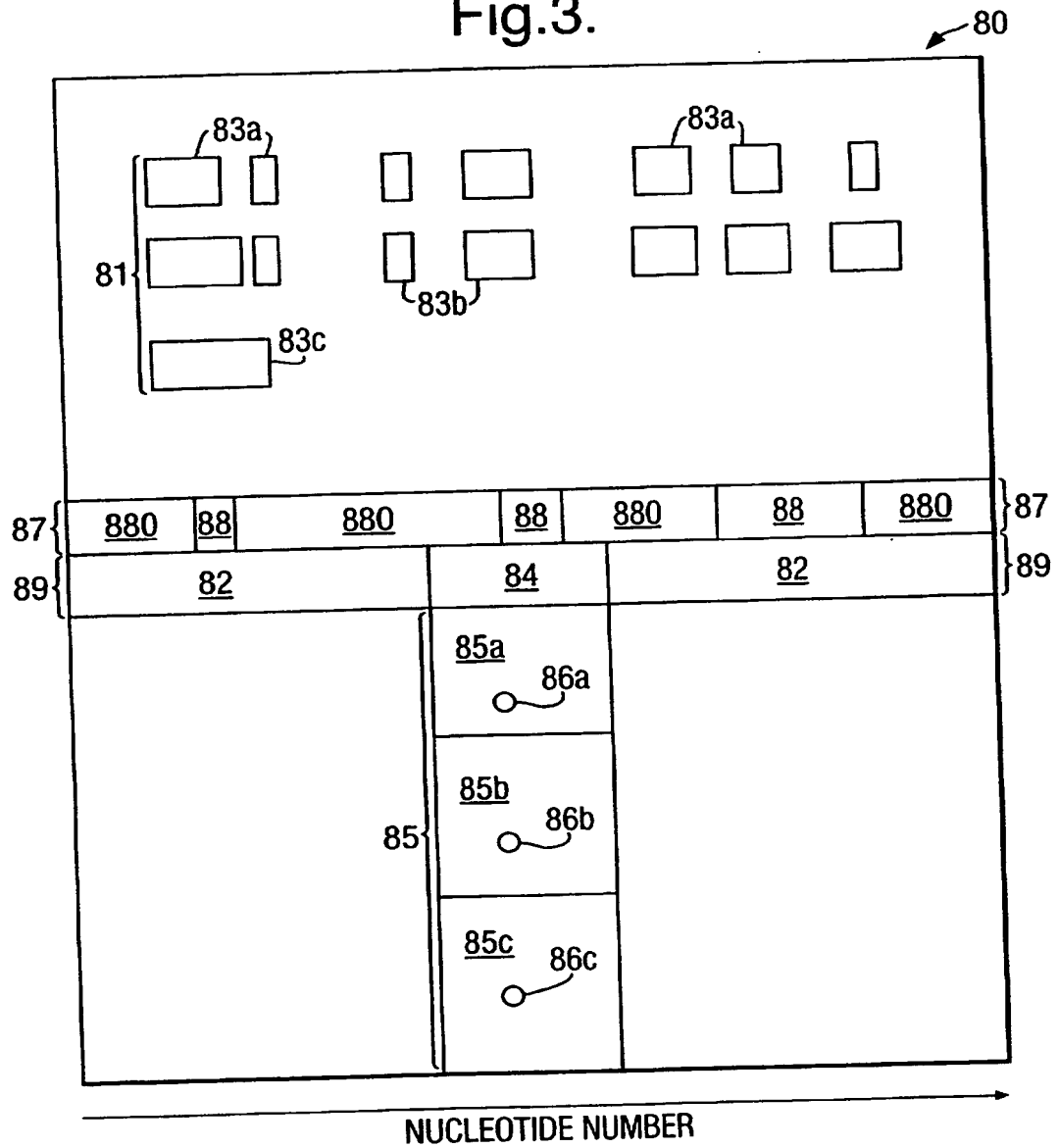




Fig.4.

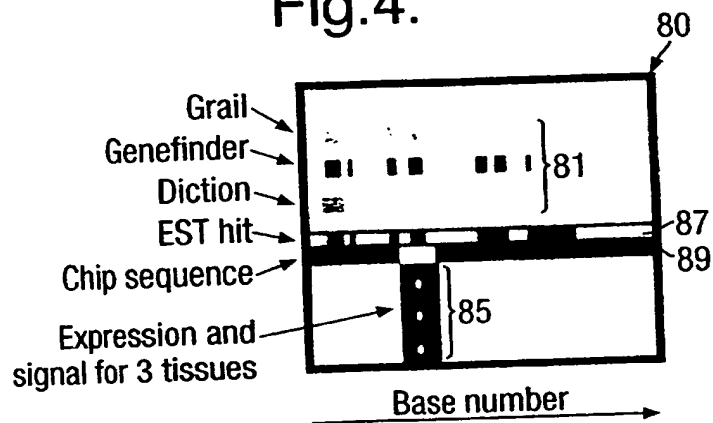


Fig.5.

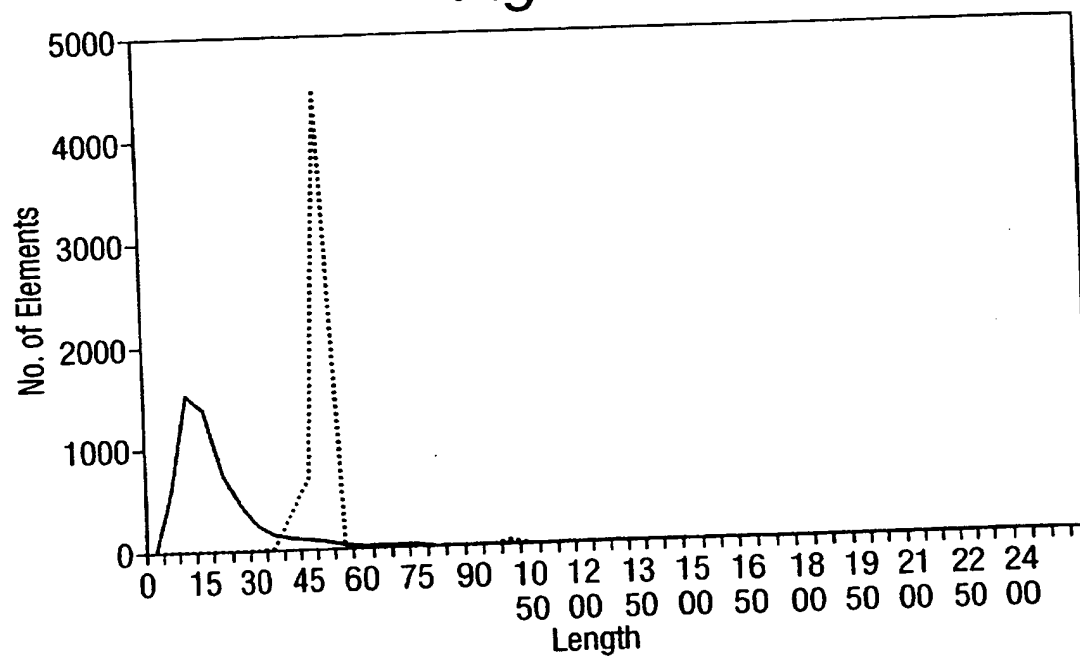


Fig.6.

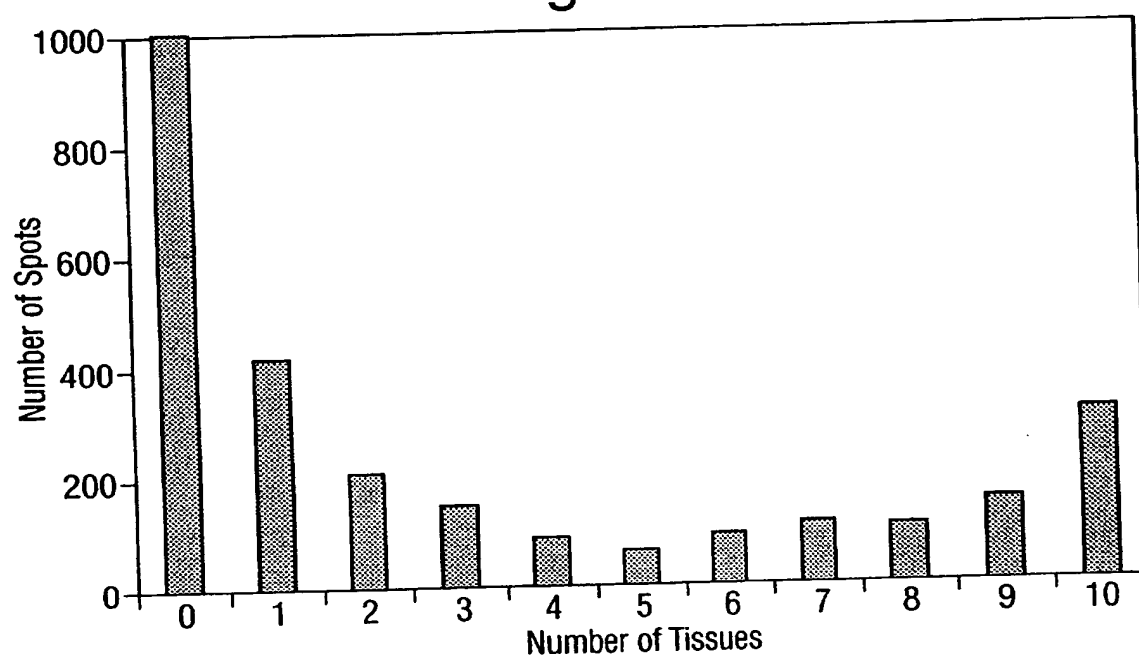


Fig.7A.

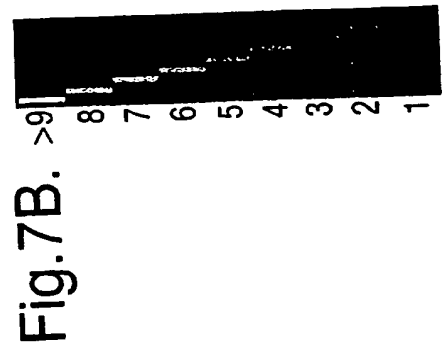
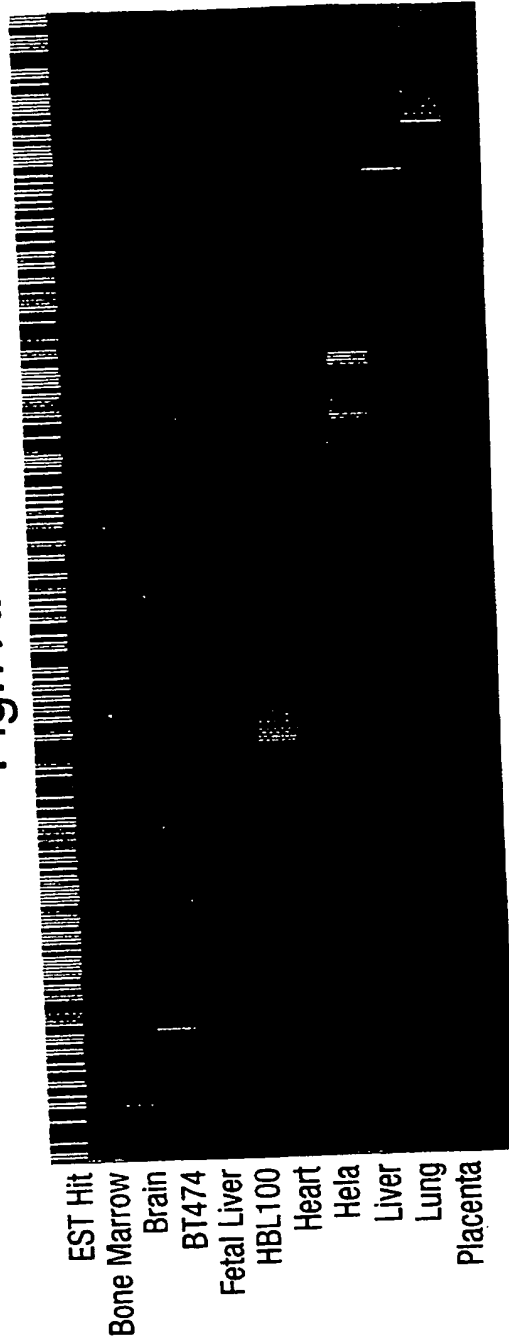


Fig.7B.

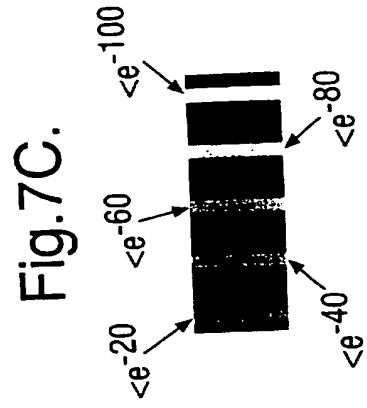


Fig.7C.

Fig.8.

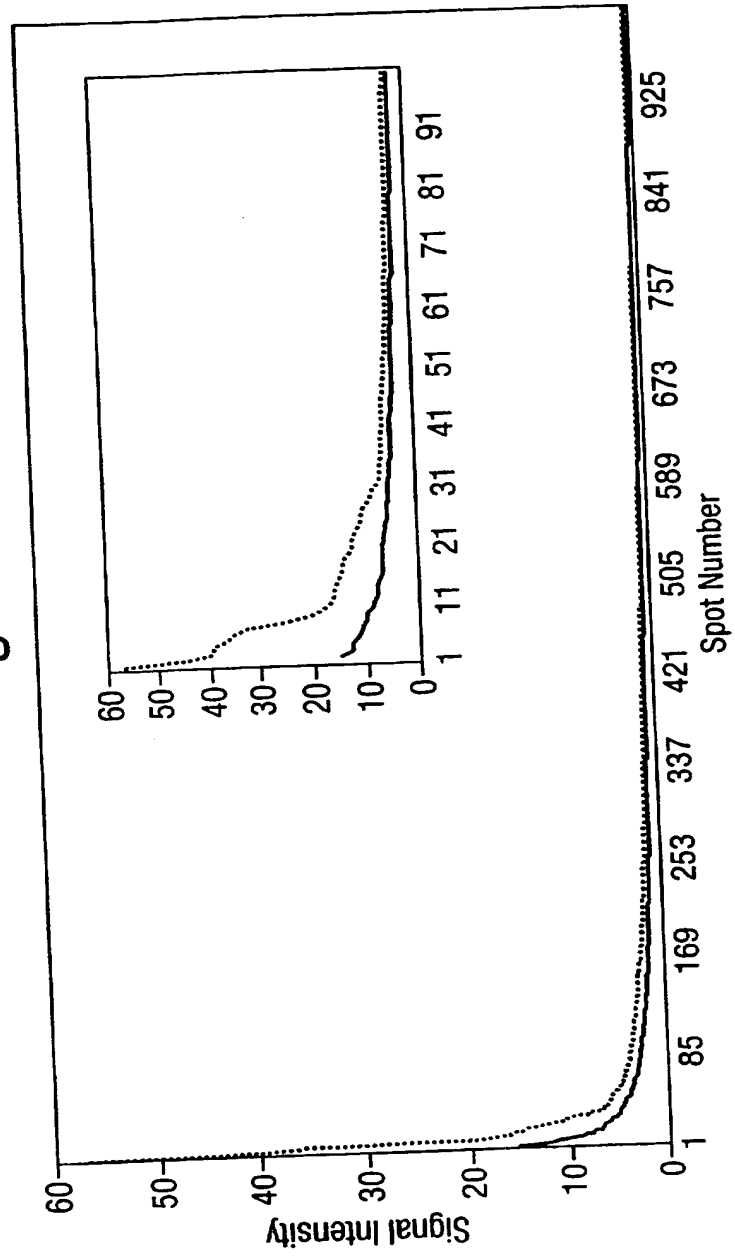


Fig.9.

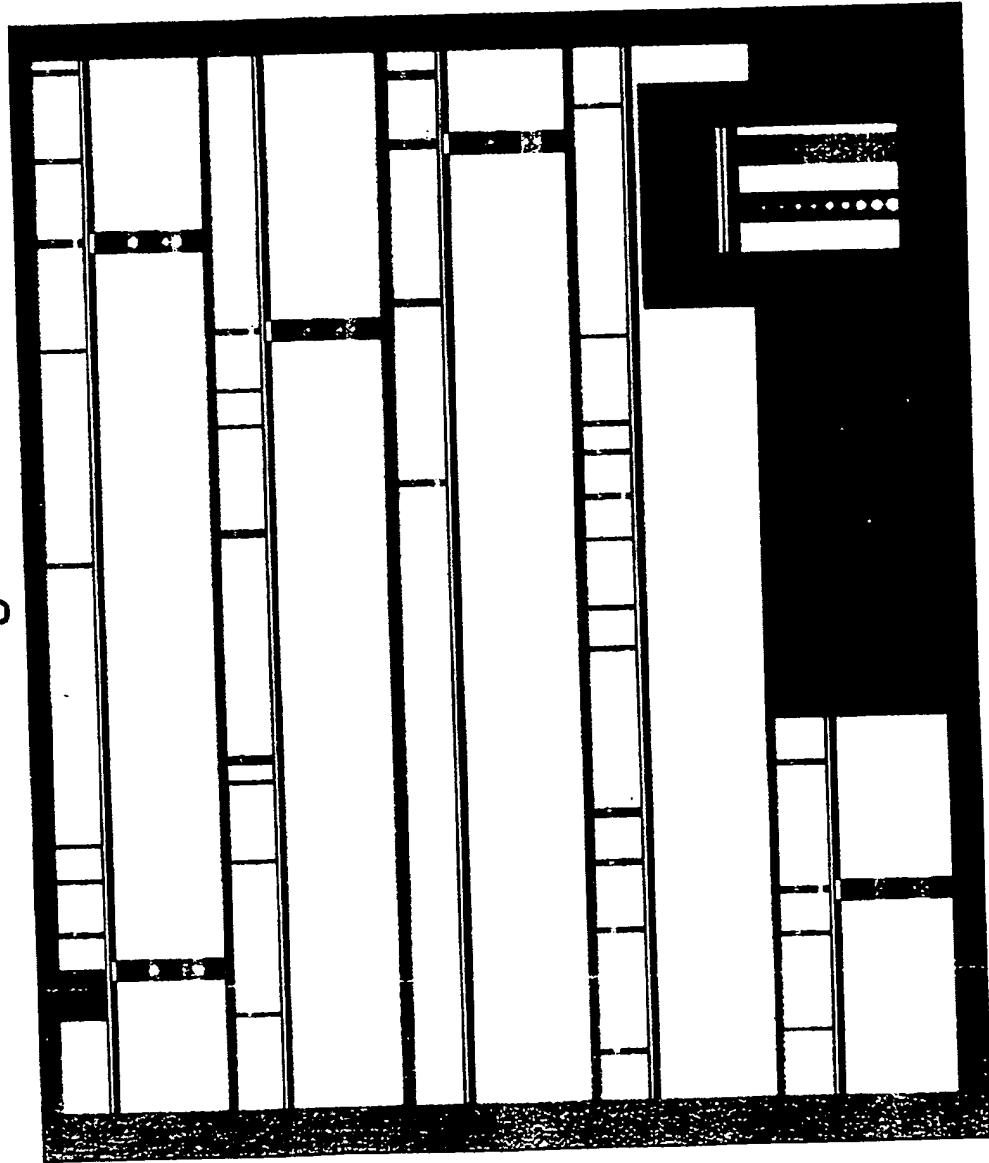
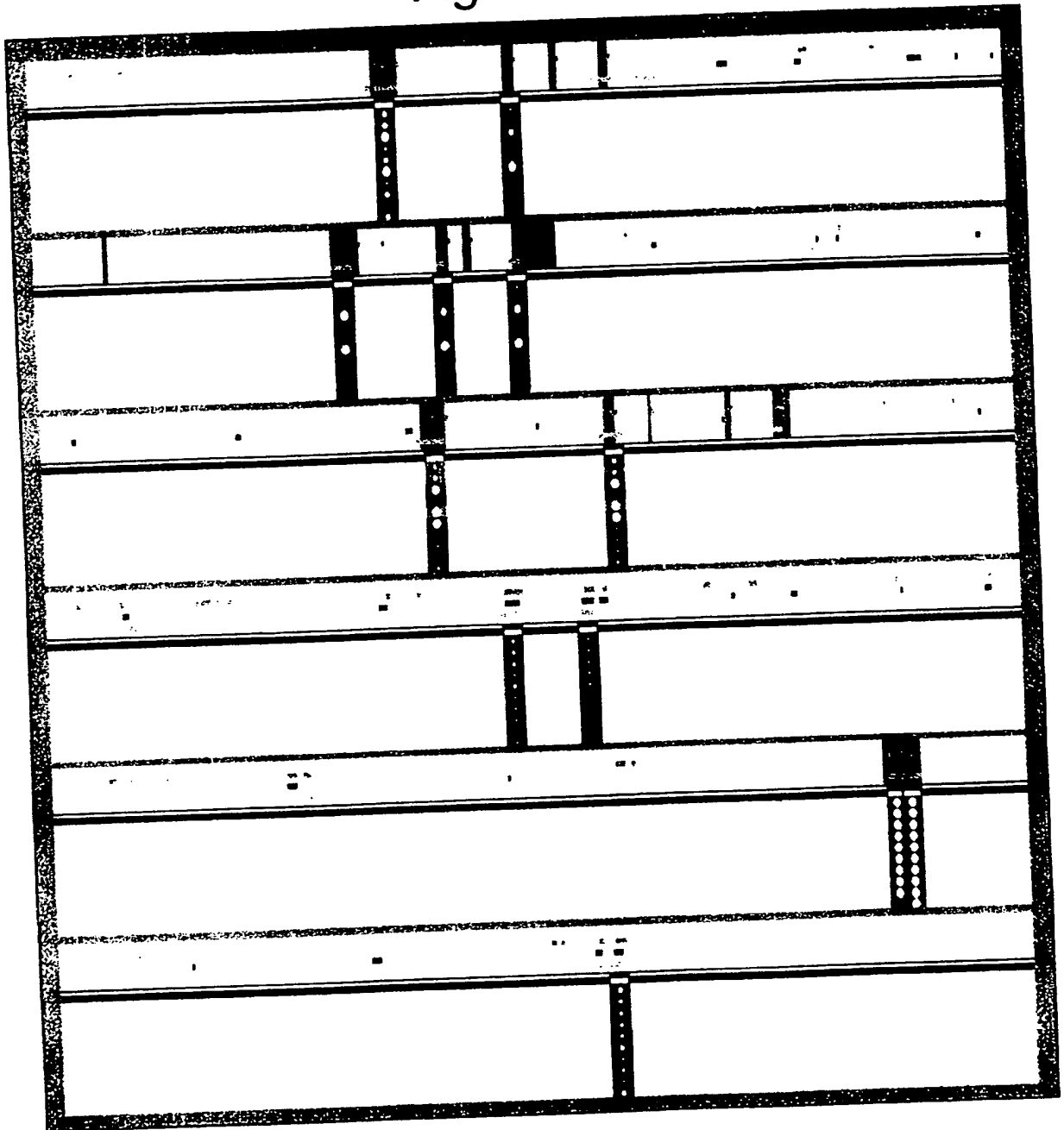


Fig.10.



HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL  
FOR ANALYSIS OF GENE EXPRESSION IN HUMAN HEART

Field of the Invention

5

The present invention relates to genome-derived single exon microarrays useful for verifying the expression of regions of genomic DNA predicted to encode protein. In particular, the present invention relates to unique genome-derived single exon nucleic acid probes expressed in human heart and single exon nucleic acid microarrays that include such probes.

Background of the Invention

15

For almost two decades following the invention of general techniques for nucleic acid sequencing, Sanger et al., *Proc. Natl. Acad. Sci. USA* 70(4):1209-13 (1973); Gilbert et al., *Proc. Natl. Acad. Sci. USA* 70(12):3581-4 (1973), these techniques were used principally as tools to further the understanding of proteins - known or suspected - about which a basic foundation of biological knowledge had already been built. In many cases, the cloning effort that preceded sequence identification had been both informed and directed by that antecedent biological understanding.

25

For example, the cloning of the T cell receptor for antigen was predicated upon its known or suspected cell type-specific expression, by its suspected membrane association, and by the predicted assembly of its gene via T cell-specific somatic recombination. Subsequent sequencing efforts at once confirmed and extended understanding of this family of proteins. Hedrick et al., *Nature* 308(5955):153-8 (1984).

30

More recently, however, the development of high

throughput sequencing methods and devices, in concert with large public and private undertakings to sequence the human and other genomes, has altered this investigational paradigm: today, sequence information often precedes  
5 understanding of the basic biology of the encoded protein product.

One of the approaches to large-scale sequencing is predicated upon the proposition that expressed sequences – that is, those accessible through isolation of  
10 mRNA – are of greatest initial interest. This "expressed sequence tag" ("EST") approach has already yielded vast amounts of sequence data (see for example Adams et al., *Science* 252:1651 (1991); Williamson, *Drug Discov. Today* 4:115 (1999)). For nucleic acids sequenced by this  
15 approach, often the only biological information that is known *a priori* with any certainty is the likelihood of biologic expression itself. By virtue of the species and tissue from which the mRNA had originally been obtained, most such sequences are also annotated with the identity of  
20 the species and at least one tissue in which expression appears likely.

More recently, the pace of genomic sequencing has accelerated dramatically. When genomic DNA serves as the initial substrate for sequencing efforts, expression cannot  
25 be presumed; often the only *a priori* biological information about the sequence includes the species and chromosome (and perhaps chromosomal map location) of origin.

With the ever-accelerating pace of sequence accumulation by directed, EST, and genomic sequencing  
30 approaches – and in particular, with the accumulation of sequence information from multiple genera, from multiple species within genera, and from multiple individuals within a species – there is an increasing need for methods that rapidly and effectively permit the functions of nucleic



sequences to be elucidated. And as such functional information accumulates, there is a further need for methods of storing such functional information in meaningful and useful relationship to the sequence itself; that is, there is an increasing need for means and apparatus for annotating raw sequence data with known or predicted functional information.

Although the increase in the pace of genomic sequencing is due in large part to technological changes in sequencing strategies and instrumentation, Service, *Science* 280:995 (1998); Pennisi, *Science* 283: 1822-1823 (1999), there is an important functional motivation as well.

While it was understood that the EST approach would rarely be able to yield sequence information about the noncoding portions of the genome, it now also appears the EST approach is capable of capturing only a fraction of a genome's actual expression complexity.

For example, when the *C. elegans* genome was fully sequenced, gene prediction algorithms identified over 19,000 potential genes, of which only 7,000 had been found by EST sequencing. *C. elegans* Sequencing Consortium, *Science* 282:2012 (1998). Analogously, the recently completed sequence of chromosome 2 of *Arabidopsis* predicts over 4000 genes, Lin et al., *Nature*, 402:761 (1999), of which only about 6% had previously been identified via EST sequencing efforts. Although the human genome has the greatest depth of EST coverage, it is still woefully short of surrendering all of its genes. One recent estimate suggests that the human genome contains more than 146,000 genes, which would at this point leave greater than half of the genes undiscovered. It is now predicted that many genes, perhaps 20 to 50%, will only be found by genomic sequencing.

There is, therefore, a need for methods that

permit the functional regions of genomic sequence – and most importantly, but not exclusively, regions that function to encode genes – to be identified.

Much of the coding sequence of the human genome is not homologous to known genes, making detection of open reading frames ("ORFs") and predictions of gene function difficult. Computational methods exist for predicting coding regions in eukaryotic genomes. Gene prediction programs such as GRAIL and GRAIL II, Uberbacher et al., *Proc. Natl. Acad. Sci. USA* 88(24):11261-5 (1991); Xu et al., *Genet. Eng.* 16:241-53 (1994); Uberbacher et al., *Methods Enzymol.* 266:259-81 (1996); GENEFINDER, Solovyev et al., *Nucl. Acids. Res.* 22:5156-63 (1994); Solovyev et al., *Ismb* 5:294-302 (1997); and GENESCAN, Burge et al., *J. Mol. Biol.* 268:78-94 (1997), predict many putative genes without known homology or function. Such programs are known, however, to give high false positive rates. Burset et al., *Genomics* 34:353-367 (1996). Using a consensus obtained by a plurality of such programs is known to increase the reliability of calling exons from genomic sequence. Ansari-Lari et al., *Genome Res.* 8(1):29-40 (1998)

Identification of functional genes from genomic data remains, however, an imperfect art. For example, in reporting the full sequence of human chromosome 21, the Chromosome 21 Mapping and Sequencing Consortium reports that prior bioinformatic estimates of human gene number may need to be revised substantially downwards. *Nature* 405:311-199 (2000); Reeves, *Nature* 405:283-284 (2000).

Thus, there is a need for methods and apparatus that permit the functions of the regions identified bioinformatically – and specifically, that permit the expression of regions predicted to encode protein – readily to be confirmed experimentally.

Recently, the development of nucleic acid

microarrays has made possible the automated and highly parallel measurement of gene expression. Reviewed in Schena (ed.), DNA Microarrays : A Practical Approach (Practical Approach Series), Oxford University Press (1999) 5 (ISBN: 0199637768); *Nature Genet.* 21(1)(suppl):1 - 60 (1999); Schena (ed.), Microarray Biochip: Tools and Technology, Eaton Publishing Company/BioTechniques Books Division (2000) (ISBN: 1881299376).

It is common for microarrays to be derived from 10 cDNA/EST libraries, either from those previously described in the literature, such as those from the I.M.A.G.E. consortium, Lennon et al., *Genomics* 33(1):151-2 (1996), or from the construction of "problem specific" libraries targeted at a particular biological question, R.S. Thomas 15 et al., *Cancer Res.* (in press). Such microarrays by definition can measure expression only of those genes found in EST libraries, and thus have not been useful as probes for genes discovered solely by genomic sequencing.

The utility of using whole genome nucleic acid 20 microarrays to answer certain biological questions has been demonstrated for the yeast *Saccharomyces cerevisiae*. De Risi et al., *Science* 278:680 (1997). The vast majority of yeast nuclear genes, approximately 95% however, are single exon genes, i.e., lack introns, Lopez et al., *RNA* 5:1135- 25 1137 (1999); Goffeau et al., *Science* 274:563-67 (1996), permitting coding regions more readily to be identified. Whole genome nucleic acid microarrays have not generally been used to probe gene expression from more complex eukaryotic genomes, and in particular from those averaging 30 more than one intron per gene.

#### Summary of the Invention

The present invention solves these and other

problems in the art by providing methods and apparatus for predicting, confirming, and displaying functional information derived from genomic sequence. The present invention also provides apparatus for verifying the  
5 expression of putative genes identified within genomic sequence.

In particular, the invention provides novel genome-derived single exon nucleic acid microarrays useful for verifying the expression of putative genes identified  
10 within genomic sequence.

The present invention also provides compositions and kits for the ready production of nucleic acids identical in sequence to, or substantially identical in sequence to, probes on the genome-derived single exon  
15 microarrays of the present invention.

Accordingly, in a first aspect of the invention, there is provided a spatially-addressable set of single exon nucleic acid probes for measuring gene expression in a sample derived from human heart, comprising a plurality of  
20 single exon nucleic acid probes according to any one of the nucleotide sequences set out in SEQ ID NOs: 1 - 5,202 or a complementary sequence, or a portion of such a sequence.

By plurality is meant at least two, suitably at least 20, most suitably at least 100, preferably at least  
25 1000 and, most preferably, upto 5000.

In one embodiment of the first aspect, each of said plurality of probes is separately and addressably amplifiable.

In an alternative embodiment, each of said  
30 plurality of probes is separately and addressably isolatable from said plurality.

In a preferred embodiment, each of said plurality of probes is amplifiable using at least one common primer. Preferably, each of said plurality of probes is amplifiable

using a first and a second common primer.

In yet another embodiment, said set of single exon nucleic acid probes comprises between 50 - 20,000 probes, for example, 50 - 5000.

5 Suitably, said set of single exon nucleic acid probes comprises at least 50 - 1000 discrete single exon nucleic acid probes having a sequence as set out in any of SEQ ID NOS.: 1 - 10,283 or a complimentary sequence, or a portion of such a sequence.

10 Preferably, the average length of the single exon nucleic acid probes is between 200 and 500 bp. It is preferred that the average length should be at least 200bp, suitably at least 250bp, most suitably at least 300bp, preferably at least 400bp and, most preferably, 500 bp.

15 In another embodiment, the single exon nucleic acid probes lack prokaryotic and bacteriophage vector sequence. It is preferred that at least 50%, suitably at least 60%, most suitably at least 70%, preferably at least 75%, more preferably at least 80, 85, 90, 95 or 99% of said  
20 single exon nucleic acid probes lack prokaryotic and bacteriophage vector sequence.

In another preferred embodiment, said single exon nucleic acid lack homopolymeric stretches of A or T. It is preferred that at least 50%, suitably at least 60%, most  
25 suitably at least 70%, preferably at least 75%, more preferably at least 80, 85, 90, 95 or 99% of said single exon nucleic acid probes lack homopolymeric stretches of A or T.

In a particularly preferred embodiment, a set of  
30 single exon nucleic acid probes in accordance with a first aspect of the invention comprises a nucleotide sequence selected from any of SEQ ID NOS.: 286, 287, 442, 871, 1029, 1280, 1597, 1619, 1694, 1715, 1721, 1848, 1935, 2119, 2233, 2893, 3003, 3003, 3149, 3403, 3471, 3513, 3607, 4102, 4164,

4184, 4184, 4242, 4730, 4779, 4976, 4988, 5473, 5608, 6019, 6169, 6410, 6723, 6745, 6818, 6838, 6844, 6966, 7052, 7230, 7340, 8044, 8155, 8298, 8545, 8612, 8654, 8746, 9228, 9290, 9310, 9367, 9842, 9889, 10079 and 10091, a sequence

5 complementary to any of said sequences, or a portion of such a sequence.

In yet another embodiment, a set of single exon nucleic acid probes in accordance with the invention comprises a nucleotide encoding a peptide having an amino  
10 acid sequence as set out in any of SEQ ID NOS.: 10603, 10741, 11179, 11571, 11893, 11913, 11999, 12017, 12023, 12152, 12245, 12439, 12552, 13144, 13255, 13256, 13407, 13653, 13724, 13841, 14313, 14370, 14390, 14391, 14934, 15149 and 15161, or portion thereof.

15 Preferably, a spatially-addressable set of single exon nucleic acid probes in accordance with the first aspect of the invention is addressably disposed upon a substrate.

Suitable substrates include a filter membrane  
20 which may, preferably, be nitrocellulose or nylon. The nylon may preferably, be positively-charged. Other suitable substrates include glass, amorphous silicon, crystalline silicon, and plastic. Further suitable materials include polymethylacrylic, polyethylene, polypropylene,  
25 polyacrylate, polymethylmethacrylate, polyvinylchloride, polytetrafluoroethylene, polystyrene, polycarbonate, polyacetal, polysulfone, celluloseacetate, cellulosenitrate, nitrocellulose, and mixtures thereof.

In a second aspect of the invention, there is  
30 provided a microarray comprising a spatially addressable set of single exon nucleic acid probes in accordance with the first aspect of the invention.

In one embodiment, a genome-derived single-exon microarray is packaged together with such an ordered set of  
35 amplifiable probes corresponding to the probes, or one or

more subsets of probes, thereon. In alternative embodiments, the ordered set of amplifiable probes is packaged separately from the genome-derived single exon microarray.

5 In another aspect, the invention provides genome-derived single exon nucleic acid probes useful for gene expression analysis, and particularly for gene expression analysis by microarray. In particular embodiments of this aspect, the present invention provides human single-exon  
10 probes that include specifically-hybridizable fragments of SEQ ID Nos. 5,203 - 10,283, wherein the fragment hybridizes at high stringency to an expressed human gene. In particular embodiments, the invention provides single exon probes comprising SEQ ID Nos. 1 - 5,202.

15 Accordingly, in a third aspect of the invention, there is provided a single exon nucleic acid probe for measuring human gene expression in a sample derived from human heart which is a nucleic acid molecule comprising a nucleotide sequence as set out in any of SEQ ID NOS.: 1 -  
20 5,202 or a complementary sequence or a fragment thereof wherein said probe hybridizes at high stringency to a nucleic acid expressed in the human heart.

In one embodiment, a single exon nucleic acid probe in accordance with the third aspect comprises a  
25 nucleotide sequence as set out in any of SEQ ID NOS.: 5,203 - 10,283 or a complementary sequence or a fragment thereof.

In a fourth aspect of the invention, there is provided a single exon nucleic acid probe for measuring human gene expression in a sample derived from human heart  
30 which is a nucleic acid molecule having a sequence encoding a peptide comprising a peptide sequence as set out in any of SEQ ID NOS.: 10,284 - 15,322 or a complementary sequence or a fragment thereof wherein said probe hybridizes at high stringency to a nucleic acid expressed in the human heart.

35 In a preferred embodiment, a single exon nucleic

acid probe for measuring human gene expression in a sample derived from human heart is selected from any of SEQ ID NOS.: 286, 287, 442, 871, 1029, 1280, 1597, 1619, 1694, 1715, 1721, 1848, 1935, 2119, 2233, 2893, 3003, 3003, 3149, 5 3403, 3471, 3513, 3607, 4102, 4164, 4184, 4184, 4242, 4730, 4779, 4976, 4988, 5473, 5608, 6019, 6169, 6410, 6723, 6745, 6818, 6838, 6844, 6966, 7052, 7230, 7340, 8044, 8155, 8298, 8545, 8612, 8654, 8746, 9228, 9290, 9310, 9367, 9842, 9889, 10079 and 10091.

10 In another embodiment, a single exon nucleic acid probe for measuring human gene expression in a sample derived from human heart is selected from a nucleotide encoding a peptide, or portion thereof, as set out in any of SEQ ID NOS.: 10603, 10741, 11179, 11571, 11893, 11913, 15 11999, 12017, 12023, 12152, 12245, 12439, 12552, 13144, 13255, 13256, 13407, 13653, 13724, 13841, 14313, 14370, 14390, 14391, 14934, 15149 and 15161.

Preferably, a single exon nucleic acid probe in accordance with the third or fourth aspects of the 20 invention comprises between at least 15 and 50 contiguous nucleotides of said SEQ ID NO:. It is preferred that the single exon nucleic acid probe comprises at least 15, suitably at least 20, more suitably at least 25 or preferably at least 50 contiguous nucleotides of said SEQ 25 ID NO:.

In another preferred embodiment, a single exon nucleic acid probe in accordance with the third or fourth aspects of the invention is between 3kb and 25kb in length. It is preferred that said probe is no more than 3kb, 30 suitably no more than 5kb, more suitably no more than 10kb, preferably 15kb, more preferably 20kb or, most preferably, no more than 20kb in length.

Preferably, a single exon nucleic acid probe in accordance with either the fifth or sixth aspect of the 35 invention is DNA, preferably single-stranded DNA, RNA or



PNA.

In another embodiment of either the third or fourth aspect of the invention, a single exon nucleic acid probe is detectably labeled. Suitable detectable labels include a radionuclide, a fluorescent label or a first member of a specific binding pair. Suitable fluorescent labels include dyes such as cyanine dyes, preferably Cy3 and Cy5 although other suitable dyes will be known to those skilled in the art.

In a particularly preferred embodiment, a single exon nucleic acid probe in accordance with either the third or fourth aspect of the invention lacks prokaryotic and bacteriophage vector sequence. In yet another embodiment, a single exon nucleic acid probe in accordance with either the third or fourth aspect of the invention lacks homopolymeric stretches of A or T.

In a fifth aspect of the invention, there is provided an amplifiable nucleic acid composition, comprising:

the single exon nucleic acid probe in accordance with either of the third or fourth aspects of the invention; and at least one nucleic acid primer; wherein said at least one primer is sufficient to prime enzymatic amplification of said probe.

In a sixth aspect of the invention, there is provided a method of measuring gene expression in a sample derived from human heart, comprising:

contacting the single exon microarray in accordance with the second aspect of the invention, with a first collection of detectably labeled nucleic acids, said first collection of nucleic acids derived from mRNA of human heart; and then

measuring the label detectably bound to each probe of said microarray.

In a seventh aspect of the invention, there is

provided a method of identifying exons in a eukaryotic genome, comprising:

algorithmically predicting at least one exon from genomic sequence of said eukaryote; and then

5 detecting specific hybridization of detectably labeled nucleic acids to a single exon probe,

wherein said detectably labeled nucleic acids are derived from mRNA from the heart of said eukaryote, said probe is a single exon probe having a fragment identical in  
10 sequence to, or complementary in sequence to, said predicted exon, said probe is included within a single exon microarray in accordance with the first aspect of the invention, and said fragment is selectively hybridizable at high stringency.

15 In a eighth aspect of the invention, there is provided a method of assigning exons to a single gene, comprising:

identifying a plurality of exons from genomic sequence in accordance with the seventh aspect of the  
20 invention; and then

measuring the expression of each of said exons in a plurality of tissues and/or cell types using hybridization to single exon microarrays having a probe with said exon,

25 wherein a common pattern of expression of said exons in said plurality of tissues and/or cell types indicates that the exons should be assigned to a single gene.

In an ninth aspect of the invention, there is  
30 provided a nucleic acid sequence as set out in any of SEQ ID NOs: 1 - 10,283 wherein said sequence encodes a peptide.

In a tenth aspect of the invention, there is provided a peptide encoded by a sequence comprising a sequence as set out in any of SEQ ID NOs: 5,203 - 10,283,  
35 or a complementary sequence or coding portion thereof.

In a preferred embodiment, a peptide may be encoded by a sequence comprising a sequence set out in any of SEQ ID NOS.: 1 - 5,202.

In a further aspect, the invention provides  
 5 peptides comprising an amino acid sequence translated from the DNA fragments, said amino acid sequences comprising SEQ ID NOS.: 10,283 - 15,322.

Accordingly in a eleventh aspect of the invention there is provided a peptide comprising a sequence as set  
 10 out in any of SEQ ID NOS: 10,284 - 15,322, or fragment thereof.

In another aspect, the invention provides means for displaying annotated sequence, and in particular, for displaying sequence annotated according to the methods and  
 15 apparatus of the present invention. Further, such display can be used as a preferred graphical user interface for electronic search, query, and analysis of such annotated sequence.

20

## Detailed Description of the Invention

### Definitions

As used herein, the term "microarray" and phrase  
 25 "nucleic acid microarray" refer to a substrate-bound collection of plural nucleic acids, hybridization to each of the plurality of bound nucleic acids being separately detectable. The substrate can be solid or porous, planar or non-planar, unitary or distributed.

As so defined, the term "microarray" and phrase  
 30 "nucleic acid microarray" include all the devices so called in Schena (ed.), DNA Microarrays: A Practical Approach (Practical Approach Series), Oxford University Press (1999) (ISBN: 0199637768); Nature Genet. 21(1)(suppl):1 - 60

(1999); and Schena (ed.), Microarray Biochip: Tools and Technology, Eaton Publishing Company/BioTechniques Books Division (2000) (ISBN: 1881299376). As so defined, the term "microarray" and phrase "nucleic acid microarray" further include substrate-bound collections of plural nucleic acids in which the nucleic acids are distributably disposed on a plurality of beads, rather than on a unitary planar substrate, as is described, *inter alia*, in Brenner et al., *Proc. Natl. Acad. Sci. USA* 97(4):166501670 (2000); in such case, the term "microarray" and phrase "nucleic acid microarray" refer to the plurality of beads in aggregate.

As used herein with respect to a nucleic acid microarray, the term "probe" refers to the nucleic acid that is, or is intended to be, bound to the substrate; in such context, the term "target" thus refers to nucleic acid intended to be bound thereto by Watson-Crick complementarity. As used herein with respect to solution phase hybridization, the term "probe" refers to the nucleic acid of known sequence that is detectably labeled.

As used herein, the expression "probe comprising SEQ ID NO.", and variants thereof, intends a nucleic acid probe, at least a portion of which probe has either (i) the sequence directly as given in the referenced SEQ ID NO., or (ii) a sequence complementary to the sequence as given in the referenced SEQ ID NO., the choice as between sequence directly as given and complement thereof dictated by the requirement that the probe hybridize to mRNA.

As used herein, the term "ORF" refers to a nucleic acid sequence that, in at least one reading frame, does not possess stop codons; the term does not require that the ORF encode the entirety of a natural protein. In the absence of a consensus prediction, all six frames of an exon are examined for stop codons and the longest ORF is

selected.

As used herein, the term "amplicon" refers to a PCR product amplified from human genomic DNA, containing the predicted exon.

5 As used herein the term "exon" refers to the consensus prediction of the various exon and gene predicting algorithms.

As used herein, the term "peptide" refers to a sequence of amino acids. The sequences referred to as  
10 PEPTIDE SEQ ID NOS.: are the predicted peptide sequences that would be translated from one of the exons, or a portion thereof set out in exon SEQ ID NOS... The codons encoding the peptide are wholly contained within the exon.

As used herein, a "portions" of a defined  
15 nucleotide sequence or sequences can be and, preferably, are fragments unique to that sequence or to one or a combination of those sequences. A fragment unique to a nucleic acid molecule is one that is a signature for the larger nucleic acid molecule.

20 As used herein, the phrase "expression of a probe" and its linguistic variants means that the ORF present within the probe, or its complement, is present within a target mRNA.

As used herein, "stringent conditions" refers to  
25 parameters well known to those skilled in the art. When a nucleic acid molecule is said to be hybridisable to another of a given sequence under "stringent conditions" it is meant that it is homologous to the given sequence.

As used herein, the phrase "specific binding  
30 pair" intends a pair of molecules that bind to one another with high specificity. Binding pairs are said to exhibit specific binding when they exhibit avidity of at least  $10^7$ , preferably at least  $10^8$ , more preferably at least  $10^9$  liters/mole. Nonlimiting examples of specific binding  
35 pairs are: antibody and antigen; biotin and avidin; and

biotin and streptavidin.

As used herein with respect to the visual display of annotated genomic sequence, the term "rectangle" means any geometric shape that has at least a first and a second border, wherein the first and second borders each are capable of mapping uniquely to a point of another visual object of the display.

As used herein, a "Mondrian" means a visual display in which a single genomic sequence is annotated with predicted and experimentally confirmed functional information.

#### Brief Description of the Drawings

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The present invention is further illustrated with reference to the following non-limiting figures and examples in which:

FIG. 1 illustrates a process for predicting functional regions from genomic sequence, confirming the functional activity of such regions experimentally, and associating and displaying the data so obtained in meaningful and useful relationship to the original sequence data;

25

FIG. 2 further elaborates that portion of the process schematized in FIG. 1 for predicting functional regions from genomic sequence;

FIG. 3 illustrates a Mondrian visual display;

FIG. 4 presents a Mondrian showing a hypothetical annotated genomic sequence;

30

FIG. 5 is a histogram showing the distribution of ORF length and PCR products as obtained, with ORF length shown in black and PCR product length shown in dotted lines;

35

FIG. 6 is a histogram showing the distribution,

among exons predicted according to the methods described,  
 of expression as measured using simultaneous two color  
 hybridization to a genome-derived single exon microarray.  
 The graph shows the number of sequence-verified products  
 5 that were either not expressed ("0"), expressed in one or  
 more but not all tested tissues ("1" - "9"), or expressed  
 in all tissues tested ("10");

FIG. 7 is a pictorial representation of the  
 expression of verified sequences that showed expression  
 10 with signal intensity greater than 3 in at least one  
 tissue, with: FIG. 7A showing the expression as measured by  
 microarray hybridization in each of the 10 measured  
 tissues, and the expression as measured "bioinformatically"  
 by query of EST, NR and SwissProt databases; with FIG. 7B  
 15 showing the legend for display of physical expression  
 (ratio) in FIG. 7A; and with FIG. 7C showing the legend for  
 scoring EST hits as depicted in FIG. 7A;

FIG. 8 shows a comparison of normalized CY3  
 signal intensity for arrayed sequences that were identical  
 20 to sequences in existing EST, NR and SwissProt databases or  
 that were dissimilar (unknown), where black denotes the  
 signal intensity for all sequence-verified products with a  
 BLAST Expect ("E") value of greater than  $1e-30$  ( $1 \times 10^{-30}$ )  
 ("unknown") and a dotted line denotes sequence-verified  
 25 spots with a BLAST expect ("E") value of less than  $1e-30$  ( $1$   
 $\times 10^{-30}$ ) ("known");

FIG. 9 presents a Mondrian of BAC AC008172 (bases  
 25,000 to 130,000), containing the carbamyl phosphate  
 synthetase gene (AF154830.1); and

30 FIG. 10 is a Mondrian of BAC A049839.

Methods and Apparatus for Predicting, Confirming,  
Annotating, and Displaying Functional Regions From Genomic  
 35 Sequence Data

FIG. 1 is a flow chart illustrating in broad outline a process for predicting functional regions from genomic sequence, confirming and characterizing the functional activity of such regions experimentally, and then associating and displaying the information so obtained in meaningful and useful relationship to the original sequence data.

The initial input into process 10 of the present invention is drawn from one or more databases 100 containing genomic sequence data. Because genomic sequence is usually obtained from subgenomic fragments, the sequence data typically will be stored in a series of records corresponding to these subgenomic sequenced fragments. Some fragments will have been catenated to form larger contiguous sequences ("contigs"); others will not. A finite percentage of sequence data in the database will typically be erroneous, consisting *inter alia* of vector sequence, sequence created from aberrant cloning events, sequence of artificial polylinkers, and sequence that was erroneously read.

Each sequence record in database 100 will minimally contain as annotation a unique sequence identifier (accession number), and will typically be annotated further to identify the date of accession, species of origin, and depositor. Because database 100 can contain nongenomic sequence, each sequence will typically be annotated further to permit query for genomic sequence. Chromosomal origin, optionally with map location, can also be present. Data can be, and over time increasingly will be, further annotated with additional information, in part through use of the present invention, as described below. Annotation can be present within the data records, in information external to database 100 and linked to the



records thereto, or through a combination of the two.

Databases useful as genomic sequence database 100 in the present invention include GenBank, and particularly include several divisions thereof, including the  
5 htgs(draft), NT (nucleotide, command line), and NR (nonredundant) divisions. GenBank is produced by the National Institutes of Health and is maintained by the National Center for Biotechnology Information (NCBI).  
Databases of genomic sequence from species other than  
10 human, such as mouse, rat, *Arabidopsis*, *C. elegans*, *C. brigssii*, *Drosophila*, zebra fish, and other higher eukaryotic organisms will also prove useful as genomic sequence database 100.

Genomic sequence obtained by query of genomic  
15 sequence database 100 is then input into one or more processes 200 for identification of regions therein that are predicted to have a biological function as specified by the user. Such functions include, but are not limited to, encoding protein, regulating transcription, regulating  
20 message transport after transcription into mRNA, regulating message splicing after transcription into mRNA, of regulating message degradation after transcription into mRNA, and the like. Other functions include directing  
somatic recombination events, contributing to chromosomal  
25 stability or movement, contributing to allelic exclusion or X chromosome inactivation, and the like.

The particular genomic sequence to be input into process 200 will depend upon the function for which relevant sequence is to be identified as well as upon the  
30 approach chosen for such identification. Process step 200 can be iterated to identify different functions within a given genomic region. In such case, the input often will be different for the several iterations.

Sequences predicted to have the requisite

function by process 200 are then input into process 300, where a subset of the input sequences suitable for experimental confirmation is identified. Experimental confirmation can involve physical and/or bioinformatic assay. Where the subsequent experimental assay is bioinformatic, rather than physical, there are fewer constraints on the sequences that can be tested, and in this latter case therefore process 300 can output the entirety of the input sequence.

10           The subset of sequences output from process 300 is then used in process 400 for experimental verification and characterization of the function predicted in process 200, which experimental verification can, and often will, include both physical and bioinformatic assay.

15           Process 500 annotates the sequence data with the functional information obtained in the physical and/or bioinformatic assays of process 400. Such annotation can be done using any technique that usefully relates the functional information to the sequence, as, for example, by incorporating the functional data into the sequence data record itself, by linking records in a hierarchical or relational database, by linking to external databases, by a combination thereof, or by other means well known within the database arts. The data can even be submitted for  
20           incorporation into databases maintained by others, such as GenBank, which is maintained by NCBI.

          As further noted in FIG. 1, additional annotation can be input into process 500 from external sources 600.

          The annotated data is then displayed in process  
30       800, either before, concomitantly with, or after optional storage 700 on nontransient media, such as magnetic disk, optical disc, magnetooptical disk, flash memory, or the like.

          FIG. 1 shows that the experimental data output  
35       from process 400 can be used in each preceding step of

process 10: e.g., facilitating identification of functional sequences in process 200, facilitating identification of an experimentally suitable subset thereof in process 300, and facilitating creation of physical and/or informational substrates for, and performance of subsequent assay, of functional sequences in process 400.

Information from each step can be passed directly to the succeeding process, or stored in permanent or interim form prior to passage to the succeeding process. Often, data will be stored after each, or at least a plurality, of such process steps. Any or all process steps can be automated.

FIG. 2 further elaborates the prediction of functional sequence within genomic sequence according to process 200.

Genomic sequence database 100 is first queried for genomic sequence.

The sequence required to be returned by query 20 will depend, in the first instance, upon the function to be identified.

For example, genomic sequences that function to encode protein can be identified *inter alia* using gene prediction approaches, comparative sequence analysis approaches, or combinations of the two. In gene prediction analysis, sequence from one genome is input into process 200 where at least one, preferably a plurality, of algorithmic methods are applied to identify putative coding regions. In comparative sequence analysis, by contrast, corresponding, e.g., syntenic, sequence from a plurality of sources, typically a plurality of species, is input into process 200, where at least one, possibly a plurality, of algorithmic methods are applied to compare the sequences and identify regions of least variability.

The exact content of query 20 will also depend

upon the database queried. For example, if the database contains both genomic and nongenomic sequence, perhaps derived from multiple species, and the function to be determined is protein coding regions in human genomic sequence, the query will accordingly require that the  
5 sequence returned be genomic and derived from humans.

Query 20 can also incorporate criteria that compel return of sequence that meets operative requirements of the subsequent analytical method. Alternatively, or in  
10 addition, such operative criteria can be enforced in subsequent preprocess step 24.

For example, if the function sought to be identified is protein coding, query 20 can incorporate criteria that return from genomic sequence database 100  
15 only those sequences present within contigs sufficiently long as to have obviated substantial fragmentation of any given exon among a plurality of separate sequence fragments.

Such criteria can, for example, consist of a  
20 required minimal individual genomic sequence fragment length, such as 10 kb, more typically 20 kb, 30 kb, 40kb, and preferably 50 kb or more, as well as an optional further or alternative requirement that sequence from any given clone, such as a bacterial artificial chromosome  
25 ("BAC"), be presented in no more than a finite maximal number of fragments, such as no more than 20 separate pieces, more typically no more than 15 fragments, even more typically no more than about 10 - 12 fragments.

Results using the present invention have shown  
30 that genomic sequence from bacterial artificial chromosomes (BACs) is sufficient for gene prediction analysis according to the present invention if the sequence is at least 50 kb in length, and if additionally the sequence from any given BAC is presented in fewer than 15, and preferably fewer  
35 than 10, fragments. Accordingly, query 20 can incorporate

a requirement that data accessioned from BAC sequencing be in fewer than 15, preferably fewer than 10, fragments.

An additional criterion that can be incorporated into the query can be the date, or range of dates, of sequence accession. Although the process has been described above as if genomic sequence database 100 were static, it is of course understood that the genomic sequence databases need not be static, and indeed are typically updated on a frequent, even hourly, basis. Thus, as further described in Examples 1 and 2, *infra*, it is possible to query the database for newly added sequence, either newly added after an absolute date, or newly added relative to a prior analysis performed using the methods and apparatus of the present invention. In this way, the process herein described can incorporate a dynamic, temporal component.

One utility of such temporal limitation is to identify, from newly accessioned genomic sequence, the presence of novel genes, particularly those not previously identified by EST sequencing (or other sequencing efforts that are similarly based upon gene expression). As further described in Example 1, such an approach has shown that newly accessioned human genomic sequence, when analyzed for sequences that function to encode protein, readily identifies genes that are novel over those in existing EST and other expression databases. This makes the methods of the present invention extremely powerful gene discovery tools. And as would be appreciated, such gene discovery can be performed using genomic sequence from species other than human.

If query 20 incorporates multiple criteria, such as above-described, the multiple criteria can be performed as a series of separate queries or as a single query, depending in part upon the query language, the complexity

of the query, and other considerations well known in the database arts.

If query 20 returns no genomic sequence meeting the query criteria, the negative result can be reported by process 22, and process 200 (and indeed, entire process 10) ended 23, as shown. Alternatively, or in addition to report and termination of the initial inquiry, a new query 20 can be generated that takes into account the initial negative result.

When query 20 returns sequence meeting the query criteria, the returned sequence is then passed to optional preprocessing 24, suitable and specific for the desired analytical approach and the particular analytical methods thereof to be used in process 25.

Preprocessing 24 can include processes suitable for many approaches and methods thereof, as well as processes specifically suited for the intended subsequent analysis.

Preprocessing 24 suitable for most approaches and methods will include elimination of sequence irrelevant to, or that would interfere with, the subsequent analysis. Such sequence includes repetitive sequence, such as Alu repeats and LINE elements, vector sequence, artificial sequence, such as artificial polylinkers, and the like. Such removal can readily be performed by identification and subsequent masking of the undesired sequence.

Identification can be effected by comparing the genomic sequence returned by query 20 with public or private databases containing known repetitive sequence, vector sequence, artificial sequence, and other artifactual sequence. Such comparison can readily be done using programs well known in the art, such as CROSS\_MATCH, or by proprietary sequence comparison programs the engineering of which is well within the skill in the art.

Alternatively, or in addition, undesirable,

including artifactual, sequence can be identified algorithmically without comparison to external databases and thereafter removed. For example, synthetic polylinker sequence can be identified by an algorithm that identifies  
5 a significantly higher than average density of known restriction sites. As another example, vector sequence can be identified by algorithms that identify nucleotide or codon usage at variance with that of the bulk of the genomic sequence.

10 Once identified, undesired sequence can be removed. Removal can usefully be done by masking the undesired sequence as, for example, by converting the specific nucleotide references to one that is unrecognized by the subsequent bioinformatic algorithms, such as "X".  
15 Alternatively, but at present less preferred, the undesired sequence can be excised from the returned genomic sequence, leaving gaps.

Preprocessing 24 can further include selection from among duplicative sequences of that one sequence of  
20 highest quality. Higher quality can be measured as a lower percentage of, fewest number of, or least densely clustered occurrence of ambiguous nucleotides, defined as those nucleotides that are identified in the genomic sequence using symbols indicating ambiguity. Higher quality can  
25 also or alternatively be valued by presence in the longest contig.

Preprocessing 24 can, and often will, also include formatting of the data as specifically appropriate for passage to the analytical algorithms of process 25.  
30 Such formatting can and typically will include, inter alia, addition of a unique sequence identifier, either derived from the original accession number in genomic sequence database 100, or newly applied, and can further include additional annotation. Formatting can include conversion

from one to another sequence listing standard, such as conversion to or from FASTA or the like, depending upon the input expected by the subsequent process.

Preprocessing, which can be optional depending upon the function desired to be identified and the informational requirements of the methods for effecting such identification, is followed by sequence processing 25, where sequences with the desired function are identified within the genomic sequence.

As mentioned above, such functions can include, but are not limited to, encoding protein, regulating transcription, regulating message transport after transcription into mRNA, regulating message splicing after transcription, of regulating message degradation, and the like. Other functions include directing somatic recombination events, contributing to chromosomal stability or movement, contributing to allelic exclusion or X chromosome inactivation, or the like.

The methods of the present invention are particularly useful for gene discovery, that is, for identifying, from genomic sequence, regions that function to encode genes, and in a particularly useful embodiment, for identifying regions that function to encode genes not hitherto identified by expression-based or directed cloning and sequencing. In conjunction with verification using the novel single exon microarrays of the present invention, as further described below, the methods herein described become powerful gene discovery tools.

Accordingly, in a preferred embodiment of the present invention, process 25 is used to identify putative coding regions. Two preferred approaches in process 25 for identifying sequence that encodes putative genes are gene prediction and comparative sequence analysis.

Gene prediction can be performed using any of a number of algorithmic methods, embodied in one or more



software programs, that identify open reading frames (ORFs) using a variety of heuristics, such as GRAIL, DICTION, and GENEFINDER. Comparative sequence analysis similarly can be performed using any of a variety of known programs that  
 5 identify regions with lower sequence variability.

As further described in Example 1, below, gene finding software programs yield a range of results. For the newly accessioned human genomic sequence input in Example 1, for example, GRAIL identified the greatest  
 10 percentage of genomic sequence as putative coding region, 2% of the data analyzed; GENEFINDER was second, calling 1%; and DICTION yielded the least putative coding region, with 0.8% of genomic sequence called as coding region.

Increased reliability can be obtained when  
 15 consensus is required among several such methods. Although discussed herein particularly with respect to exon calling, consensus among methods will in general increase reliability of predicting other functions as well.

Thus, as indicated by query 26, sequence  
 20 processing 25, optionally with preprocessing 24, can be repeated with a different method, with consensus among such iterations determined and reported in process 27.

Process 27 compares the several outputs for a given input genomic sequence and identifies consensus among  
 25 the separately reported results. The consensus itself, as well as the sequence meeting that consensus, is then stored in process 29a, displayed in process 29b, and/or output to process 300 for subsequent identification of a subset thereof suitable for assay.

30 Multiple levels of consensus can be calculated and reported by process 27. For example, as further described in Example 1, *infra*, process 27 can report consensus as between all specific pairs of methods of gene prediction, as consensus among any one or more of the pairs

of methods of gene prediction, or as among all of the gene prediction algorithms used. Thus, in Example 1, process 27 reported that GRAIL and GENEFINDER programs agreed on 0.7% of genomic sequence, that GRAIL and DICTION agreed on 0.5% of genomic sequence, and that the three programs together  
5 agreed on 0.25% of the data analyzed. Put another way, 0.25% of the genomic sequence was identified by all three of the programs as containing putative coding region.

Furthermore, consensus can be required among  
10 different approaches to identifying a chosen function.

For example, if the function desired to be identified is coding of protein sequence, and a first used approach to exon calling is gene prediction, the process can be repeated on the same input sequence, or subset  
15 thereof, with another approach, such as comparative sequence analysis. In such a case, where comparative sequence analysis follows gene prediction, the comparison can be performed not only on genomic nucleic acid sequence, but additionally or alternatively can be performed on the  
20 predicted amino acid sequence translated from the ORFs prior identified by the gene prediction approach.

Although shown as an iterative process, the multiple analyses required to achieve consensus can be done in series, in parallel, or some combination thereof.

25 Predicted functional sequence, optionally representing a consensus among a plurality of methods and approaches for determination thereof, is passed to process 300 for identification of a subset thereof for functional assay.

30 In the preferred embodiment of the methods of the present invention, wherein the function sought to be identified is protein coding, process 300 is used to identify a subset thereof suitable for experimental verification by physical and/or bioinformatic approaches.

35 For example, putative ORFs identified in process

200 can be classified, or binned, bioinformatically into putative genes. This binning can be based *inter alia* upon consideration of the average number of exons/gene in the species chosen for analysis, upon density of exons that have been called on the genomic sequence, and other empirical rules. Thereafter, one or more among the gene-specific ORFs can be chosen for subsequent use in gene expression assay.

Where such subsequent gene expression assay uses amplified nucleic acid, considerations such as desired amplicon length, primer synthesis requirements, putative exon length, sequence GC content, existence of possible secondary structure, and the like can be used to identify and select those ORFs that appear most likely successfully to amplify. Where subsequent gene expression assay relies upon nucleic acid hybridization, whether or not using amplified product, further considerations involving hybridization stringency can be applied to identify that subset of sequences that will most readily permit sequence-specific discrimination at a chosen hybridization and wash stringency. One particular such consideration is avoidance of putative exons that span repetitive sequence; such sequence can hybridize spuriously to nonspecific message, reducing specific signal in the hybridization.

For bioinformatic assay, there are fewer constraints on the sequences that can be tested experimentally, and in this latter case therefore process 300 can output the entirety of the input sequence.

The subset of sequences identified by process 300 as suitable for use in assay is then used in process 400 to create the physical and/or informational substrate for experimental verification of the predictions made in process 200, and thereafter to assay those substrates.

As mentioned, the methods of the present

invention are particularly useful for identifying potential coding regions within genomic sequence. In a preferred embodiment of process 400, therefore, the expression of the sequences predicted to encode protein is verified. The  
5 combination of the predictive and experimental methods provides a powerful gene discovery engine.

Thus, in another aspect, the present invention provides methods and apparatus for verifying the expression of putative genes identified within genomic sequence. In  
10 particular, the invention provides a novel method of verifying gene expression in which expression of predicted ORFs is measured and confirmed using a novel type of nucleic acid microarray, the genome-derived single exon nucleic acid microarrays of the present invention.

15 Putative ORFs as predicted by a consensus of gene calling, particularly gene prediction, algorithms in process 200, and as further identified as suitable by process 300, are amplified from genomic DNA using the polymerase chain reaction (PCR). Although PCR is  
20 conveniently used, other amplification approaches can also be used.

Amplification schemes can be designed to capture the entirety of each predicted ORF in an amplicon with minimal additional (that is, intronic or intergenic)  
25 sequence. Because ORFs predicted from human genomic sequence using the methods of the present invention differ in length, such an approach results in amplicons of varying length.

However, most predicted ORFs are shorter than 500  
30 bp in length, and although amplicons of at least about 100 or 200 base pairs can be immobilized as probes on nucleic acid microarrays, early experimental results using the methods of the present invention have suggested that longer amplicons, at least about 400 or 500 base pairs, are more  
35 effective. Furthermore, certain advantages derive from

application to the microarray of amplicons of defined size.

Therefore, amplification schemes can alternatively, and preferably, be designed to amplify regions of defined size, preferably at least about 300, 400  
5 or 500 bp, centered about each predicted ORF. Such an approach results in a population of amplicons of limited size diversity, but that typically contain intronic and/or intergenic nucleic acid in addition to putative ORF.

Conversely, somewhat fewer than 10% of ORFs  
10 predicted from human genomic sequence according to the methods of the present invention exceed 500 bp in length. Portions of such extended ORFs, preferably at least about 300, 400 or 500 bp in length, can be amplified. However, it has been discovered that the percentage success at  
15 amplifying pieces of such ORFs is low, and that such putative exons are more effectively amplified when larger fragments, at least about 1000 or 1500 bp, and even as large as 2000 bp are amplified.

The putative ORFs selected in process 300 are  
20 thus input into one or more primer design programs, such as PRIMER3 (available online for use at <http://www-genome.wi.mit.edu/cgi-bin/primer/> ), with a goal of amplifying at least about 500 base pairs of genomic sequence centered within or about ORFs predicted to be no  
25 more than about 500 bp, or at least about 1000 - 1500 bp of genomic sequence for ORFs predicted to exceed 500 bp in length, and the primers synthesized by standard techniques. Primers with the requisite sequences can be purchased commercially or synthesized by standard techniques.

30 Conveniently, a first predetermined sequence can be added commonly to the ORF-specific 5' primer and a second, typically different, predetermined sequence commonly added to each 3' ORF-unique primer. This serves to immortalize the amplicon, that is, serves to permit  
35 further amplification of any amplicon using a single set of

primers complementary respectively to the common 5' and common 3' sequence elements. The presence of these "universal" priming sequences further facilitates later sequence verification, providing a sequence common to all  
 5 amplicons at which to prime sequencing reactions. The common 5' and 3' sequences further serve to add a cloning site should any of the ORFs warrant further study.

Such predetermined sequence is usefully at least about 10, 12 or 15 nt in length, and usually does not  
 10 exceed about 25 nt in length. The "universal" priming sequences used in the examples presented *infra* were each 16 nt long.

The genomic DNA to be used as substrate for amplification will come from the eukaryotic species from  
 15 which the genomic sequence data had originally been obtained, or a closely related species, and can conveniently be prepared by well known techniques from somatic or germline tissue or cultured cells of the organism. See, e.g., Short Protocols in Molecular Biology  
 20 : A Compendium of Methods from Current Protocols in Molecular Biology, Ausubel et al. (eds.), 4<sup>th</sup> edition (April 1999), John Wiley & Sons (ISBN: 047132938X) and Maniatis et al., Molecular Cloning : A Laboratory Manual, 2<sup>nd</sup> edition (December 1989), Cold Spring Harbor Laboratory  
 25 Press (ISBN: 0879693096). Many such prepared genomic DNAs are available commercially, with the human genomic DNAs additionally having certification of donor informed consent.

Although the intronic and intergenic material  
 30 flanking putative coding regions in the amplicons could potentially interfere with hybridizations during microarray experiments, we have found, surprisingly, that differential expression ratios are not significantly affected. Rather, the predominant effect of exon size is to alter the

absolute signal intensity, rather than its ratio. Equally surprising, the art had suggested that single exon probes would not provide sufficient signal intensity for high stringency hybridization analyses; we find that such probes  
5 not only provide adequate signal, but have substantial advantages, as herein described.

After partial purification, as by size exclusion spin column, with or without confirmation as to amplicon quality as by gel electrophoresis, each amplicon (single  
10 exon probe) is disposed in an array upon a support substrate.

Methods for creating microarrays by deposition and fixation of nucleic acids onto support substrates are well known in the art (Reviewed by Schena et al., see  
15 above).

Typically, the support substrate will be glass, although other materials, such as amorphous or crystalline silicon or plastics. Such plastics include  
20 polymethylacrylic, polyethylene, polypropylene, polyacrylate, polymethylmethacrylate, polyvinylchloride, polytetrafluoroethylene, polystyrene, polycarbonate, polyacetal, polysulfone, celluloseacetate, cellulosenitrate, nitrocellulose, or mixtures thereof, can also be used. Typically, the support will be rectangular,  
25 although other shapes, particularly circular disks and even spheres, present certain advantages. Particularly advantageous alternatives to glass slides as support substrates for array of nucleic acids are optical discs, as described in WO 98/12559.

30 The amplified nucleic acids can be attached covalently to a surface of the support substrate or, more typically, applied to a derivatized surface in a chaotropic agent that facilitates denaturation and adherence by presumed noncovalent interactions, or some combination  
35 thereof.

Robotic spotting devices useful for arraying nucleic acids on support substrates can be constructed using public domain specifications (The MGuide, version 2.0, <http://cmgm.stanford.edu/pbrown/mguide/index.html>), or  
5 can conveniently be purchased from commercial sources (MicroArray GenII Spotter and MicroArray GenIII Spotter, Molecular Dynamics, Inc., Sunnyvale, CA). Spotting can also be effected by printing methods, including those using ink jet technology.

10 As is well known in the art, microarrays typically also contain immobilized control nucleic acids. For controls useful in providing measurements of background signal for the genome-derived single exon microarrays of the present invention, a plurality of *E. coli* genes can  
15 readily be used. As further described in Example 1, 16 or 32 *E. coli* genes suffice to provide a robust measure of background noise in such microarrays.

As is well known in the art, the amplified product disposed in arrays on a support substrate to create  
20 a nucleic acid microarray can consist entirely of natural nucleotides linked by phosphodiester bonds, or alternatively can include either nonnative nucleotides, alternative internucleotide linkages, or both, so long as complementary binding can be obtained in the hybridization.  
25 If enzymatic amplification is used to produce the immobilized probes, the amplifying enzyme will impose certain further constraints upon the types of nucleic acid analogs that can be generated.

Although particularly described herein as using  
30 high density microarrays constructed on planar substrates, the methods of the present invention for confirming the expression of ORFs predicted from genomic sequence can use any of the known types of microarrays, as herein defined, including lower density planar arrays, and microarrays on



nonplanar, nonunitary, distributed substrates.

For example, gene expression can be confirmed using hybridization to lower density arrays, such as those constructed on membranes, such as nitrocellulose, nylon, and positively-charged derivatized nylon membranes. Further, gene expression can also be confirmed using nonplanar, bead-based microarrays such as are described in Brenner et al., *Proc. Natl. Acad. Sci. USA* 97(4):166501670 (2000); U.S. Patent No. 6,057,107; and U.S. Patent No. 5,736,330. In theory, a packed collection of such beads provides in aggregate a higher density of nucleic acid probe than can be achieved with spotting or lithography techniques on a single planar substrate.

Planar microarrays on solid substrates, however, provide certain useful advantages, including high throughput and compatibility with existing readers. For example, each standard microscope slide can include at least 1000, typically at least 2000, preferably 5000 and upto 10,000 - 50,000 or more nucleic acid probes of discrete sequence. The number of sequences deposited will depend on their required application.

Each putative gene can be represented in the array by a single predicted ORF. Alternatively, genes can be represented by more than one predicted ORF. For purposes of measuring differential splicing, more than one predicted ORF will be provided for a putative gene. And as is well known in the art, each probe of defined sequence, representing a single predicted ORF, can be deposited in a plurality of locations on a single microarray to provide redundancy of signal.

The genome-derived single exon microarrays described above differ in several fundamental and advantageous ways from microarrays presently used in the gene expression art, including (1) those created by

deposition of mRNA-derived nucleic acids, (2) those created by *in situ* synthesis of oligonucleotide probes, and (3) those constructed from yeast genomic DNA.

Most nucleic acid microarrays that are in use for  
 5 study of eukaryotic gene expression have as immobilized probes nucleic acids that are derived – either directly or indirectly – from expressed message. As discussed above, it is common, for example, for such microarrays to be derived from cDNA/EST libraries, either from those  
 10 previously described in the literature, see Lennon et al., or from the *de novo* construction of "problem specific" libraries targeted at a particular biological question, R.S. Thomas et al., *Cancer Res.* (in press). Such microarrays are herein collectively denominated "EST  
 15 microarrays".

Such EST microarrays by definition can measure expression only of those genes found in EST libraries, shown herein to represent only a fraction of expressed genes. Furthermore, such libraries – and thus microarrays  
 20 based thereupon – are biased by the tissue or cell type of message origin, by the expression levels of the respective genes within the tissues, and by the ability of the message successfully to have been reverse-transcribed and cloned.

Thus, as further discussed in Example 1, the  
 25 methods of the present invention enable sequences that do not appear in EST or other expression databases to be determined – subsequently arrayed for expression measurements could not, therefore, have been represented as probes on an EST microarray. And as further demonstrated  
 30 in the examples, *infra*, the remaining population of genes identified from genomic sequence by the methods of the present invention – that is, the one third of sequences that had previously been accessioned in EST or other expression databases – are biased toward genes with higher

expression levels.

Representation of a message in an EST and/or cDNA library depends upon the successful reverse transcription, optionally but typically with subsequent successful  
5 cloning, of the message. This introduces substantial bias into the population of probes available for arraying in EST microarrays.

In contrast, neither reverse transcription nor cloning is required to produce the probes arrayed on the  
10 genome-derived single exon microarrays of the present invention. And although the ultimate deposition of a probe on the genome-derived single exon microarray of the present invention depends upon a successful amplification from genomic material, *a priori* knowledge of the sequence of the  
15 desired amplicon affords greater opportunity to recover any given probe sequence recalcitrant to amplification than is afforded by the requirement for successful reverse transcription and cloning of unknown message in EST approaches.

20 Thus, the genome-derived single exon microarrays of the present invention present a far greater diversity of probes for measuring gene expression, with far less bias, than do EST microarrays presently used in the art.

As a further consequence of their ultimate origin  
25 from expressed message, the probes in EST microarrays often contain poly-A (or complementary poly-T) stretches derived from the poly-A tail of mature mRNA. These homopolymeric stretches contribute to cross-hybridization, that is, to a spurious signal occasioned by hybridization to the  
30 homopolymeric tail of a labeled cDNA that lacks sequence homology to the gene-specific portion of the probe.

In contrast, the probes arrayed in the genome-derived single exon microarrays of the present invention lack homopolymeric stretches derived from message

polyadenylation, and thus can provide more specific signal. Typically, at least about 50, 60 or 75% of the probes on the genome-derived single exon microarrays of the present invention lack homopolymeric regions consisting of A or T, where a homopolymeric region is defined for purposes herein as stretches of 25 or more, typically 30 or more, identical nucleotides.

A further distinction, which also affects the specificity of hybridization, is occasioned by the typical derivation of EST microarray probes from cloned material. Because much of the probe material disposed as probes on EST microarrays is excised or amplified from plasmid, phage, or phagemid vectors, EST microarrays typically include a fair amount of vector sequence, more so when the probes are amplified, rather than excised, from the vector.

In contrast, the vast majority of probes in the genome-derived single exon microarrays of the present invention contain no prokaryotic or bacteriophage vector sequence, having been amplified directly or indirectly from genomic DNA. Typically, therefore, at least about 50, 60, 70 or 80% or more of individual exon-including probes disposed on a genome-derived single exon microarray of the present invention lack vector sequence, and particularly lack sequences drawn from plasmids and bacteriophage. Preferably, at least about 85, 90 or more than 90% of exon-including probes in the genome-derived single exon microarray of the present invention lack vector sequence. With attention to removal of vector sequences through preprocessing 24, percentages of vector-free exon-including probes can be as high as 95 - 99%. The substantial absence of vector sequence from the genome-derived single exon microarrays of the present invention results in greater specificity during hybridization, since spurious cross-hybridization to a probe vector sequence is reduced.

As a further consequence of excision or

amplification of probes from vectors in construction of EST microarrays, the probes arrayed thereon often contain artificial sequence, derived from vector polylinker multiple cloning sites, at both 5' and 3' ends. The probes  
5 disposed upon the genome-derived single exon microarrays need have no such artificial sequence appended thereto.

As mentioned above, however, the ORF-specific primers used to amplify putative ORFs can include artificial sequences, typically 5' to the ORF-specific  
10 primer sequence, useful for "universal" (that is, independent of ORF sequence) priming of subsequent amplification or sequencing reactions. When such "universal" 5' and/or 3' priming sequences are appended to the amplification primers, the probes disposed upon the  
15 genome-derived single exon microarray will include artificial sequence similar to that found in EST microarrays. However, the genome-derived single exon microarray of the present invention can be made without such sequences, and if so constructed, presents an even  
20 smaller amount of nonspecific sequence that would contribute to nonspecific hybridization.

Yet another consequence of typical use of cloned material as probes in EST microarrays is that such microarrays contain probes that result from cloning  
25 artifacts, such as chimeric molecules containing coding region of two separate genes. Derived from genomic material, typically not thereafter cloned, the probes of the genome-derived single exon microarrays of the present invention lack such cloning artifacts, and thus provide  
30 greater specificity of signal in gene expression measurements.

A further consequence of the cloned origin of probes on many EST microarrays is that the individual probes often have disparate sizes, which can cause the  
35 optimal hybridization stringency to vary among probes on a

single microarray. In contrast, as discussed above, the probes arrayed on the genome-derived single exon microarrays of the present invention can readily be designed to have a narrow distribution in sizes, with the  
5 range of probe sizes no greater than about 10% of the average size, typically no greater than about 5% of the average probe size.

Because of their origin from fully- or partially-spliced message, probes disposed upon EST arrays will often  
10 include multiple exons. The percentage of such exon-spanning probes in an EST microarray can be calculated, on average, based upon the predicted number of exons/gene for the given species and the average length of the immobilized probes. For human genes, the near-complete sequence of  
15 human chromosome 22, Dunham et al., *Nature* 402(6761):489-95 (1999), predicts that human genes average 5.5 exons/gene. Even with probes of 200 - 500 bp, the vast majority of human EST microarray probes include more than one exon.

In contrast, by virtue of their origin from  
20 algorithmically identified ORFs in genomic sequence, the probes in the genome-derived single exon microarrays of the present invention can consist of individual exons. Thus, in contrast to EST microarrays, at least about 50, 60, 70, 75, 80, 85, 95 or 99% of probes deposited in the genome-  
25 derived microarray of the present invention consist of, or include, no more than one predicted ORF.

This provides the ability, not readily achieved using EST microarrays, to use the genome-derived single exon microarrays of the present invention to measure  
30 tissue-specific expression of individual exons, which in turn allows differential splicing events to be detected and characterized, and in particular, allows the correlation of differential splicing to tissue-specific expression patterns.

Furthermore, the exons that are represented in EST microarrays are often biased toward the 3' or 5' end of their respective genes, since sequencing strategies used for EST identification are so biased. In contrast, no such  
5 3' or 5' bias necessarily inheres in the selection of exons for disposition on the genome-derived single exon microarrays of the present invention.

Conversely, the probes provided on the genome-derived single exon microarrays of the present invention  
10 typically, but need not necessarily, include intronic and/or intergenic sequence that is absent from EST microarrays, which are derived from mature mRNA. Typically, at least about 50, 60, 70, 80 or 90% of the exon-including probes on the genome-derived single exon  
15 microarrays of the present invention include sequence drawn from noncoding regions. As discussed above, the additional presence of noncoding region does not significantly interfere with measurement of gene expression, and provides the additional opportunity to assay prespliced RNA, and  
20 thus measure such phenomena such as nuclear export control.

The genome-derived single exon microarrays of the present invention are also quite different from *in situ* synthesis microarrays, where probe size is severely constrained by inadequacies in the photolithographic  
25 synthesis process.

Typically, probes arrayed on *in situ* synthesis microarrays are limited to a maximum of about 25 bp. As a well known consequence, hybridization to such chips must be performed at low stringency. In order, therefore, to  
30 achieve unambiguous sequence-specific hybridization results, the *in situ* synthesis microarray requires substantial redundancy, with concomitant programmed arraying for each probe of probe analogues with altered (*i.e.*, mismatched) sequence.

In contrast, the longer probe length of the genome-derived single exon microarrays of the present invention allows much higher stringency hybridization and wash. Typically, therefore, exon-including probes on the  
5 genome-derived single exon microarrays of the present invention average at least about 100, 200, 300, 400 or 500 bp in length. By obviating the need for substantial probe redundancy, this approach permits a higher density of probes for discrete exons or genes to be arrayed on the  
10 microarrays of the present invention than can be achieved for *in situ* synthesis microarrays.

A further distinction is that the probes in *in situ* synthesis microarrays typically are covalently linked to the substrate surface. In contrast, the probes disposed  
15 on the genome-derived microarray of the present invention typically are, but need not necessarily be, bound noncovalently to the substrate.

Furthermore, the short probe size on *in situ* microarrays causes large percentage differences in the  
20 melting temperature of probes hybridized to their complementary target sequence, and thus causes large percentage differences in the theoretically optimum stringency across the array as a whole.

In contrast, the larger probe size in the  
25 microarrays of the present invention create lower percentage differences in melting temperature across the range of arrayed probes.

A further significant advantage of the microarrays of the present invention over *in situ*  
30 synthesized arrays is that the quality of each individual probe can be confirmed before deposition. In contrast, the quality of probes cannot be assessed on a probe-by-probe basis for the *in situ* synthesized microarrays presently being used.



The genome-derived single exon microarrays of the present invention are also distinguished over, and present substantial benefits over, the genome-derived microarrays from lower eukaryotes such as yeast. Lashkari et al.,

5 Proc. Natl. Acad. Sci. USA 94:13057-13062 (1997).

Only about 220 - 250 of the 6100 or so nuclear genes in *Saccharomyces cerevisiae* - that is, only about 4 - 5% - have standard, spliceosomal, introns, Lopez et al., Nucl. Acids Res. 28:85-86 (2000); Spingola et al., RNA  
10 5(2):221-34 (1999). Furthermore, the entire yeast genome has already been sequenced. These two facts permit the ready amplification and disposition of single-ORF amplicons on such microarray without the requirement for antecedent use of gene prediction and/or comparative sequence  
15 analyses.

Thus, a significant aspect of the present invention is the ability to identify and to confirm expression of predicted coding regions in genomic sequence drawn from eukaryotic organisms that have a higher  
20 percentage of genes having introns than do yeast such as *Saccharomyces cerevisiae*, particularly in genomic sequence drawn from eukaryotes in which at least about 10, 20 or 50% of protein-encoding genes have introns. In preferred embodiments, the methods and apparatus of the present  
25 invention are used to identify and confirm expression of novel genes from genomic sequence of eukaryotes in which the average number of introns per gene is at least about one, two or three or more.

After the physical substrate is prepared,  
30 experimental verification of predicted function is performed.

In a preferred embodiment of the present invention, where the function sought to be identified in genomic sequence is protein coding, experimental

verification is performed by measuring expression of the putative ORFs, typically through nucleic acid hybridization experiments, and in particularly preferred embodiments, through hybridization to genome-derived single exon  
5 microarrays prepared as above- described.

Expression is conveniently measured and expressed for each probe in the microarray as a ratio of the expression measured concurrently in a plurality of mRNA sources, according to techniques well known in the  
10 microarray art, Reviewed in Schena et al., and as further described in Example 2, below. The mRNA source for the reference against which specific expression is measured can be drawn from a homogeneous mRNA source, such as a single cultured cell-type, or alternatively can be heterogeneous,  
15 as from a pool of mRNA derived from multiple tissues and/or cell types, as further described in Example 2, *infra*.

mRNA can be prepared by standard techniques, see Ausubel et al. and Maniatis et al., or purchased commercially. The mRNA is then typically reverse-  
20 transcribed in the presence of labeled nucleotides: the index source (that in which expression is desired to be measured) is reverse transcribed in the presence of nucleotides labeled with a first label, typically a fluorophore (fluorochrome; fluor; fluorescent dye); the  
25 reference source is reverse transcribed in the presence of a second label, typically a fluorophore, typically fluorometrically-distinguishable from the first label. As further described in Example 2, *infra*, Cy3 and Cy5 dyes prove particularly useful in these methods. After partial  
30 purification of the index and reference targets, hybridization to the probe array is conducted according to standard techniques, typically under a coverslip.

After wash, microarrays are conveniently scanned using a commercial microarray scanning device, such as a

Gen3 Scanner (Molecular Dynamics, Sunnyvale, CA). Data on expression is then passed, with or without interim storage, to process 500, where the results for each probe are related to the original sequence.

5           Often, hybridization of target material to the genome-derived single exon microarray will identify certain of the probes thereon as of particular interest. Thus, it is often desirable that the user be able readily to obtain sufficient quantities of an individual probe, either for  
10 subsequent arrayed deposition upon an additional support substrate, often as part of a microarray having a plurality of probes so identified, or alternatively or additionally as a solitary solid-phase or solution-phase probe, for further use.

15           Thus, in another aspect, the present invention provides compositions and kits for the ready production of nucleic acids identical in sequence to, or substantially identical in sequence to, probes on the genome-derived single exon microarrays of the present invention.

20           In this aspect, a small quantity of each probe is disposed, typically without attachment to substrate, in a spatially-addressable ordered set, typically one per well of a microtiter dish. Although a 96 well microtiter plate can be used, greater efficiency is obtained using higher  
25 density arrays, such as are provided by microtiter plates having 384, 864, 1536, 3456, 6144, or 9600 wells, and although microtiter plates having physical depressions (wells) are conveniently used, any device that permits addressable withdrawal of reagent from fluidly-  
30 noncommunicating areas can be used.

          In this aspect of the invention, therefore, a fluidly noncommunicating addressable ordered set of individual probes, corresponding to those on a genome-derived single exon microarray, is provided, with each  
35 probe in sufficient quantity to permit amplification, such

as by PCR. As earlier mentioned, the ORF-specific 5' primers used for genomic amplification can have a first common sequence added thereto, and the ORF-specific 3' primers used for genomic amplification can have a second, different, common sequence added thereto, thus permitting, in this preferred embodiment, the use of a single set of 5' and 3' primers to amplify any one of the probes from the amplifiable ordered set.

Each discrete amplifiable probe can also be packaged with amplification primers, solutes, buffers, etc., and can be provided in dry (e.g., lyophilized) form or wet, in the latter case typically with addition of agents that retard evaporation.

In another aspect of the present invention, a genome-derived single-exon microarray is packaged together with such an ordered set of amplifiable probes corresponding to the probes, or one or more subsets of probes, thereon. In alternative embodiments, the ordered set of amplifiable probes is packaged separately from the genome-derived single exon microarray.

In some embodiments, the microarray and/or ordered probe set are further packaged with recordable media that provide probe identification and addressing information, and that can additionally contain annotation information, such as gene expression data. Such recordable media can be packaged with the microarray, with the ordered probe set, or with both.

If the microarray is constructed on a substrate that incorporates recordable media, such as is described in international patent application no. WO 98/12559, then separate packaging of the genome-derived single exon microarray and the bioinformatic information is not required.

The amount of amplifiable probe material should

be sufficient to permit at least one amplification sufficient for subsequent hybridization assay.

Although the use of high density genome-derived microarrays on solid planar substrates is presently a preferred approach for the physical confirmation and characterization of the expression of sequences predicted to encode protein, other types of microarrays (as herein defined) can also be used.

Furthermore, as earlier mentioned, experimental verification of the function predicted from genomic sequence in process 200 can be bioinformatic, rather than, or additional to, physical verification.

For example, where the function desired to be identified is protein coding, the predicted ORFs can be compared bioinformatically to sequences known or suspected of being expressed.

Thus, the sequences output from process 300 (or process 200), can be used to query expression databases, such as EST databases, SNP ("single nucleotide polymorphism") databases, known cDNA and mRNA sequences, SAGE ("serial analysis of gene expression") databases, and more generalized sequence databases that allow query for expressed sequences. Such query can be done by any sequence query algorithm, such as BLAST ("basic local alignment search tool"). The results of such query - including information on identical sequences and information on nonidentical sequences that have diffuse or focal regions of sequence homology to the query sequence - can then be passed directly to process 500, or used to inform analyses subsequently undertaken in process 200, process 300, or process 400.

Experimental data, whether obtained by physical or bioinformatic assay in process 400, is passed to process 500 where it is usefully related to the sequence data itself, a process colloquially termed "annotation". Such

annotation can be done using any technique that usefully relates the functional information to the sequence, as, for example, by incorporating the functional data into the record itself, by linking records in a hierarchical or relational database, by linking to external databases, or by a combination thereof. Such database techniques are well within the skill in the art.

The annotated sequence data can be stored locally, uploaded to genomic sequence database 100, and/or displayed 800.

The methods and apparatus of the present invention rapidly produce functional information from genomic sequence. Coupled with the escalating pace at which sequence now accumulates, the rapid pace of sequence annotation produces a need for methods of displaying the information in meaningful ways.

FIG. 3 shows visual display 80 presenting a single genomic sequence annotated according to the present invention. Because of its nominal resemblance to artistic works of Piet Mondrian, visual display 80 is alternatively described herein as a "Mondrian".

Each of the visual elements of display 80 is aligned with respect to the genomic sequence being annotated (hereinafter, the "annotated sequence"). Given the number of nucleotides typically represented in an annotated sequence, representation of individual nucleotides would rarely be readable in hard copy output of display 80. Typically, therefore, the annotated sequence is schematized as rectangle 89, extending from the left border of display 80 to its right border. By convention herein, the left border of rectangle 89 represents the first nucleotide of the sequence and the right border of rectangle 89 represents the last nucleotide of the sequence.

As further discussed below, however, the Mondrian

visual display of annotated sequence can serve as a convenient graphical user interface for computerized representation, analysis, and query of information stored electronically. For such use, the individual nucleotides  
5 can conveniently be linked to the X axis coordinate of rectangle 89. This permits the annotated sequence at any point within rectangle 89 readily to be viewed, either automatically – for example, by time-delayed appearance of a small overlaid window upon movement of a cursor or other  
10 pointer over rectangle 89 – or through user intervention, as by clicking a mouse or other pointing device at a point in rectangle 89.

Visual display 80 is generated after user specification of the genomic sequence to be displayed.  
15 Such specification can consist of or include an accession number for a single clone (e.g., a single BAC accessioned into GenBank), wherein the starting and stopping nucleotides are thus absolutely identified, or alternatively can consist of or include an anchor or  
20 fulcrum point about which a chosen range of sequence is anchored, thus providing relative endpoints for the sequence to be displayed. For example, the user can anchor such a range about a given chromosomal map location, gene name, or even a sequence returned by query for similarity  
25 or identity to an input query sequence. When visual display 80 is used as a graphical user interface to computerized data, additional control over the first and last displayed nucleotide will typically be dynamically selectable, as by use of standard zooming and/or selection  
30 tools.

Field 81 of visual display 80 is used to present the output from process 200, that is, to present the bioinformatic prediction of those sequences having the desired function within the genomic sequence. Functional

sequences are typically indicated by at least one rectangle 83 (83a, 83b, 83c), the left and right borders of which respectively indicate, by their X-axis coordinates, the starting and ending nucleotides of the region predicted to have function.

Where a single bioinformatic method or approach identifies a plurality of regions having the desired function, a plurality of rectangles 83 is disposed horizontally in field 81. Where multiple methods and/or approaches are used to identify function, each such method and/or approach can be represented by its own series of horizontally disposed rectangles 83, each such horizontally disposed series of rectangles offset vertically from those representing the results of the other methods and approaches.

Thus, rectangles 83a in FIG. 3 represent the functional predictions of a first method of a first approach for predicting function, rectangles 83b represent the functional predictions of a second method and/or second approach for predicting that function, and rectangles 83c represent the predictions of a third method and/or approach.

Where the function desired to be identified is protein coding, field 81 is used to present the bioinformatic prediction of sequences encoding protein. For example, rectangles 83a can represent the results from GRAIL or GRAIL II, rectangles 83b can represent the results from GENEFINDER, and rectangles 83c can represent the results from DICTION.

Optionally, and preferably, rectangles 83 collectively representing predictions of a single method and/or approach are identically colored and/or textured, and are distinguishable from the color and/or texture used for a different method and/or approach.

Alternatively, or in addition, the color, hue,



density, or texture of rectangles 83 can be used further to report a measure of the bioinformatic reliability of the prediction. For example, many gene prediction programs will report a measure of the reliability of prediction.

5 Thus, increasing degrees of such reliability can be indicated, e.g., by increasing density of shading. Where display 80 is used as a graphical user interface, such measures of reliability, and indeed all other results output by the program, can additionally or alternatively be  
10 made accessible through linkage from individual rectangles 83, as by time-delayed window ("tool tip" window), or by pointer (e.g., mouse)-activated link.

As earlier described, increased predictive reliability can be achieved by requiring consensus among  
15 methods and/or approaches to determining function. Thus, field 81 can include a horizontal series of rectangles 83 that indicate one or more degrees of consensus in predictions of function.

Although FIG. 3 shows three series of  
20 horizontally disposed rectangles in field 81, display 80 can include as few as one such series of rectangles and as many as can discriminably be displayed, depending upon the number of methods and/or approaches used to predict a given function.

25 Furthermore, field 81 can be used to show predictions of a plurality of different functions. However, the increased visual complexity occasioned by such display makes more useful the ability of the user to select a single function for display. When display 80 is used as  
30 a graphical user interface for computer query and analysis, such function can usefully be indicated and user-selectable, as by a series of graphical buttons or tabs (not shown in FIG. 3).

Rectangle 89 is shown in FIG. 3 as including

interposed rectangle 84. Rectangle 84 represents the portion of annotated sequence for which predicted functional information has been assayed physically, with the starting and ending nucleotides of the assayed material indicated by the X axis coordinates of the left and right borders of rectangle 84. Rectangle 85, with optional inclusive circles 86 (86a, 86b, and 86c) displays the results of such physical assay.

Although a single rectangle 84 is shown in FIG. 3, physical assay is not limited to just one region of annotated genomic sequence. It is expected that an increasing percentage of regions predicted to have function by process 200 will be assayed physically, and that display 80 will accordingly, for any given genomic sequence, have an increasing number of rectangles 84 and 85, representing an increased density of sequence annotation.

Where the function desired to be identified is protein coding, rectangle 84 identifies the sequence of the probe used to measure expression. In embodiments of the present invention where expression is measured using genome-derived single exon microarrays, rectangle 84 identifies the sequence included within the probe immobilized on the support surface of the microarray. As noted *supra*, such probe will often include a small amount of additional, synthetic, material incorporated during amplification and designed to permit reamplification of the probe, which sequence is typically not shown in display 80.

Rectangle 87 is used to present the results of bioinformatic assay of the genomic sequence. For example, where the function desired to be identified is protein coding, process 400 can include bioinformatic query of expression databases with the sequences predicted in process 200 to encode exons. And as earlier discussed, because bioinformatic assay presents fewer constraints than

does physical assay, often the entire output of process 200 can be used for such assay, without further subsetting thereof by process 300. Therefore, rectangle 87 typically need not have separate indicators therein of regions submitted for bioinformatic assay; that is, rectangle 87 typically need not have regions therein analogous to rectangles 84 within rectangle 89.

Rectangle 87 as shown in FIG. 3 includes smaller rectangles 880 and 88. Rectangles 880 indicate regions that returned a positive result in the bioinformatic assay, with rectangles 88 representing regions that did not return such positive results. Where the function desired to be predicted and displayed is protein coding, rectangles 880 indicate regions of the predicted exons that identify sequence with significant similarity in expression databases, such as EST, SNP, SAGE databases, with rectangles 88 indicating genes novel over those identified in existing expression data bases.

Rectangles 880 can further indicate, through color, shading, texture, or the like, additional information obtained from bioinformatic assay.

For example, where the function assayed and displayed is protein coding, the degree of shading of rectangles 880 can be used to represent the degree of sequence similarity found upon query of expression databases. The number of levels of discrimination can be as few as two (identity, and similarity, where similarity has a user-selectable lower threshold). Alternatively, as many different levels of discrimination can be indicated as can visually be discriminated.

Where display 80 is used as a graphical user interface, rectangles 880 can additionally provide links directly to the sequences identified by the query of expression databases, and/or statistical summaries thereof. As with each of the precedingly-discussed uses of display

80 as a graphical user interface, it should be understood that the information accessed via display 80 need not be resident on the computer presenting such display, which often will be serving as a client, with the linked  
5 information resident on one or more remotely located servers.

Rectangle 85 displays the results of physical assay of the sequence delimited by its left and right borders.

10           Rectangle 85 can consist of a single rectangle, thus indicating a single assay, or alternatively, and increasingly typically, will consist of a series of rectangles (85a, 85b, 85c) indicating separate physical assays of the same sequence.

15           Where the function assayed is gene expression, and where gene expression is assayed as herein described using simultaneous two-color fluorescent detection of hybridization to genome-derived single exon microarrays, individual rectangles 85 can be colored to indicate the  
20 degree of expression relative to control. Conveniently, shades of green can be used to depict expression in the sample over control values, and shades of red used to depict expression less than control, corresponding to the spectra of the Cy3 and Cy5 dyes conventionally used for  
25 respective labeling thereof. Additional functional information can be provided in the form of circles 86 (86a, 86b, 86c), where the diameter of the circle can be used to indicate expression intensity. As discussed *infra*, such relative expression (expression ratios) and absolute  
30 expression (signal intensity) can be expressed using normalized values.

Where display 80 is used as a graphical user interface, rectangle 85 can be used as a link to further information about the assay. For example, where the assay

is one for gene expression, each rectangle 85 can be used to link to information about the source of the hybridized mRNA, the identity of the control, raw or processed data from the microarray scan, or the like.

5           FIG. 4 is rendition of display 80 representing gene prediction and gene expression for a hypothetical BAC, showing conventions used in the Examples presented infra. BAC sequence ("Chip seq.") 89 is presented, with the physically assayed region thereof (corresponding to  
10 rectangle 84 in FIG. 3) shown in white. Algorithmic gene predictions are shown in field 81, with predictions by GRAIL shown, predictions by GENEFINDER, and predictions by DICTION shown. Within rectangle 87, regions of sequence that, when used to query expression databases, return  
15 identical or similar sequences ("EST hit") are shown as white rectangles (corresponding to rectangles 880 in FIG. 3), gray indicates low homology, and black indicates unknowns (where black and gray would correspond to rectangles 88 in FIG. 3).

20           Although FIGS. 3 and 4 show a single stretch of sequence, uninterrupted from left to right, longer sequences are usefully represented by vertical stacking of such individual Mondrians, as shown in FIGS. 9 and 10.

## 25   Single Exon Probes Useful For Measuring Gene Expression

          The methods and apparatus of the present invention rapidly produce functional information from genomic sequence. Where the function to be identified is  
30 protein coding, the methods and apparatus of the present invention rapidly identify and confirm the expression of portions of genomic sequence that function to encode protein. As a direct result, the methods and apparatus of the present invention rapidly yield large numbers of

single-exon nucleic acid probes, the majority from previously unknown genes, each of which is useful for measuring and/or surveying expression of a specific gene in one or more tissues or cell types.

5           It is, therefore, another aspect of the present invention to provide genome-derived single exon nucleic acid probes useful for gene expression analysis, and particularly for gene expression analysis by microarray.

10           Using the methods and genome-derived single-exon microarrays of the present invention, we have for example readily identified a large number of unique ORFs from human genomic sequence. Using single exon probes that encompass these ORFs, we have demonstrated, through microarray hybridization analysis, the expression of 5,081 of these  
15 ORFs in heart.

          As would immediately be appreciated by one of skill in the art, each single exon probe having demonstrable expression in heart is currently available for use in measuring the level of its ORF's expression in  
20 heart. The utility is specific to the probe; at sufficiently high hybridization stringency, which stringencies are well known in the art — see Ausubel et al. and Maniatis et al. — each probe reports the level of expression of message specifically containing that ORF.

25           It should be appreciated, however, that the probes of the present invention, for which expression in the heart has been demonstrated are useful for both measurement in the heart and for survey of expression in other tissues.

30           Significant among such advantages is the presence of probes for novel genes.

          As mentioned above and further detailed in Examples 1 and 2, the methods described enable ORFs which are not present in existing expression databases to be

identified. And the fewer the number of tissues in which the ORF can be shown to be expressed, the more likely the ORF will prove to be part of a novel gene: as further discussed in Example 2, ORFs whose expression was measurable in only a single of the tested tissues were represented in existing expression databases at a rate of only 11%, whereas 36% of ORFs whose expression was measurable in 9 tissues were present in existing expression databases, and fully 45% of those ORFs expressed in all ten tested tissues were present in existing expressed sequence databases.

Either as tools for measuring gene expression or tools for surveying gene expression, the genome-derived single exon probes of the present invention have significant advantages over the cDNA or EST-based probes that are currently available for achieving these utilities.

The genome-derived single exon probes of the present invention are useful in constructing genome-derived single exon microarrays; the genome-derived single exon microarrays, in turn, are useful devices for measuring and for surveying gene expression in the human.

Gene expression analysis using microarrays — conventionally using microarrays having probes derived from expressed message — is well-established as useful in the biological research arts (see Lockhart et al. *Nature* 405, 827-836).

Microarrays have been used to determine gene expression profiles in cells in response to drug treatment (see, for example, Kaminski et al., "Global Analysis of Gene Expression in Pulmonary Fibrosis Reveals Distinct Programs Regulating Lung Inflammation and Fibrosis," *Proc. Natl. Acad. Sci. USA* 97(4):1778-83 (2000); Bartosiewicz et al., "Development of a Toxicological Gene Array and Quantitative Assessment of This Technology," *Arch. Biochem.*

*Biophys.* 376(1):66-73 (2000)), viral infection (see for example, Geiss et al., "Large-scale Monitoring of Host Cell Gene Expression During HIV-1 Infection Using cDNA Microarrays," *Virology* 266(1):8-16 (2000)) and during cell  
 5 processes such as differentiation, senescence and apoptosis (see, for example, Shelton et al., "Microarray Analysis of Replicative Senescence," *Curr. Biol.* 9(17):939-45 (1999); Voehringer et al., "Gene Microarray Identification of Redox and Mitochondrial Elements That Control Resistance or  
 10 Sensitivity to Apoptosis," *Proc. Natl. Acad. Sci. USA* 97(6):2680-5 (2000)).

Microarrays have also been used to determine abnormal gene expression in diseased tissues (see, for example, Alon et al., "Broad Patterns of Gene Expression  
 15 Revealed by Clustering Analysis of Tumor and Normal Colon Tissues Probed by Oligonucleotide Arrays," *Proc. Natl. Acad. Sci. USA* 96(12):6745-50 (1999); Perou et al., "Distinctive Gene Expression Patterns in Human Mammary Epithelial Cells and Breast Cancers, *Proc. Natl. Acad. Sci.*  
 20 *USA* 96(16):9212-7 (1999); Wang et al., "Identification of Genes Differentially Over-expressed in Lung Squamous Cell Carcinoma Using Combination of cDNA Subtraction and Microarray Analysis," *Oncogene* 19(12):1519-28 (2000); Whitney et al., "Analysis of Gene Expression in Multiple  
 25 Sclerosis Lesions Using cDNA Microarrays," *Ann. Neurol.* 46(3):425-8 (1999)), in drug discovery screens (see, for example, Scherf et al., "A Gene Expression Database for the Molecular Pharmacology of Cancer," *Nat. Genet.* 24(3):236-44 (2000)) and in diagnosis to determine appropriate treatment  
 30 strategies (see, for example, Sgroi et al., "In vivo Gene Expression Profile Analysis of Human Breast Cancer Progression," *Cancer Res.* 59(22):5656-61 (1999)).

In microarray-based gene expression screens of pharmacological drug candidates upon cells, each probe



provides specific useful data. In particular, it should be appreciated that even those probes that show no change in expression are as informative as those that do change, serving, in essence, as negative controls.

- 5 For example, where gene expression analysis is used to assess toxicity of chemical agents on cells, the failure of the agent to change a gene's expression level is evidence that the drug likely does not affect the pathway of which the gene's expressed protein is a part.
- 10 Analogously, where gene expression analysis is used to assess side effects of pharmacological agents – whether in lead compound discovery or in subsequent screening of lead compound derivatives – the inability of the agent to alter a gene's expression level is evidence that the drug does
- 15 not affect the pathway of which the gene's expressed protein is a part.

WO 99/58720 provides methods for quantifying the relatedness of a first and second gene expression profile and for ordering the relatedness of a plurality of gene

20 expression profiles. The methods so described permit useful information to be extracted from a greater percentage of the individual gene expression measurements from a microarray than methods previously used in the art.

Other uses of microarrays are described in

25 Gerhold et al., *Trends Biochem. Sci.* 24(5):168-173 (1999) and Zweiger, *Trends Biotechnol.* 17(11):429-436 (1999); Schena et al.

The invention particularly provides genome-derived single-exon probes known to be expressed in heart.

- 30 The individual single exon probes can be provided in the form of substantially isolated and purified nucleic acid, typically, but not necessarily, in a quantity sufficient to perform a hybridization reaction.

Such nucleic acid can be in any form directly

hybridizable to the message that contains the probe's ORF, such as double stranded DNA, single-stranded DNA complementary to the message, single-stranded RNA complementary to the message, or chimeric DNA/RNA molecules  
5 so hybridizable. The nucleic acid can alternatively or additionally include either nonnative nucleotides, alternative internucleotide linkages, or both, so long as complementary binding can be obtained. For example, probes can include phosphorothioates, methylphosphonates,  
10 morpholino analogs, and peptide nucleic acids (PNA), as are described, for example, in U.S. Patent Nos. 5,142,047; 5,235,033; 5,166,315; 5,217,866; 5,184,444; 5,861,250.

Usefully, however, such probes are provided in a form and quantity suitable for amplification, where the  
15 amplified product is thereafter to be used in the hybridization reactions that probe gene expression. Typically, such probes are provided in a form and quantity suitable for amplification by PCR or by other well known amplification technique. One such technique additional to  
20 PCR is rolling circle amplification, as is described, *inter alia*, in U.S. Patent Nos. 5,854,033 and 5,714,320 and international patent publications WO 97/19193 and WO 00/15779. As is well understood, where the probes are to be provided in a form suitable for amplification, the  
25 range of nucleic acid analogues and/or internucleotide linkages will be constrained by the requirements and nature of the amplification enzyme.

Where the probe is to be provided in form suitable for amplification, the quantity need not be  
30 sufficient for direct hybridization for gene expression analysis, and need be sufficient only to function as an amplification template, typically at least about 1, 10 or 100 pg or more.

Each discrete amplifiable probe can also be

packaged with amplification primers, either in a single composition that comprises probe template and primers, or in a kit that comprises such primers separately packaged therefrom. As earlier mentioned, the ORF-specific  
5 5' primers used for genomic amplification can have a first common sequence added thereto, and the ORF-specific 3' primers used for genomic amplification can have a second, different, common sequence added thereto, thus permitting, in this embodiment, the use of a single set of 5' and 3'  
10 primers to amplify any one of the probes. The probe composition and/or kit can also include buffers, enzyme, etc., required to effect amplification.

As mentioned earlier, when intended for use on a genome-derived single exon microarray of the present  
15 invention, the genome-derived single exon probes of the present invention will typically average at least about 100, 200, 300, 400 or 500 bp in length, including (and typically, but not necessarily centered about) the ORF. Furthermore, when intended for use on a genome-derived  
20 single exon microarray of the present invention, the genome-derived single exon probes of the present invention will typically not contain a detectable label.

When intended for use in solution phase hybridization, however — that is, for use in a  
25 hybridization reaction in which the probe is not first bound to a support substrate (although the target may indeed be so bound) — length constraints that are imposed in microarray-based hybridization approaches will be relaxed, and such probes will typically be labeled.

30 In such case, the only functional constraint that dictates the minimum size of such probe is that each such probe must be capable of specifically identifying in a hybridization reaction the exon from which it is drawn. In theory, a probe of as little as 17 nucleotides is capable

of uniquely identifying its cognate sequence in the human genome. For hybridization to expressed message – a subset of target sequence that is much reduced in complexity as compared to genomic sequence – even fewer nucleotides are  
5 required for specificity.

Therefore, the probes of the present invention can include as few as 20, 25 or 50 bp or ORF, or more. In particular embodiments, the ORF sequences are given in SEQ ID NOS. 5,203 – 10,283, respectively, for probe SEQ ID NOS.  
10 1 – 5,202. The minimum amount of ORF required to be included in the probe of the present invention in order to provide specific signal in either solution phase or microarray-based hybridizations can readily be determined for each of ORF SEQ ID NOS. 5,203 – 10,283 individually by  
15 routine experimentation using standard high stringency conditions.

Such high stringency conditions are described, *inter alia*, in Ausubel et al. and Maniatis et al. For microarray-based hybridization, standard high stringency  
20 conditions can usefully be 50% formamide, 5X SSC, 0.2  $\mu\text{g}/\mu\text{l}$  poly(dA), 0.2  $\mu\text{g}/\mu\text{l}$  human c<sub>0</sub>t1 DNA, and 0.5 % SDS, in a humid oven at 42°C overnight, followed by successive washes of the microarray in 1X SSC, 0.2% SDS at 55°C for 5 minutes, and then 0.1X SSC, 0.2% SDS, at 55°C for 20  
25 minutes. For solution phase hybridization, standard high stringency conditions can usefully be aqueous hybridization at 65°C in 6X SSC. Lower stringency conditions, suitable for cross-hybridization to mRNA encoding structurally- and functionally-related proteins, can usefully be the same as  
30 the high stringency conditions but with reduction in temperature for hybridization and washing to room temperature (approximately 25°C).

When intended for use in solution phase hybridization, the maximum size of the single exon probes

of the present invention is dictated by the proximity of other expressed exons in genomic DNA: although each single exon probe can include intergenic and/or intronic material contiguous to the ORF in the human genome, each probe of  
5 the present invention will include portions of only one expressed exon.

Thus, each single exon probe will include no more than about 25 kb of contiguous genomic sequence, more typically no more than about 20 kb of contiguous genomic  
10 sequence, more usually no more than about 15 kb, even more usually no more than about 10 kb. Usually, probes that are maximally about 5 kb will be used, more typically no more than about 3 kb.

It will be appreciated that the Sequence Listing  
15 appended hereto presents, by convention, only that strand of the probe and ORF sequence that can be directly translated reading from 5' to 3' end. As would be well understood by one of skill in the art, single stranded probes must be complementary in sequence to the ORF as  
20 present in an mRNA; it is well within the skill in the art to determine such complementary sequence. It will further be understood that double stranded probes can be used in both solution-phase hybridization and microarray-based hybridization if suitably denatured.

25 Thus, it is an aspect of the present invention to provide single-stranded nucleic acid probes that have sequence complementary to those described herein above and below, and double-stranded probes one strand of which has sequence complementary to the probes described herein.

30 The probes can, but need not, contain intergenic and/or intronic material that flanks the ORF, on one or both sides, in the same linear relationship to the ORF that the intergenic and/or intronic material bears to the ORF in genomic DNA. The probes do not, however, contain nucleic  
35 acid derived from more than one expressed ORF.

And when intended for use in solution hybridization, the probes of the present invention can usefully have detectable labels. Nucleic acid labels are well known in the art, and include, *inter alia*, radioactive  
5 labels, such as  $^3\text{H}$ ,  $^{32}\text{P}$ ,  $^{33}\text{P}$ ,  $^{35}\text{S}$ ,  $^{125}\text{I}$ ,  $^{131}\text{I}$ ; fluorescent labels, such as Cy3, Cy5, Cy5.5, Cy7, SYBR<sup>®</sup>

Green and other labels described in Haugland, *Handbook of Fluorescent Probes and Research Chemicals*, 7th ed., Molecular Probes Inc., Eugene, OR (2000), or  
10 fluorescence resonance energy transfer tandem conjugates thereof; labels suitable for chemiluminescent and/or enhanced chemiluminescent detection; labels suitable for ESR and NMR detection; and labels that include one member of a specific binding pair, such as biotin, digoxigenin, or  
15 the like.

The probes, either in quantity sufficient for hybridization or sufficient for amplification, can be provided in individual vials or containers.

Alternatively, such probes can usefully be  
20 packaged as a plurality of such individual genome-derived single exon probes.

When provided as a collection of plural individual probes, the probes are typically made available in amplifiable form in a spatially-addressable ordered set,  
25 typically one per well of a microtiter dish. Although a 96 well microtiter plate can be used, greater efficiency is obtained using higher density arrays.

If, as earlier mentioned, the ORF-specific 5' primers used for genomic amplification had a first  
30 common sequence added thereto, and the ORF-specific 3' primers used for genomic amplification had a second, different, common sequence added thereto, a single set of 5' and 3' primers can be used to amplify all of the probes from the amplifiable ordered set.

Such collections of genome-derived single exon probes can usefully include a plurality of probes chosen for the common attribute of expression in the human heart.

In such defined subsets, typically at least 50,  
5 60, 75, 80, 85, 90 or 95% or more of the probes will be chosen by their expression in the defined tissue or cell type.

The single exon probes of the present invention, as well as fragments of the single exon probes comprising  
10 selectively hybridizable portions of the probe ORF, can be used to obtain the full length cDNA that includes the ORF by (i) screening of cDNA libraries; (ii) rapid amplification of cDNA ends ("RACE"); or (iii) other conventional means, as are described, *inter alia*, in  
15 Ausubel et al. and Maniatis et al.

It is another aspect of the present invention to provide genome-derived single exon nucleic acid microarrays useful for gene expression analysis, where the term "microarray" has the meaning given in the definitional  
20 section of this description, *supra*.

The invention particularly provides genome-derived single-exon nucleic acid microarrays comprising a plurality of probes known to be expressed in human heart. In preferred embodiments, the present invention provides  
25 human genome-derived single exon microarrays comprising a plurality of probes drawn from the group consisting of SEQ ID NOS.: 1 - 5,202.

When used for gene expression analysis, the genome-derived single exon microarrays provide greater  
30 physical informational density than do the genome-derived single exon microarrays that have lower percentages of probes known to be expressed commonly in the tested tissue. At a fixed probe density, for example, a given microarray surface area of the defined subset genome-derived single

exon microarray can yield a greater number of expression measurements. Alternatively, at a given probe density, the same number of expression measurements can be obtained from a smaller substrate surface area. Alternatively, at a fixed probe density and fixed surface area, probes can be provided redundantly, providing greater reliability in signal measurement for any given probe. Furthermore, with a higher percentage of probes known to be expressed in the assayed tissue, the dynamic range of the detection means can be adjusted to reveal finer levels discrimination among the levels of expression.

Although particularly described with respect to their utility as probes of gene expression, particularly as probes to be included on a genome-derived single exon microarray, each of the nucleic acids having SEQ ID NOS.: 1 - 5,202 contains an open-reading frame, set forth respectively in SEQ ID NOS.: 5,203 - 10,283, that encodes a protein domain. Thus, each of SEQ ID NOS. 1 - 5,202 can be used, or that portion thereof in SEQ ID NOS. 5,203 - 10,283 used, to express a protein domain by standard *in vitro* recombinant techniques. See Ausubel et al. and Maniatis et al.

Additionally, kits are available commercially that readily permit such nucleic acids to be expressed as protein in bacterial cells, insect cells, or mammalian cells, as desired (e.g., HAT™ Protein Expression & Purification System, ClonTech Laboratories, Palo Alto, CA; Adeno-X™ Expression System, ClonTech Laboratories, Palo Alto, CA; Protein Fusion & Purification (pMAL™) System, New England Biolabs, Beverley, MA)

Furthermore, shorter peptides can be chemically synthesized using commercial peptide synthesizing equipment and well known techniques. Procedures are described, *inter alia*, in Chan et al. (eds.), Fmoc Solid Phase Peptide



Synthesis: A Practical Approach (Practical Approach Series, (Paper)), Oxford Univ. Press (March 2000) (ISBN: 0199637245); Jones, Amino Acid and Peptide Synthesis (Oxford Chemistry Primers, No 7) , Oxford Univ. Press (August 1992) (ISBN: 0198556683); and Bodanszky, Principles of Peptide Synthesis (Springer Laboratory), Springer Verlag (December 1993) (ISBN: 0387564314).

It is, therefore, another aspect of the invention to provide peptides comprising an amino acid sequence translated from SEQ ID NOS.: 5,203 - 10,283. Such amino acid sequences are set out in SEQ ID NOS: 10,284 - 15,322. Any such recombinantly-expressed or synthesized peptide of at least 8, and preferably at least about 15, amino acids, can be conjugated to a carrier protein and used to generate antibody that recognizes the peptide. Thus, it is a further aspect of the invention to provide peptides that have at least 8, preferably at least 15, consecutive amino acids.

The following examples are offered by way of illustration and not by way of limitation.

#### EXAMPLE 1

Preparation of Single Exon Microarrays from ORFs Predicted in Human Genomic Sequence

#### Bioinformatics Results

All human BAC sequences in fewer than 10 pieces that had been accessioned in a five month period immediately preceding this study were downloaded from GenBank. This corresponds to ~2200 clones, totaling ~350 MB of sequence, or approximately 10% of the human genome.

After masking repetitive elements using the program CROSS\_MATCH, the sequence was analyzed for open reading frames using three separate gene finding programs.

The three programs predict genes using independent algorithmic methods developed on independent training sets: GRAIL uses a neural network, GENEFINDER uses a hidden Markoff model, and DICTION, a program proprietary to  
 5 Genetics Institute, operates according to a different heuristic. The results of all three programs were used to create a prediction matrix across the segment of genomic DNA.

The three gene finding programs yielded a range  
 10 of results. GRAIL identified the greatest percentage of genomic sequence as putative coding region, 2% of the data analyzed. GENEFINDER was second, calling 1%, and DICTION yielded the least putative coding region, with 0.8% of genomic sequence called as coding region.

15 The consensus data were as follows. GRAIL and GENEFINDER agreed on 0.7% of genomic sequence, GRAIL and DICTION agreed on 0.5% of genomic sequence, and the three programs together agreed on 0.25% of the data analyzed. That is, 0.25% of the genomic sequence was identified by  
 20 all three of the programs as containing putative coding region.

ORFs predicted by any two of the three programs ("consensus ORFs") were assorted into "gene bins" using two criteria: (1) any 7 consecutive exons within a 25 kb window  
 25 were placed together in a bin as likely contributing to a single gene, and (2) all ORFs within a 25 kb window were placed together in a bin as likely contributing to a single gene if fewer than 7 exons were found within the 25 kb window.

30

#### PCR

The largest ORF from each gene bin that did not span repetitive sequence was then chosen for amplification, as were all consensus ORFs longer than 500 bp. This method  
 35 approximated one exon per gene; however, a number of genes

were found to be represented by multiple elements.

Previously, we had determined that DNA fragments fewer than 250 bp in length do not bind well to the amino-modified glass surface of the slides used as support substrate for construction of microarrays; therefore, amplicons were designed in the present experiments to approximate 500 bp in length.

Accordingly, after selecting the largest ORF per gene bin, a 500 bp fragment of sequence centered on the ORF was passed to the primer picking software, PRIMER3 (available online for use at <http://www-genome.wi.mit.edu/cgi-bin/primer/>). A first additional sequence was commonly added to each ORF-unique 5' primer, and a second, different, additional sequence was commonly added to each ORF-unique 3' primer, to permit subsequent reamplification of the amplicon using a single set of "universal" 5' and 3' primers, thus immortalizing the amplicon. The addition of universal priming sequences also facilitates sequence verification, and can be used to add a cloning site should some ORFs be found to warrant further study.

The ORFs were then PCR amplified from genomic DNA, verified on agarose gels, and sequenced using the universal primers to validate the identity of the amplicon to be spotted in the microarray.

Primers were supplied by Operon Technologies (Alameda, CA). PCR amplification was performed by standard techniques using human genomic DNA (Clontech, Palo Alto, CA) as template. Each PCR product was verified by SYBR<sup>®</sup> green (Molecular Probes, Inc., Eugene, OR) staining of agarose gels, with subsequent imaging by Fluorimager (Molecular Dynamics, Inc., Sunnyvale, CA). PCR amplification was classified as successful if a single band appeared.

The success rate for amplifying ORFs of interest

directly from genomic DNA using PCR was approximately 75%.  
FIG. 5 graphs the distribution of predicted ORF (exon)  
length and distribution of amplified PCR products, with ORF  
length shown in red and PCR product length shown in blue  
5 (which may appear black in the figure). Although the range  
of ORF sizes is readily seen to extend to beyond 900 bp,  
the mean predicted exon size was only 229 bp, with a median  
size of 150 bp (n=9498). With an average amplicon size of  
475  $\pm$  25 bp, approximately 50% of the average PCR  
10 amplification product contained predicted coding region,  
with the remaining 50% of the amplicon containing either  
intron, intergenic sequence, or both.

Using a strategy predicated on amplifying about  
500 bp, it was found that long exons had a higher PCR  
15 failure rate. To address this, the bioinformatics process  
was adjusted to amplify 1000, 1500 or 2000 bp fragments  
from exons larger than 500 bp. This improved the rate of  
successful amplification of exons exceeding 500 bp,  
constituting about 9.2% of the exons predicted by the gene  
20 finding algorithms.

Approximately 75% of the probes disposed on the  
array (90% of those that successfully PCR amplified) were  
sequence-verified by sequencing in both the forward and  
reverse direction using MegaBACE sequencer (Molecular  
25 Dynamics, Inc., Sunnyvale, CA), universal primers, and  
standard protocols.

Some genomic clones (BACs) yielded very poor PCR  
and sequencing results. The reasons for this are unclear,  
but may be related to the quality of early draft sequence  
30 or the inclusion of vector and host contamination in some  
submitted sequence data.

Although the intronic and intergenic material  
flanking coding regions could theoretically interfere with  
hybridization during microarray experiments, subsequent  
35 empirical results demonstrated that differential expression

ratios were not significantly affected by the presence of noncoding sequence. The variation in exon size was similarly found not to affect differential expression ratios significantly; however, variation in exon size was  
5 observed to affect the absolute signal intensity (data not shown).

The 350 MB of genomic DNA was, by the above-described process, reduced to 9750 discrete probes, which were spotted in duplicate onto glass slides using  
10 commercially available instrumentation (MicroArray GenII Spotter and/or MicroArray GenIII Spotter, Molecular Dynamics, Inc., Sunnyvale, CA). Each slide additionally included either 16 or 32 *E. coli* genes, the average hybridization signal of which was used as a measure of  
15 background biological noise.

Each of the probe sequences was BLASTed against the human EST data set, the NR data set, and SwissProt GenBank (May 7, 1999 release 2.0.9).

One third of the probe sequences (as amplified)  
20 produced an exact match (BLAST Expect ("E") values less than  $1 \text{ e}^{-100}$ ) to either an EST (20% of sequences) or a known mRNA (13% of sequences). A further 22% of the probe sequences showed some homology to a known EST or mRNA (BLAST E values from  $1 \text{ e}^{-5}$  to  $1 \text{ e}^{-99}$ ). The remaining 45% of  
25 the probe sequences showed no significant sequence homology to any expressed, or potentially expressed, sequences present in public databases.

All of the probe sequences (as amplified) were then analyzed for protein similarities with the SwissProt  
30 database using BLASTX, Gish et al., Nature Genet. 3:266 (1993). The predicted functional breakdowns of the 2/3 of probes identical or homologous to known sequences are presented in Table 1.

Table 1

Function of Predicted ORFs As Deduced From Comparative Sequence Analysis			
Total	V6 chip	V7 chip	Function Predicted from Comparative Sequence Analysis
211	96	115	Receptor
120	43	77	Zinc Finger
30	11	19	Homeobox
25	9	16	Transcription Factor
17	11	7	Transcription
118	57	61	Structural
95	39	56	Kinase
36	18	18	Phosphatase
83	31	52	Ribosomal
45	19	26	Transport
21	17	14	Growth Factor
17	12	5	Cytochrome
50	33	17	Channel

As can be seen, the two most common types of genes were transcription factors and receptors, making up 2.2% and 1.8% of the arrayed elements, respectively.

#### EXAMPLE 2

Gene Expression Measurements From Genome-Derived Single Exon Microarrays

The two genome-derived single exon microarrays prepared according to Example 1 were hybridized in a series of simultaneous two-color fluorescence experiments to (1)

Cy3-labeled cDNA synthesized from message drawn individually from each of brain, heart, liver, fetal liver, placenta, lung, bone marrow, HeLa, BT 474, or HBL 100 cells, and (2) Cy5-labeled cDNA prepared from message  
 5 pooled from all ten tissues and cell types, as a control in each of the measurements. Hybridization and scanning were carried out using standard protocols and Molecular Dynamics equipment.

Briefly, mRNA samples were bought from commercial  
 10 sources (Clontech, Palo Alto, CA and Amersham Pharmacia Biotech (APB)). Cy3-dCTP and Cy5-dCTP (both from APB) were incorporated during separate reverse transcriptions of 1  $\mu$ g of polyA<sup>+</sup> mRNA performed using 1  $\mu$ g oligo(dT)12-18 primer and 2  $\mu$ g random 9mer primers as follows. After heating to  
 15 70°C, the RNA:primer mixture was snap cooled on ice. After snap cooling on ice, added to the RNA to the stated final concentration was: 1X Superscript II buffer, 0.01 M DTT, 100  $\mu$ M dATP, 100  $\mu$ M dGTP, 100  $\mu$ M dTTP, 50  $\mu$ M dCTP, 50  $\mu$ M Cy3-dCTP or Cy5-dCTP 50  $\mu$ M, and 200 U Superscript II  
 20 enzyme. The reaction was incubated for 2 hours at 42°C. After 2 hours, the first strand cDNA was isolated by adding 1 U Ribonuclease H, and incubating for 30 minutes at 37°C. The reaction was then purified using a Qiagen PCR cleanup column, increasing the number of ethanol washes to 5.  
 25 Probe was eluted using 10 mM Tris pH 8.5.

Using a spectrophotometer, probes were measured for dye incorporation. Volumes of both Cy3 and Cy5 cDNA corresponding to 50 pmoles of each dye were then dried in a Speedvac, resuspended in 30  $\mu$ l hybridization solution  
 30 containing 50% formamide, 5X SSC, 0.2  $\mu$ g/ $\mu$ l poly(dA), 0.2  $\mu$ g/ $\mu$ l human c<sub>o</sub>t1 DNA, and 0.5 % SDS.

Hybridizations were carried out under a coverslip, with the array placed in a humid oven at 42°C overnight. Before scanning, slides were washed in 1X SSC,  
 35 0.2% SDS at 55°C for 5 minutes, followed by 0.1X SSC, 0.2%

SDS, at 55°C for 20 minutes. Slides were briefly dipped in water and dried thoroughly under a gentle stream of nitrogen.

Slides were scanned using a Molecular Dynamics  
 5 Gen3 scanner, as described. Schena (ed.), Microarray  
 Biochip: Tools and Technology, Eaton Publishing  
 Company/BioTechniques Books Division (2000) (ISBN:  
 1881299376).

Although the use of pooled cDNA as a reference  
 10 permitted the survey of a large number of tissues, it  
 attenuates the measurement of relative gene expression,  
 since every highly expressed gene in the tissue/cell type-  
 specific fluorescence channel will be present to a level of  
 at least 10% in the control channel. Because of this fact,  
 15 both signal and expression ratios (the latter hereinafter,  
 "expression" or "relative expression") for each probe were  
 normalized using the average ratio or average signal,  
 respectively, as measured across the whole slide.

Data were accepted for further analysis only when  
 20 signal was at least three times greater than biological  
 noise, the latter defined by the average signal produced by  
 the *E. coli* control genes.

The relative expression signal for these probes  
 was then plotted as function of tissue or cell type, and is  
 25 presented in FIG. 6.

FIG. 6 shows the distribution of expression  
 across a panel of ten tissues. The graph shows the number  
 of sequence-verified products that were either not  
 expressed ("0"), expressed in one or more but not all  
 30 tested tissues ("1" - "9"), and expressed in all tissues  
 tested ("10").

Of 9999 arrayed elements on the two microarrays  
 (including positive and negative controls and "failed"  
 products), 2353 (51%) were expressed in at least one tissue



or cell type. Of the gene elements showing significant signal — where expression was scored as "significant" if the normalized Cy3 signal was greater than 1, representing signal 5-fold over biological noise (0.2) — 39% (991) were  
 5 expressed in all 10 tissues. The next most common class (15%) consisted of gene elements expressed in only a single tissue.

The genes expressed in a single tissue were further analyzed, and the results of the analyses are  
 10 compiled in FIG. 7.

FIG. 7A is a matrix presenting the expression of all verified sequences that showed expression greater than 3 in at least one tissue. Each clone is represented by a column in the matrix. Each of the 10 tissues assayed is  
 15 represented by a separate row in the matrix, and relative expression of a clone in that tissue is indicated at the respective node by intensity of green shading, with the intensity legend shown in panel B. The top row of the matrix ("EST Hit") contains "bioinformatic" rather than  
 20 "physical" expression data — that is, presents the results returned by query of EST, NR and SwissProt databases using the probe sequence. The legend for "bioinformatic expression" (i.e., degree of homology returned) is presented in panel C. Briefly, white is known, black is  
 25 novel, with gray depicting nonidentical with significant homology (white: E values <  $1e-100$ ; gray: E values from  $1e-05$  to  $1e-99$ ; black: E values >  $1e-05$ ).

As FIG. 7 readily shows, heart and brain were demonstrated to have the greatest numbers of genes that  
 30 were shown to be uniquely expressed in the respective tissue. In brain, 200 uniquely expressed genes were identified; in heart, 150. The remaining tissues gave the following figures for uniquely expressed genes: liver, 100; lung, 70; fetal liver, 150; bone marrow, 75; placenta, 100;

HeLa, 50; HBL, 100; and BT474, 50.

It was further observed that there were many more "novel" genes among those that were up-regulated in only one tissue, as compared with those that were down-regulated in only one tissue. In fact, it was found that ORFs whose expression was measurable in only a single of the tested tissues were represented in sequencing databases at a rate of only 11%, whereas 36% of the ORFs whose expression was measurable in 9 of the tissues were present in public databases. As for those ORFs expressed in all ten tissues, fully 45% were present in existing expressed sequence databases. These results are not unexpected, since genes expressed in a greater number of tissues have a higher likelihood of being, and thus of having been, discovered by EST approaches.

#### Comparison of Signal from Known and Unknown Genes

The normalized signal of the genes found to have high homology to genes present in the GenBank human EST database were compared to the normalized signal of those genes not found in the GenBank human EST database. The data are shown in FIG. 8.

FIG. 8 shows the normalized Cy3 signal intensity for all sequence-verified products with a BLAST Expect ("E") value of greater than  $1e-30$  (designated "unknown") upon query of existing EST, NR and SwissProt databases, and shows in blue the normalized Cy3 signal intensity for all sequence-verified products with a BLAST Expect value of less than  $1e-30$  ("known"). Note that biological background noise has an averaged normalized Cy3 signal intensity of 0.2.

As expected, the most highly expressed of the ORFs were "known" genes. This is not surprising, since very high signal intensity correlates with very commonly-expressed genes, which have a higher likelihood of being

found by EST sequence.

However, a significant point is that a large number of even the high expressers were "unknown". Since the genomic approach used to identify genes and to confirm  
 5 their expression does not bias exons toward either the 3' or 5' end of a gene, many of these high expression genes will not have been detected in an end-sequenced cDNA library.

The significant point is that presence of the  
 10 gene in an EST database is not a prerequisite for incorporation into a genome-derived microarray, and further, that arraying such "unknown" exons can help to assign function to as-yet undiscovered genes.

#### 15 Verification of Gene Expression

To ascertain the validity of the approach described above to identify genes from raw genomic sequence, expression of two of the probes was assayed using reverse transcriptase polymerase chain reaction (RT PCR)  
 20 and northern blot analysis.

Two microarray probes were selected on the basis of exon size, prior sequencing success, and tissue-specific gene expression patterns as measured by the microarray experiments. The primers originally used to amplify the  
 25 two respective ORFs from genomic DNA were used in RT PCR against a panel of tissue-specific cDNAs (Rapid-Scan gene expression panel 24 human cDNAs) (OriGene Technologies, Inc., Rockville, MD).

Sequence AL079300\_1 was shown by microarray  
 30 hybridization to be present in cardiac tissue, and sequence AL031734\_1 was shown by microarray experiment to be present in placental tissue (data not shown). RT-PCR on these two sequences confirmed the tissue-specific gene expression as measured by microarrays, as ascertained by the presence of

a correctly sized PCR product from the respective tissue type cDNAs.

Clearly, all microarray results cannot, and indeed should not, be confirmed by independent assay methods, or the high throughput, highly parallel advantages of microarray hybridization assays will be lost. However, in addition to the two RT-PCR results presented above, the observation that 1/3 of the arrayed genes exist in expression databases provides powerful confirmation of the power of our methodology – which combines bioinformatic prediction with expression confirmation using genome-derived single exon microarrays – to identify novel genes from raw genomic data.

To verify that the approach further provides correct characterization of the expression patterns of the identified genes, a detailed analysis was performed of the microarrayed sequences that showed high signal in brain.

For this latter analysis, sequences that showed high (normalized) signal in brain, but which showed very low (normalized) signal (less than 0.5, determined to be biological noise) in all other tissues, were further studied. There were 82 sequences that fit these criteria, approximately 2% of the arrayed elements. The 10 sequences showing the highest signal in brain in microarray hybridizations are detailed in Table 2, along with assigned function, if known or reasonably predicted.

Table 2

Function of the Most Highly Expressed Genes Expressed Only in Brain				
Microarray Sequence Name	Normalized Signal	Expression Ratio	Homology to EST present	Gene Function as described by GenBank

in GenBank				
AP000217-1	5.2	+7.7	High	S-100 protein, b-chain, $\text{Ca}^{2+}$ binding protein expressed in central nervous system
AP000047-1	2.3		High	Unknown Function
AC006548-9	1.7		High	Similar to mouse membrane glyco-protein M6, expressed in central nervous system
AC007245-5	1.5		High	Similar to amphiphysin, a synaptic vesicle-associated protein. Ref 21
L44140-4	1.2	+2.0	High	Endothelial actin-binding protein found in nonmuscle filamin
AC004689-9	1.2	+3.5	High	Protein Phosphatase PP2A, neuronal/ downregulates activated protein kinases
AL031657-1	1.2	+3.0	High	Unknown

				function/ Contains the anhyrin motif, a common protein sequence motif
AC009266-2	1.1	+3.7	Low	Low homology to the Synaptotagmin I protein in rat/present at low levels throughout rat brain
AP000086-1	1.0	+2.7	Low	Unknown, very poor homology to collagen
AC004689-3	1.0		High	Protein Phosphatase PP2A, neuronal/ downregulates activated protein kinases

Of the ten sequences studied by these latter confirmatory approaches, eight were previously known. Of these eight, six had previously been reported to be  
5 important in the central nervous system or brain. The exon giving the highest signal (AP00217-1) was found to be the gene encoding an S100B  $\text{Ca}^{2+}$  binding protein, reported in the literature to be highly and uniquely expressed in the central nervous system. Heizmann, *Neurochem. Res.* 9:1097  
10 (1997).

A number of the brain-specific probe sequences

(including AC006548-9, AC009266-2) did not have homology to any known human cDNAs in GenBank but did show homology to rat and mouse cDNAs. Sequences AC004689-9 and AC004689-3 were both found to be phosphatases present in neurons  
 5 (Millward et al., *Trends Biochem. Sci.* 24(5):186-191 (1999)). Two microarray sequences, AP000047-1 and AP000086-1 have unknown function, with AP000086-1 being absent from GenBank. Functionality can now be narrowed down to a role in the central nervous system for both of  
 10 these genes, showing the power of designing microarrays in this fashion.

Next, the function of the chip sequences with the highest (normalized) signal intensity in brain, regardless of expression in other tissues, was assessed. In this  
 15 latter analysis, we found expression of many more common genes, since the sequences were not limited to those expressed only in brain. For example, looking at the 20 highest signal intensity spots in brain, 4 were similar to tubulin (AC00807905; AF146191-2; AC007664-4; AF14191-2), 2  
 20 were similar to actin (AL035701-2; AL034402-1), and 6 were found to be homologous to glyceraldehyde-3-phosphate dehydrogenase (GAPDH) (AL035604-1; Z86090-1; AC006064-L, AC006064-K; AC035604-3; AC006064-L). These genes are often used as controls or housekeeping genes in microarray  
 25 experiments of all types.

Other interesting genes highly expressed in brain were a ferritin heavy chain protein, which is reported in the literature to be found in brain and liver (Joshi et al., *J. Neurol. Sci.* 134(Suppl):52-56 (1995)), a result  
 30 duplicated with the array. Other highly expressed chip sequences included a translation elongation factor 1 (AC007564-4), a DEAD-box homolog (AL023804-4), and a Y-chromosome RNA-binding motif (Chai et al., *Genomics* 49(2):283-89 (1998)) (AC007320-3). A low homology analog

(AP00123-1/2) to a gene, DSCR1, thought to be involved in trisomy 21 (Down's syndrome), showed high expression in both brain and heart, in agreement with the literature (Fuentes et al., *Mol. Genet.* 4(10):1935-44 (1995)).

5           As a further validation of the approach, we selected the BAC AC006064 to be included on the array. This BAC was known to contain the GAPDH gene, and thus could be used as a control for the ORF selection process. The gene finding and exon selection algorithms resulted in  
10 choosing 25 exons from BAC AC006064 for spotting onto the array, of which four were drawn from the GAPDH gene. Table 3 shows the comparison of the average expression ratio for the 4 exons from BAC006064 compared with the average  
15 expression ratio for 5 different dilutions of a commercially available GAPDH cDNA (Clontech).

Table 3

Comparison of Expression Ratio, for each tissue, of GAPDH		
	AC006064 (n = 4)	Control ( n = 5)
Bone Marrow	-1.81 $\pm$ 0.11	-1.85 $\pm$ 0.08
Brain	-1.41 $\pm$ 0.11	-1.17 $\pm$ 0.05
BT474	1.85 $\pm$ 0.09	1.66 $\pm$ 0.12
Fetal Liver	-1.62 $\pm$ 0.07	-1.41 $\pm$ 0.05
HBL100	1.32 $\pm$ 0.05	2.64 $\pm$ 0.12
Heart	1.16 $\pm$ 0.09	1.56 $\pm$ 0.10
HeLa	1.11 $\pm$ 0.06	1.30 $\pm$ 0.15
Liver	-1.62 $\pm$ 0.22	-2.07 $\pm$
Lung	-4.95 $\pm$ 0.93	-3.75 $\pm$ 0.21
Placenta	-3.56 $\pm$ 0.25	-3.52 $\pm$ 0.43



experimentally chosen exons and the control, again demonstrating the validity of the present exon mining approach. In addition, the data also show the variability of expression of GAPDH within tissues, calling into  
 5 question its classification as a housekeeping gene and utility as a housekeeping control in microarray experiments.

### EXAMPLE 3

10 Representation of Sequence and Expression Data as a "Mondrian"

For each genomic clone processed for microarray as above-described, a plethora of information was  
 15 accumulated, including full clone sequence, probe sequence within the clone, results of each of the three gene finding programs, EST information associated with the probe sequences, and microarray signal and expression for multiple tissues, challenging our ability to display the  
 20 information.

Accordingly, we devised a new tool for visual display of the sequence with its attendant annotation which, in deference to its visual similarity to the paintings of Piet Mondrian, is hereinafter termed a  
 25 "Mondrian". FIGS. 3 and 4 present the key to the information presented on a Mondrian.

FIG. 9 presents a Mondrian of BAC AC008172 (bases 25,000 to 130,000 shown), containing the carbamyl phosphate synthetase gene (AF154830.1). Purple background within the  
 30 region shown as field 81 in FIG. 3 indicates all 37 known exons for this gene.

As can be seen, GRAIL II successfully identified 27 of the known exons (73%), GENEFINDER successfully identified 37 of the known exons (100%), while DICTION  
 35 identified 7 of the known exons (19%).

Seven of the predicted exons were selected for physical assay, of which 5 successfully amplified by PCR and were sequenced. These five exons were all found to be from the same gene, the carbamyl phosphate synthetase gene (AF154830.1).

The five exons were arrayed, and gene expression measured across 10 tissues. As is readily seen in the Mondrian, the five chip sequences on the array show identical expression patterns, elegantly demonstrating the reproducibility of the system.

FIG. 10 is a Mondrian of BAC AL049839. We selected 12 exons from this BAC, of which 10 successfully sequenced, which were found to form between 5 and 6 genes. Interestingly, 4 of the genes on this BAC are protease inhibitors. Again, these data elegantly show that exons selected from the same gene show the same expression patterns, depicted below the red line. From this figure, it is clear that our ability to find known genes is very good. A novel gene is also found from 86.6 kb to 88.6 kb, upon which all the exon finding programs agree. We are confident we have two exons from a single gene since they show the same expression patterns and the exons are proximal to each other. Backgrounds in the following colors indicate a known gene (top to bottom):

- red = kallistatin protease inhibitor (P29622);
- purple = plasma serine protease inhibitor (P05154);
- turquoise =  $\alpha$ 1 anti-chymotrypsin (P01011); mauve = 40S ribosomal protein (P08865). Note that chip sequence 8 and 12 did not sequence verify.

30

#### EXAMPLE 4

Genome-Derived Single Exon Probes Useful For Measuring Human Gene Expression

The protocols set forth in Examples 1 and 2, *supra*, were applied to additional human genomic sequence as it became newly available in GenBank. 5,081 unique exons in the human genome that could be shown to be expressed at significant levels in heart tissue were identified.

These unique exons are within longer probe sequences. Each probe was completely sequenced on both strands prior to its use on a genome-derived single exon microarray; sequencing confirms the exact chemical structure of each probe. An added benefit of sequencing is that it placed us in possession of a set of single base-incremented fragments of the sequenced nucleic acid, starting from the sequencing primer 3' OH. (Since the single exon probes were first obtained by PCR amplification from genomic DNA, we were of course additionally in possession of an even larger set of single base incremented fragments of each of the 5,202 single exon probes, each fragment corresponding to an extension product from one of the two amplification primers.)

The structures of the 5,202 unique single exon probes are clearly presented in the Sequence Listing as SEQ ID Nos.: 1 - 5,202. The 16 nt 5' primer sequence and 16 nt 3' primer sequence present on the amplicon are not included in the sequence listing. The sequences of the exons present within each of these probes is presented in the Sequence Listing as SEQ ID Nos.: 5,203 - 10,283, respectively. It will be noted that some amplicons have more than one exon, some exons are contained in more than one amplicon.

As detailed in Example 2, expression was demonstrated by disposing the amplicons as single exon probes on nucleic acid microarrays and then performing two-color fluorescent hybridization analysis; significant

expression is based on a statistical confidence that the signal is significantly greater than negative biological control spots. The negative biological control is formed from spotted DNA sequences from a different species. Here,  
 5 32 sequences from E.Coli were spotted in duplicate to give a total of 64 spots.

For each hybridisation (each slide, each colour) the median value of the signal from all of the spots is determined. The normalised signal value is the arithmetic  
 10 mean of the signal from duplicate spots divided by the population median.

Control spots are eliminated if there is more than a five-fold difference between each one of the duplicate spots raw signals.

15 The median of the signal from the remaining control spots is calculated and all subsequent calculations are done with normalised signals.

Control spots having a signal of greater than median + 2.4 (the value 2.4 is roughly 12 times the  
 20 observed standard deviation of control spot populations) are eliminated. Spots with such high signals are considered to be "outliers".

The mean and standard deviation of the modified control spot populations are calculated.

25 The mean + 3x the standard deviation (mean + (3\*SD)) is used as the signal threshold qualifier for that particular hybridisation. Thus, individual thresholds are determined for each channel and each hybridisation.

This means that, assuming that the data is  
 30 distributed normally, there is a 99% confidence that any signal exceeding the threshold is significant.

The probes and their expression data are presented in Table 4, set forth respectively in Example 5. Example 5 presents the subset of probes that is  
 35 significantly expressed in the human heart and thus

presents the subset of probes that was recognized to be useful for measuring expression of their cognate genes in human heart tissue.

The sequence of each of the exon probes identified by SEQ ID NOS.: 5,203 to 10,283 was individually used as a BLAST (or, for SWISSPROT, BLASTX) query to identify the most similar sequence in each of dbEST, SwissProt (BLASTX), and NR divisions of GenBank. Because the query sequences are themselves derived from genomic sequence in GenBank, only nongenic hits from NR were scored.

The smallest in value of the BLAST (or BLASTX) expect ("E") scores for each query sequence across the three database divisions was used as a measure of the "expression novelty" of the probe's ORF. Table 4 is sorted in descending order based on this measure, reported as "Most Similar (top) Hit BLAST E Value". 29 out of the 5081 exons were found to have no similar sequences.

As sorted, Table 4 thus lists its respective probes (by "AMPLICON SEQ ID NO.:" and additionally by the SEQ ID NO.: of the exon contained within the probe:"EXON SEQ ID NO.:") from least similar to sequences known to be expressed (i.e., highest BLAST E value), at the beginning of the table, to most similar to sequences known to be expressed (i.e., lowest BLAST E value), at the bottom of the table.

Table 4 further provides, for each listed probe, the accession number of the database sequence that yielded the "Most Similar (top) Hit BLAST E Value", along with the name of the database in which the database sequence is found ("Top Hit Database Source").

Table 4 further provides SEQ ID NOS. corresponding to the predicted amino acid sequences where they have been determined for the probe and exon nucleotide

sequences. These are set out as PEPTIDE SEQ ID NOS.: The peptide sequences for a given exon are predicted as follows: Since each chip exon is a consensus sequence drawn from predictions from various exon finding programs (i.e. 5 Grail, GeneFinder and GenScan), the multiple initial ORFs are first determined in a uniform way according to each prediction. In particular, the reading frame for predicting the first amino acid in the peptide sequence always starts with the first base of any codon and ends with the last 10 base of non-termination codon. Next, for each strand of the exon, initial ORFs are merged into one or more final ORFs in an exhaustive process based on the following criteria: 1) the merging ORFs must be overlapping, and 2) the merging ORFs must be in the same frame.

15           The Sequence Listing, which is a superset of all of the data presented in Table 4, further includes, for each probe, the most similar hit, with accession number and BLAST E value, from the each of the three queried databases.

20           Table 4 further lists, for each probe, a portion of the descriptor for the top hit ("Top Hit Descriptor") as provided in the sequence database. For those ORFs that are similar in sequence, but nonidentical to known sequences (e.g., those with BLAST E values between about  $1e-05$  and 25  $1e-100$ ), the descriptor reveals the likely function of the protein encoded by the probe's ORF.

          Using BLAST E value cutoffs of  $1e-05$  (i.e.,  $1 \times 10^{-5}$ ) and  $1e-100$  (i.e.,  $1 \times 10^{-100}$ ) as evidence of similarity to sequences known to be expressed is of course arbitrary: 30 in Example 2, *supra*, a BLAST E value of  $1e-30$  was used as the boundary when only two classes were to be defined for analysis (unknown,  $>1e-30$ ; known  $<1e-30$ ) (see also FIG. 8). Furthermore, even when the "Most Similar (Top) Hit BLAST E Value" is low, e.g., less than about  $1e-100$  — which is

probative evidence that the query sequence has previously been shown to be expressed – the top hit is highly unlikely exactly to match the probe sequence.

First, such expression entries typically will not  
 5 have the intronic and/or intergenic sequence present within the single exon probes listed in the Table. Second, even the ORF itself is unlikely in such cases to be present identically in the databases, since most of the EST and mRNA clones in existing databases include multiple exons,  
 10 without any indication of the location of exon boundaries.

As noted, the data presented in Table 4 represent a proper subset of the data present within the attached sequence listing. For each amplicon probe (SEQ ID NOs.: 1 – 5,202) and probe exon (SEQ ID NOs.: 5,203 – 10,283,  
 15 respectively), the sequence listing further provides, through iterated annotation fields <220> and <223>:

(a) the accession number of the BAC from which the sequence was derived ("MAP TO"), thus providing a link to the chromosomal map location and other information about  
 20 the genomic milieu of the probe sequence;

(b) the most similar sequence provided by BLAST query of the EST database, with accession number and BLAST E value for the "hit";

(c) the most similar sequence provided by BLAST  
 25 query of the GenBank NR database, with accession number and BLAST E value for the "hit"; and

(d) the most similar sequence provided by BLASTX query of the SWISSPROT database, with accession number and BLAST E value for the "hit".

30

#### EXAMPLE 5

Genome-Derived Single Exon Probes Useful For Measuring  
 Expression of Genes in Human Heart

35

Table 4 presents expression, homology, and functional information for the genome-derived single exon probes that are expressed significantly in human heart.



Table 4

AMPLICON SEQ ID NO:	EXON SEQ ID NO:	PEPTIDE SEQ ID NO:	EXPRESSION	HIT EVALUE	HIT ACCESSION	DATASET	HIT DESCRIPTION
286	5473	10603	0.7				
287	5473	10603	0.7				
442	5608	10741	1.5				
871	6019	11178	5.8				
1029	6169		0.7				
1280	6410	11571	2.7				
1597	6723	11893	0.7				
1619	6745	11913	1.8				
1694	6818	11999	1.0				
1715	6838	12017	1.0				
1721	6844	12023	2.7				
1848	6966	12152	1.0				
1935	7052	12245	1.1				
2119	7230	12439	1.0				
2233	7340	12552	0.8				
2893	8044	13144	5.9				
3003	8155	13255	1.0				
3003	8155	13256	1.0				
3149	8298	13407	3.7				
3403	8545	13653	1.5				
3471	8612	13724	9.0				
3513	8654		0.9				
3607	8746	13841	1.0				
4102	8228	14313	1.7				
4164	9290	14370	5.9				
4184	9310	14390	0.9				
4184	9310	14391	0.9				
4242	9367		1.0				
4730	9842	14934	1.8				
4779	9889		0.8				
4976	10079	15149	5.1				
4988	10091	15161	2.1				
578	5738	10854	0.7	9.80E+00	AA442238.1	EST_HUMAN	z61901.a1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:758160.3
2631	7721	12921	1.0	9.40E+00	L11433.1	NT	Dengue virus type 3 membrane protein (prM/M)/envelope glycoprotein (E) polyprotein mRNA, partial cds
2631	7721	12921	1.0	9.40E+00	L11433.1	NT	Dengue virus type 3 membrane protein (prM/M)/envelope glycoprotein (E) polyprotein mRNA, partial cds

Table 4

433	5600	10731	0.6	8.40E+00	5031804	NT	Homo sapiens insulin receptor substrate 1 (IRS1) mRNA
2947	8098	13203	4.2	7.20E+00	L12051.1	NT	Lycopodium obscurum Mill. GTPase (SAR2) mRNA, complete cds
2947	8098	13204	4.2	7.20E+00	L12051.1	NT	Lycopodium obscurum Mill. GTPase (SAR2) mRNA, complete cds
3479	8620		0.8	5.80E+00	7661557	NT	Homo sapiens DESC1 protein (DESC1), mRNA
4675	9787	14886	1.5	5.30E+00	L43126.1	NT	Bovine immunodeficiency-like virus surface envelope gene, 5' end of cds
3972	9104		9.4	4.80E+00	AF185255.1	NT	Eucalia australis histone H3 (H3) gene, partial cds
3236	8384	13480	4.0	4.70E+00	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080
3459	8600	13713	3.9	3.90E+00	X64518.1	NT	N. labacum chitinase gene 50 for class I chitinase C
4228	9350		1.0	3.80E+00	AF055466.1	NT	Mus musculus seminal vesicle secretory protein 99 (MSVSP99) gene, promoter region
2586	7681		0.9	3.80E+00	AE001562.1	NT	Helicobacter pylori, strain J99 section 123 of 132 of the complete genome
3936	9070	14154	10.1	3.70E+00	AL161539.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 39
							Enterobacter agglomerans Cole-1-like plasmid RNA one modulator (rom) gene, complete cds
3946	9079		5.1	3.70E+00	AF014880.1	NT	Cryptosporidium felis heat shock protein 70 (HSP70) gene, partial cds
3209	8357	13466	1.0	3.50E+00	AF221538.1	NT	Brassica napus RPB5d mRNA, complete cds
1486	6622	11792	1.3	3.40E+00	AF254577.1	NT	Homo sapiens chromosome 21 segment HS21C078
2532	7626	12830	1.0	3.40E+00	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C078
5036	10136	15211	1.4	3.30E+00	7662155	NT	Homo sapiens KIAA0480 gene product (KIAA0480), mRNA
5036	10136	15212	1.4	3.30E+00	7662155	NT	Homo sapiens KIAA0480 gene product (KIAA0480), mRNA
482	5657	10780	1.4	3.20E+00	X96422.1	NT	D. rerio zp-50 POU gene
3938	5657	10780	0.8	3.20E+00	X96422.1	NT	D. rerio zp-50 POU gene
4482	9602		1.5	3.20E+00	AL403571.1	NT	M. musculus DNA for GFP-binding fragment GFPB27
2807	7959	13067	1.1	3.00E+00	8923884	NT	M. musculus hyphothetical protein PRO0889 (PRO0889), mRNA
1964	7080	12279	0.9	2.90E+00	AE002225.2	NT	Chlamydia pneumoniae AR39, section 53 of 64 of the complete genome
							Rattus norvegicus pore-forming calcium channel alpha-1B subunit variant a mRNA, alternatively spliced product, complete cds
2114	7225	12433	1.1	2.90E+00	AF05477.1	NT	Buxus harlandii maturase K (malk) gene, partial cds; chloroplast gene for chloroplast product
1441	6568	11744	2.1	2.80E+00	AF186398.1	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 52
1615	6741		1.1	2.80E+00	AL161552.2	NT	Mus musculus per-hexamer repeat gene 3 (Phx3), mRNA
230	5421	10544	1.6	2.70E+00	6678306	NT	Mus musculus per-hexamer repeat gene 3 (Phx3), mRNA
230	5421	10545	1.6	2.70E+00	6678306	NT	Mus musculus per-hexamer repeat gene 3 (Phx3), mRNA
2923	8074	13182	1.5	2.70E+00	4504548	NT	Homo sapiens hexabrachion (hemachin C, cytolactin) (HXB) mRNA
3904	9039	14130	1.5	2.70E+00	AF195052.1	NT	Danio rerio proteasome activator subunit 1 (psme1) mRNA, complete cds
461	5627	10754	1.0	2.60E+00	AE002369.1	NT	Neisseria meningitidis serogroup B strain MC58 section 11 of 206 of the complete genome
461	5627	10755	1.0	2.60E+00	AE002369.1	NT	Neisseria meningitidis serogroup B strain MC58 section 11 of 206 of the complete genome
							Homo sapiens serine palmitoyl transferase, subunit II gene, complete cds, and unknown genes
3526	8667	13771	0.8	2.60E+00	AF111168.2	NT	EST378157 MAGE resequences, MAGE Homo sapiens cDNA
3732	8669	13961	0.8	2.60E+00	AW966084.1	EST_HUMAN	EST378157 MAGE resequences, MAGE Homo sapiens cDNA
3732	8669	13962	0.8	2.60E+00	AW966084.1	EST_HUMAN	EST378157 MAGE resequences, MAGE Homo sapiens cDNA
4576	9693	14785	4.4	2.60E+00	AF068749.1	NT	Mus musculus sphingosine kinase (SPHK1b) mRNA, complete cds

Table 4

1448	6575	11748	0.8	2.50E+00	AJ271844.1	NT	Aspergillus nidulans recQ gene for DNA helicase, exons 1-4
1448	6575	11749	0.8	2.50E+00	AJ271844.1	NT	Aspergillus nidulans recQ gene for DNA helicase, exons 1-4
2503	7600		0.8	2.40E+00	P19532	SWISSPROT	TRANSCRIPTION FACTOR E3
2980	8131	13239	0.9	2.40E+00	M24282.1	NT	Chicken alpha-3 collagen type VI mRNA, 3' end
3201	8349	13462	3.0	2.40E+00	O68906	SWISSPROT	TRYPTOPHAN SYNTHASE ALPHA CHAIN
4816	9925	15017	7.6	2.40E+00	4503352	NT	Homo sapiens double C2-like domains, alpha (DOC2A) mRNA
1233	6382	11524	3.2	2.30E+00	Z46724.1	NT	G-domesticus artificial single chain antibody gene (L3)
1371	6499	11685	0.8	2.30E+00	AF180891.1	NT	Danio rerio fast skeletal muscle myosin light polypeptide 3 (myz3) mRNA, complete cds
2639	7728		1.2	2.30E+00	AL163208.2	NT	Homo sapiens chromosome 21 segment HS21C009
4031	9159		1.3	2.30E+00	AJ401081.1	NT	Bos taurus partial cytb gene for cytochrome b
4216	9340	14423	3.8	2.20E+00	D67071.1	NT	Rat gene for regucalcin, exon1 (non-coding exon)
4216	9340	14424	3.8	2.20E+00	D67071.1	NT	Rat gene for regucalcin, exon1 (non-coding exon)
557	7892	10836	2.3	2.10E+00	AF132612.2	NT	Mus musculus pre-T cell receptor alpha gene, enhancer region and upstream region
830	5979	11140	0.8	2.10E+00	6912721	NT	Homo sapiens tollid-like 1 (TLL1) mRNA
3539	8680		1.2	2.10E+00	AW449366.1	EST_HUMAN	U1-H-B13-ak1e-08-0-U1.s1 NCI_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:2734550.3
3715	8852	13942	1.6	2.10E+00	5835149	NT	Gorilla gorilla mitochondrion, complete genome
3715	8852	13943	1.6	2.10E+00	5835149	NT	Gorilla gorilla mitochondrion, complete genome
3785	8822	14016	1.3	2.10E+00	AF257470.1	NT	Equus caballus calcitonin gene related peptide II precursor mRNA, complete cds
1178	6311	11466	1.2	2.00E+00	AF180527.1	NT	Homo sapiens p22Dokdel (DOKDEL) mRNA, complete cds
1178	6311	11467	1.2	2.00E+00	AF180527.1	NT	Homo sapiens p22Dokdel (DOKDEL) mRNA, complete cds
1313	6441	11608	1.4	2.00E+00	AF204827.1	NT	Oryctolagus cuniculus Na+-K+-ATPase beta 1 subunit mRNA, complete cds
1557	6684		1.1	2.00E+00	P25582	SWISSPROT	PUTATIVE RNA METHYLTRANSFERASE SPB1
2102	7213	12422	1.7	2.00E+00	Z78279.1	NT	R.norvegicus mRNA for collagen alpha1 type I
2102	7213	12423	1.7	2.00E+00	Z78279.1	NT	R.norvegicus mRNA for collagen alpha1 type I
4011	9142	14224	2.1	2.00E+00	AW664496.1	EST_HUMAN	h13c05.x1 NCI_CGAP_GU1 Homo sapiens cDNA clone IMAGE:2972168.3 similar to gb:X01677 Glyceroldehyde 3-phosphate dehydrogenase, liver (HUMAN);
4011	9142	14225	2.1	2.00E+00	AW664496.1	EST_HUMAN	h13c05.x1 NCI_CGAP_GU1 Homo sapiens cDNA clone IMAGE:2972168.3 similar to gb:X01677 Glyceroldehyde 3-phosphate dehydrogenase, liver (HUMAN);
1980	7106		0.7	1.80E+00	AJ010045.1	NT	Mus musculus mRNA for Rho guanine nucleotide-exchange factor, splice variant NET1A
3054	8205	13305	1.7	1.80E+00	P21004	SWISSPROT	PROTEIN B8 PRECURSOR
3082	8233	13331	4.5	1.80E+00	U04356.1	NT	Synechococcus sp. PCC7942 copper transporting P-ATPase (c1aA) and ATP synthase epsilon subunit (a1pE) genes, complete cds
3082	8233	13332	4.5	1.80E+00	U04356.1	NT	Synechococcus sp. PCC7942 copper transporting P-ATPase (c1aA) and ATP synthase epsilon subunit (a1pE) genes, complete cds
564	5726	10842	0.6	1.70E+00	Q14137	SWISSPROT	HYPOTHETICAL PROTEIN KIAA0124
564	5726	10843	0.6	1.70E+00	Q14137	SWISSPROT	HYPOTHETICAL PROTEIN KIAA0124
565	5726	10842	1.1	1.70E+00	Q14137	SWISSPROT	HYPOTHETICAL PROTEIN KIAA0124
565	5726	10843	1.1	1.70E+00	Q14137	SWISSPROT	HYPOTHETICAL PROTEIN KIAA0124

Table 4

1092	6230	11381	0.7	1.70E+00	Q60114	SWISSPROT	LEVANSUCRASE (BETA-D-FRUCTOFURANOSYL TRANSFERASE) (SUCROSE 6-FRUCTOSYL TRANSFERASE)
2225	7332	12545	1.2	1.70E+00	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080
2321	7424	12633	1.0	1.70E+00	AI141067.1	EST_HUMAN	oz43h05.x1 Soares, fetal heart, NbHH19W Homo sapiens cDNA clone IMAGE:1678137.3'
4356	9478	14569	0.8	1.70E+00	Q60114	SWISSPROT	LEVANSUCRASE (BETA-D-FRUCTOFURANOSYL TRANSFERASE) (SUCROSE 6-FRUCTOSYL TRANSFERASE)
5059	10157		1.1	1.70E+00	AA747059.1	EST_HUMAN	in85c08.a1 NC_CGAP_AAV1 Homo sapiens cDNA clone IMAGE:1267118 similar to gb:D00723 GLYCINE CLEAVAGE SYSTEM H PROTEIN PRECURSOR (HUMAN);
1989	7104	12307	6.1	1.60E+00	AF199339.1	NT	Homo sapiens lens epithelium-derived growth factor gene, alternatively spliced, complete cds
1997	7113	12315	1.3	1.60E+00	AF077374.1	NT	Homo sapiens small proline-rich protein (SPRR3) gene, exons 1, 2, and 3 and complete cds
2003	7118	12320	0.7	1.60E+00	Y11344.1	NT	Mus musculus ST6GaiNacIII gene, exon 2
2238	7344		0.5	1.60E+00	X98373.1	NT	B. napus gene encoding endo-polygalacturonase
2931	8082	13190	2.5	1.60E+00	W59426.1	EST_HUMAN	zd25f01.1 Soares, fetal heart, NbHH19W Homo sapiens cDNA clone IMAGE:341689.5' similar to gb:D29805 N-ACETYLACTOSAMINE SYNTHASE (HUMAN);
3795	8932	14026	1.3	1.60E+00	D64006.1	NT	Synechocystis sp. PCC6803 complete genome, 25/27, 3138804-3270709
4255	9380	14460	1.4	1.60E+00	AF155827.1	NT	Homo sapiens proliferation-associated SNF2-like protein (SMARCA6) mRNA, complete cds
4255	9380	14461	1.4	1.60E+00	AF155827.1	NT	Homo sapiens proliferation-associated SNF2-like protein (SMARCA6) mRNA, complete cds
4359	9481	14572	1.2	1.60E+00	U34070.1	NT	Human CCAATenhancer binding protein alpha gene, complete cds
5018	10118	15189	3.1	1.60E+00	Y11344.1	NT	Mus musculus ST6GaiNacIII gene, exon 2
5018	10118	15190	3.1	1.60E+00	Y11344.1	NT	Mus musculus ST6GaiNacIII gene, exon 2
30	5239	10344	1.5	1.50E+00	U53449.1	NT	Rattus norvegicus jun dimerization protein 2 (jdp-2) mRNA, complete cds
231	5422	10546	0.6	1.50E+00	AE002201.2	NT	Chlamydomonas reinhardtii ACP39, section 32 of 94 of the complete genome
605	5763		0.6	1.50E+00	6752961	NT	Mus musculus a disintegrin and metalloproteinase domain (ADAM) 15 (metargidin) (Adam15), mRNA
2359	7461	12667	0.9	1.50E+00	AJ131402.1	NT	Potato virus A RNA complete genome, isolate U
2468	7566	12769	0.7	1.50E+00	6678350	NT	Mus musculus T-cell lymphoma invasion and metastasis 1 (Tiam1), mRNA
3099	7461	12667	2.2	1.50E+00	AJ131402.1	NT	Potato virus A RNA complete genome, isolate U
3329	8473	13586	0.8	1.50E+00	AE001945.1	NT	Deinococcus radiodurans R1 section 82 of 229 of the complete chromosome 1
27	5236	10340	1.3	1.40E+00	7661685	NT	Homo sapiens DKFZP586M0122 protein (DKFZP586M0122), mRNA
27	5236	10341	1.3	1.40E+00	7661685	NT	Homo sapiens DKFZP586M0122 protein (DKFZP586M0122), mRNA
2231	7338		1.0	1.40E+00	AF053357.1	NT	Helicobacter pylori glutamine synthetase (glnA) gene, complete cds
2286	7391		3.4	1.40E+00	U67922.1	NT	Ovis aries prion protein gene, complete cds
2634	7723	12826	0.6	1.40E+00	X74463.1	NT	Human papillomavirus type 7 genomic DNA
2746	7830	13032	1.2	1.40E+00	AF064564.2	NT	Fugu rubripes neurofibromatosis type 1 (NF1), A-kinase anchor protein (AKAP84), BAW protein (BAW), and WSB1 protein (WSB1) genes, complete cds
2746	7830	13033	1.2	1.40E+00	AF064564.2	NT	Fugu rubripes neurofibromatosis type 1 (NF1), A-kinase anchor protein (AKAP84), BAW protein (BAW), and WSB1 protein (WSB1) genes, complete cds

Table 4

3034	8186	13287	1.0	1.40E+00	AE002324.2	NT	Chlamydia muridarum, section 55 of the complete genome
3034	8186	13288	1.0	1.40E+00	AE002324.2	NT	Chlamydia muridarum, section 55 of the complete genome
3291	8437		0.9	1.40E+00	5453733	NT	Homo sapiens Mad4 homolog (MAD4) mRNA
4162	9288	14367	1.1	1.40E+00	AW900455.1	EST_HUMAN	CMU-NN1005-140300-286-106 NN1005 Homo sapiens cDNA
4162	9288	14368	1.1	1.40E+00	AW900455.1	EST_HUMAN	CMU-NN1005-140300-286-106 NN1005 Homo sapiens cDNA
5137	10232		0.8	1.40E+00	Q07869	SWISSPROT	PEROXISOME PROLIFERATOR ACTIVATED RECEPTOR ALPHA (PPAR-ALPHA)
248	5436	10582	0.6	1.30E+00	U67587.1	NT	Methanococcus jannaschii section 129 of 150 of the complete genome
248	5436	10583	0.6	1.30E+00	U67587.1	NT	Methanococcus jannaschii section 129 of 150 of the complete genome
558	5720		0.6	1.30E+00	Z73840.1	NT	M. muscauda gene encoding 4-Dihydroxyethyl-trisporate dehydrogenase
572	7862		0.8	1.30E+00	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
884	6032	11191	0.9	1.30E+00	AL271192.1	NT	Cantharellus sp. partial 25S rRNA gene, isolate Tibet
1113	6250		5.6	1.30E+00	Y19213.1	NT	Homo sapiens putative psin-H4 pseudogene for hair keratin, exons 2 to 7
1275	6405	11565	3.7	1.30E+00	4507998	NT	Homo sapiens zinc finger protein 157 (HZF22) (ZNF157) mRNA
1275	6405	11566	3.7	1.30E+00	4507998	NT	Homo sapiens zinc finger protein 157 (HZF22) (ZNF157) mRNA
1334	6463		0.6	1.30E+00	U61730.2	NT	Cox lacryma-jobi dihydrodipicolinate synthase (dapA) gene, complete cds
							ic24e03.x1 Soares_t04us_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:2065564 3' similar to contains Alu repetitive element; contains element MERR22 repetitive element ;
1361	6489		1.4	1.30E+00	AI375930.1	EST_HUMAN	Chlamydia muridarum, section 66 of 85 of the complete genome
1593	6719		0.8	1.30E+00	AE002338.2	NT	Cyprinus carpio MRPB and MASP genes for mannose-binding lectin-associated serine protease (MASP) and MASP-related protein, complete cds
2196	7305		2.1	1.30E+00	AB030447.1	NT	Mus musculus alpha-spectrin 1, erythroid (Spna1) mRNA
2809	8059	13164	1.1	1.30E+00	6755621	NT	Mus musculus alpha-spectrin 1, erythroid (Spna1) mRNA
							Fugu rubripes gamma-aminobutyric acid receptor beta subunit gene, partial cds; 55kd erythrocyte membrane protein (P55), synaptic vesicle-associated integral membrane protein (VAMP-1), procollagen C-proteinase enhancer protein (PCOLCE) genes, complete c>
3547	8688	13790	1.0	1.30E+00	AF016494.1	NT	Synechocystis sp. PCC6803 complete genome, 10/27, 1188886-1311234
3902	9037	14128	1.0	1.30E+00	D90908.1	NT	Mus musculus alpha-spectrin 1, erythroid (Spna1) mRNA
4502	8059	13164	0.8	1.30E+00	6755621	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 2
4623	9737	14833	1.3	1.30E+00	AL161472.2	NT	Plasmodium relictum partial 83/AMA-1 gene for apical membrane antigen 1
4864	10087	15139	1.0	1.30E+00	AJ252087.1	NT	Plasmodium relictum partial 83/AMA-1 gene for apical membrane antigen 1
4864	10087	15140	1.0	1.30E+00	AJ252087.1	NT	Zf22d08.s1 Soares_f04el_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:431535
							3'
634	5793	10918	2.8	1.20E+00	AA676246.1	EST_HUMAN	HISTIDINE-RICH PROTEIN PRECURSOR (CLONE PFHRP-II)
806	5957	11110	1.3	1.20E+00	P05228	SWISSPROT	HISTIDINE-RICH PROTEIN PRECURSOR (CLONE PFHRP-II)
806	5957	11111	1.3	1.20E+00	P05228	SWISSPROT	HISTIDINE-RICH PROTEIN PRECURSOR (CLONE PFHRP-II)
806	5957	11112	1.3	1.20E+00	P05228	SWISSPROT	HISTIDINE-RICH PROTEIN PRECURSOR (CLONE PFHRP-II)
860	6008		0.8	1.20E+00	8924234	NT	Homo sapiens hypothetical protein PRO3077 (PRO3077) mRNA
1145	6280	11433	1.9	1.20E+00	AF080245.2	NT	Elaeis oleifera sesquiterpene synthase mRNA, complete cds
1187	6319	11475	0.6	1.20E+00	AJ252242.1	NT	pes seed-borne mosaic virus complete genome
1187	6319	11476	0.6	1.20E+00	AJ252242.1	NT	pes seed-borne mosaic virus complete genome
1563	7079	12278	1.1	1.20E+00	AF140631.1	NT	Homo sapiens G-protein coupled receptor 14 (GPR14) gene, complete cds

Table 4

3072	8223	13321	1.0	1.20E+00	AB020681.1	NT	Homo sapiens mRNA for KIAA0874 protein, partial cds
3128	8277	13383	5.4	1.20E+00	AL161563.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 63
3128	8277	13384	5.4	1.20E+00	AL161563.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 63
3249	8396		2.9	1.20E+00	PS4910	SWISSPROT	CONUGAL TRANSFER PROTEIN TRBE PRECURSOR
3311	8456	13570	0.8	1.20E+00	AF188740.1	NT	Homo sapiens LHX3 gene, intron 2
3312	8457		1.0	1.20E+00	M81778.1	NT	G.gallus T-cadherin mRNA, complete cds
3650	8769	13882	7.3	1.20E+00	U75902.1	NT	Mus musculus subtilisin-like serine protease LPC (PC7) gene, exons 1 to 9, partial cds
4201	8456	13570	1.1	1.20E+00	AF188740.1	NT	Homo sapiens LHX3 gene, intron 2
4298	9422	14513	1.4	1.20E+00		NT	Rattus norvegicus Glycine receptor alpha 2 subunit (glycine receptor, neonatal) (Gir2), mRNA
4371	9493		1.6	1.20E+00	M87060.1	NT	Rattus rattus cardiac AEC3 gene, exons 1-23
4422	9542	14634	1.3	1.20E+00	AL161509.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 21
4460	9580	14677	1.8	1.20E+00	AF156495.1	NT	Homo sapiens post-synaptic density 95 (DLG4) gene, complete cds
4485	9605		5.4	1.20E+00	Y09200.1	NT	T.pinnatum chloroplast rbcL gene, partial
4584	8457		0.9	1.20E+00	M81779.1	NT	G.gallus T-cadherin mRNA, complete cds
4584	8457	10749	1.1	1.10E+00	D86980.1	NT	Human mRNA for KIAA0227 gene, partial cds
4584	8457	10749	1.1	1.10E+00	D86980.1	NT	Human mRNA for KIAA0227 gene, partial cds
1726	6849	12028	1.4	1.10E+00	AW995393.1	EST_HUMAN	QV0-BN0042-170300-163-g12 BN0042 Homo sapiens cDNA
1857	6975	12160	0.9	1.10E+00	AW575889.1	EST_HUMAN	U1-HF-BR0p-alk-1-02-Q-U1.1 NIH_MGC_52 Homo sapiens cDNA clone IMAGE:3074834.3'
2870	8021	13123	1.0	1.10E+00	AB040955.1	NT	Homo sapiens mRNA for KIAA1522 protein, partial cds
2971	8122	13229	0.8	1.10E+00		NT	Homo sapiens alcohol dehydrogenase 7 (class IV), mu or sigma polypeptide (ADH7) mRNA
2971	8122	13229	0.8	1.10E+00	4501940	NT	Homo sapiens alcohol dehydrogenase 7 (class IV), mu or sigma polypeptide (ADH7) mRNA
2971	8122	13230	0.8	1.10E+00	4501940	NT	Homo sapiens alcohol dehydrogenase 7 (class IV), mu or sigma polypeptide (ADH7) mRNA
3288	8433	13541	6.6	1.10E+00	AL163213.2	NT	Homo sapiens chromosome 21 segment HS21C013
3288	8433	13542	6.6	1.10E+00	AL163213.2	NT	Homo sapiens chromosome 21 segment HS21C013
3441	8583	13697	0.9	1.10E+00	8922641	NT	Homo sapiens hypothetical protein FLJ10749 (FLJ10749), mRNA
3468	8609	13721	1.0	1.10E+00	N84066.1	EST_HUMAN	KK4629F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA clone KK4629.5' similar to ORF-RELATED TO ACTIN BUNDLING PROTEIN (DEMATIN)
3510	8651		1.3	1.10E+00	8922973	NT	Homo sapiens hypothetical protein FLJ11280 (FLJ11280), mRNA
3531	8672	13776	1.0	1.10E+00	AI808360.1	EST_HUMAN	Homo sapiens hypothetical protein FLJ11280 (FLJ11280), mRNA
3557	8796	13889	1.2	1.10E+00	AE003886.1	NT	w54h11.1, x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2359461.3' similar to SW:P531_HUMAN Q12888 P53-BINDING PROTEIN 53BP1
3657	8796	13890	1.2	1.10E+00	AE003886.1	NT	Xyella fastidiosa, section 32 of 229 of the complete genome
3678	8817	13910	17.8	1.10E+00	5729757	NT	Xyella fastidiosa, section 32 of 229 of the complete genome
3682	8998	14097	1.0	1.10E+00	8922641	NT	Homo sapiens calpain 9 (mCL-4) (CAPN9) mRNA
4122	9248		5.9	1.10E+00	5835331	NT	Homo sapiens hypothetical protein FLJ10749 (FLJ10749), mRNA
4860	9867	15052	1.2	1.10E+00	L23195.1	NT	R.unicornis complete mitochondrial genome
4821	10028	15105	2.9	1.10E+00	U18466.1	NT	Drosophila melanogaster cytoplasmic dynein heavy chain mRNA, complete cds
4999	10102	15170	1.2	1.10E+00	X78425.1	NT	African swine fever virus, complete genome
92	5289		1.2	1.00E+00	U23808.1	NT	E.faecalis pbp5 gene
							Xenopus laevis rhodopsin gene, complete cds

Table 4

108	5311	10436	1.1	1.00E+00	D88425.1	NT	Cavia cobaya mRNA for serine/threonine kinase, complete cds
412	5580		0.7	1.00E+00	AB021684.1	NT	Marchantia polymorpha genes for 26S rRNA, 5S rRNA, 16S rRNA, 5.8S rRNA and 26S rRNA
562	5724	10840	1.1	1.00E+00	AL251660.1	NT	Giardia tigrina mRNA for homeodomain transcription factor (so gene)
661	5817	10945	1.5	1.00E+00	AL163218.2	NT	Homo sapiens chromosome 21 segment HS21C018
663	5819		1.0	1.00E+00	AF125984.1	NT	Aedes aegypti mucin-like protein MUC1 mRNA, complete cds
1364	7914		1.0	1.00E+00	X80416.1	NT	V-center Algal-CAM mRNA
1722	6845	12024	1.3	1.00E+00	AB006531.1	NT	Plautia stali intestine virus RNA for nonstructural polyprotein, capsid protein precursor, complete cds
1977	7092		0.5	1.00E+00	P02704	SWISSPROT	PROCOLIPASE A PRECURSOR
2435	7534	12740	0.5	1.00E+00	P48355	SWISSPROT	DNA GYRASE SUBUNIT B
2435	7534	12741	0.5	1.00E+00	P48355	SWISSPROT	DNA GYRASE SUBUNIT B
2651	7740	12940	1.1	1.00E+00	AF131205.1	NT	Mus musculus Serf1 protein (Serf1), survival of motor neuron protein (Snm), neuronal apoptosis inhibitory protein-rs6 (Nalp-rs6), and neuronal apoptosis inhibitory protein-rs3 (Nalp-rs3) genes, complete cds
2646	7997	13093	3.5	1.00E+00	P24008	SWISSPROT	3-OXO-5-ALPHA-STEROID 4-DEHYDROGENASE 1 (STEROID 5-ALPHA-REDUCTASE 1) (SR TYPE 1)
2846	7997	13094	3.5	1.00E+00	P24008	SWISSPROT	3-OXO-5-ALPHA-STEROID 4-DEHYDROGENASE 1 (STEROID 5-ALPHA-REDUCTASE 1) (SR TYPE 1)
2938	8069		1.0	1.00E+00	O14226	SWISSPROT	HYPOTHETICAL 67.9 KD PROTEIN C6F12.08C IN CHROMOSOME 1
3162	8311	13423	1.2	1.00E+00	AA628453.1	EST_HUMAN	af26g08.s1 Soares_tetal Telus_Nb2H-F8_9w Homo sapiens cDNA clone IMAGE:1032830 3' similar to WP-C42D8.3 CE04204 :contains element MER22 MER22 repetitive element ;
3277	8422	13530	1.9	1.00E+00	AF260827.1	NT	Ipomoea batatas cysteine protease mRNA, complete cds
3327	8471		0.8	1.00E+00	AF222761.1	NT	Rattus norvegicus neuromedin U precursor (NimU) gene, exons 5 and 6
3548	5299		1.2	1.00E+00	U23808.1	NT	Xenopus laevis rhodopsin gene, complete cds
3627	8766	13860	1.4	1.00E+00	AL223816.1	NT	Agaricus bisporus mRNA for tyrosinase
3683	8822	13915	1.3	1.00E+00	U89198.1	NT	Geococcyx velox cytochrome b (cytb) gene, mitochondrial gene encoding mitochondrial protein, complete cds
3683	8822	13916	1.3	1.00E+00	U89198.1	NT	Geococcyx velox cytochrome b (cytb) gene, mitochondrial gene encoding mitochondrial protein, complete cds
3978	9110	14192	0.9	1.00E+00	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
4178	9304		0.8	1.00E+00	8822245	NT	Homo sapiens hypothetical protein FLJ10139 (FLJ10139), mRNA
4632	9746		5.9	1.00E+00	Q09472	SWISSPROT	E1A-ASSOCIATED PROTEIN P300
4815	9824		0.9	1.00E+00	U75741.1	NT	Taenia ovis 45IV antigen (TOW4) gene, complete cds
4862	9869	15054	0.9	1.00E+00	AL163281.2	NT	Homo sapiens chromosome 21 segment HS21C081
4951	10056		0.9	1.00E+00	D10852.1	NT	Rattus norvegicus mRNA for N-acetylglucosaminyltransferase III, complete cds
5139	10234	15309	0.9	1.00E+00	AL223978.1	NT	Bacillus subtilis 42.7kD DNA fragment from ysaA to ysaA
1553	6680	11847	0.8	9.90E-01	AF245455.1	NT	Drosophila melanogaster regulator of G-protein signalling LOGO III mRNA, complete cds
1553	6680	11848	0.8	9.90E-01	AF245455.1	NT	Drosophila melanogaster regulator of G-protein signalling LOCO III mRNA, complete cds

Table 4

2598	7689	12892	0.9	9.90E-01	AL163302.2	NT	Homo sapiens chromosome 21 segment HS21C102
3553	8693		1.2	9.90E-01	AF174585.1	NT	Apple mosaic virus RNA 2 putative polymerase gene, complete cds
512	5676	10797	0.8	9.80E-01	P22667	SWISSPROT	AMINO-ACID ACETYLTRANSFERASE (N-ACETYLGLUTAMATE SYNTHASE) (AGS)
5106	10202		1.0	9.70E-01	AI660384.1	EST_HUMAN	we62e04.x1 Soares thyroid NHPTb Homo sapiens cDNA clone IMAGE:2345694.3
2645	7734	12935	0.6	9.60E-01	AJ400877.1	NT	Homo sapiens ASC3 gene, CEGP1 gene, C11orf14 gene, C11orf15 gene, C11orf16 gene and C11orf17 gene
4337	9460	14548	6.8	9.60E-01	AF197925.1	NT	Bromus inermis putative cytosolic phosphoglucomutase (pgm1) mRNA, complete cds
4337	9460	14549	6.8	9.60E-01	AF197925.1	NT	Bromus inermis putative cytosolic phosphoglucomutase (pgm1) mRNA, complete cds
4355	9477	14568	1.3	9.60E-01	AW799674.1	EST_HUMAN	PM2-UM0053-240300-005-112 UM0053 Homo sapiens cDNA
5083	10181	15261	0.9	9.60E-01	7662375	NT	Homo sapiens KIAA0914 gene product (KIAA0914), mRNA
3186	8335	13447	1.5	9.50E-01	P22149	SWISSPROT	IRON-REGULATED TRANSCRIPTIONAL REPRESSOR AFT1
1087	6225	11376	0.8	9.40E-01	6671685	NT	Mus musculus calenin src (Cats), mRNA
1087	6225	11377	0.8	9.40E-01	6671685	NT	Mus musculus calenin src (Cats), mRNA
3165	8314		3.4	9.40E-01	AF165990.1	NT	Bartonella clarridgeiae RNA polymerase beta subunit (rpoB) gene, partial cds
3181	8330		1.7	9.40E-01	AF080585.1	NT	Pimplinella brachycarpa zinc finger protein (ZFP1) mRNA, complete cds
1700	6623		1.1	9.30E-01	AF242382.1	NT	Homo sapiens phytanoyl-CoA hydroxylase (PHYH) gene, exon 5
2594	7686	12889	1.1	9.30E-01	BE071172.1	EST_HUMAN	RC5-BT0503-271199-011-B01 BT0503 Homo sapiens cDNA
3949	9082	14162	0.8	9.30E-01	M20219.1	NT	Bovine papillomavirus type 2, complete genome
3949	9082	14163	0.8	9.30E-01	M20219.1	NT	Bovine papillomavirus type 2, complete genome
4567	9685	14779	1.3	9.30E-01	X06083.1	NT	Calothrix cpeB3 and cpeA3 gene for phycoerythrin 3 subunits beta and alpha
5155	10250		1.5	9.30E-01	AF075615.1	NT	Equus caballus microsatellite LEX013
3658	8797	13891	1.0	9.20E-01	Z74263.1	NT	S. cerevisiae chromosome IV reading frame ORF YDL215c
2077	7189		0.5	9.10E-01	8923056	NT	Homo sapiens hypothetical protein FLJ20048 (FLJ20048), mRNA
3169	8318	13430	1.0	9.10E-01	T26418.1	EST_HUMAN	AB2006GR Infant brain, LLNL array of Dr. M. Soares 1N1B Homo sapiens cDNA clone LAB200G8 5'
3169	8318	13431	1.0	9.10E-01	T26418.1	EST_HUMAN	AB2006GR Infant brain, LLNL array of Dr. M. Soares 1N1B Homo sapiens cDNA clone LAB200G8 5'
4310	9433	14523	0.9	9.10E-01	U68172.1	NT	Rattus norvegicus mucin (MUC2) gene, partial cds
1285	6415	11578	4.8	9.00E-01	R02285.1	EST_HUMAN	ye65e12.s1 Soares fetal liver spleen 1N1FLS Homo sapiens cDNA clone IMAGE:124558.3 similar to gb:K03002.60S RIBOSOMAL PROTEIN L32 (HUMAN);
3170	8319	13432	0.9	9.00E-01	7661625	NT	Homo sapiens DKFZP564M2423 protein (DKFZP564M2423), mRNA
4282	9407	14491	2.4	9.00E-01	AF099810.1	NT	Homo sapiens neurexin III-alpha gene, partial cds
4919	10026	15104	1.5	9.00E-01	UB4903.1	NT	Mus musculus L23 mitochondrial-related protein (L23mrp) gene, complete cds
4945	10050	15121	0.8	9.00E-01	AF017729.1	NT	Oryctolagus cuniculus Rad51 (RAD51) mRNA, complete cds
1064	6202	11356	0.7	8.80E-01	AE001358.1	NT	Chlamydia trachomatis section 85 of 87 of the complete genome
1064	6202	11357	0.7	8.80E-01	AE001358.1	NT	Chlamydia trachomatis section 85 of 87 of the complete genome
3988	9120	14204	1.5	8.80E-01	AF079764.1	NT	Drosophila melanogaster enhancer of polycomb (E(Pc)) mRNA, complete cds
4442	9562	14658	3.3	8.80E-01	O26350	SWISSPROT	PUTATIVE F420-DEPENDENT NADP REDUCTASE
457	5623	10750	0.5	8.70E-01	AF106953.2	NT	Homo sapiens SOS1 (SOS1) gene, partial cds
2353	7455	12662	1.1	8.70E-01	5901893	NT	Homo sapiens AT-binding transcription factor 1 (ATBF1), mRNA



Table 4

2845	7996	13092	4.6	8.70E-01	AA595863.1	EST_HUMAN	nm0511.s1 NCI_CGAP_P4.1 Homo sapiens cDNA clone IMAGE:107877
4938	10044		2.5	8.70E-01	AF121970.1	NT	Pseudomonas aeruginosa topoisomerase (top), putative transcriptional regulatory protein
466	5631		0.6	8.60E-01	X17012.1	NT	OhbR (ohbR), ortho-halobenzoate 1,2-dioxygenase beta-ISP protein OhbA (ohbA), OhbC (ohbC), ortho-halobenzoate 1,2-dioxygenase alpha-ISP protein OhbB (ohbB), and putative
840	5989	11150	1.2	8.60E-01	W69089.1	EST_HUMAN	Rat GFII gene for insulin-like growth factor II
2224	7331	12544	1.0	8.60E-01	4503210	NT	zd44a03.r1 Soares_fetal_heart_NbHH19W Homo sapiens cDNA clone IMAGE:343516.5
3566	8707	13805	0.8	8.60E-01	AL161565.2	NT	Homo sapiens cytochrome P450, subfamily XXVIIA (steroid 27-hydroxylase, cerebrotendinous xanthomatosis), polypeptide 1 (CYP27A1b) mRNA
3730	8867	13959	1.3	8.60E-01	U49724.1	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 65
5046	10146	15224	1.0	8.60E-01	AE002239.2	NT	Drosophila melanogaster merlin (Dmerlin) mRNA, complete cds
3930	9084	14151	3.1	8.50E-01	AI215418.1	EST_HUMAN	Chlamydia pneumoniae AR39, section 67 of 94 of the complete genome
2006	7120	12321	1.1	8.40E-01	AA078112.1	EST_HUMAN	qh11b01.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1844329.3
4108	9234	14317	0.8	8.40E-01	AF143509.1	NT	7H14C04 Chromosome 7 HeLa cDNA Library Homo sapiens cDNA clone 7H14C04
5045	10145	15223	1.0	8.40E-01	AA078112.1	EST_HUMAN	Mus musculus NK cell receptor 2B4 gene, promoter region and partial cds
724	5878	11018	0.8	8.30E-01	M93437.1	NT	7H14C04 Chromosome 7 HeLa cDNA Library Homo sapiens cDNA clone 7H14C04
3056	8207	13306	2.6	8.30E-01	AL161508.2	NT	Thermus thermophilus cytochrome c-552 (cyca) and Cyb8 (cycb) genes, complete cds
3739	8876	13966	1.0	8.30E-01	AB010878.1	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 18
4628	9742		1.9	8.30E-01	AF083221.1	NT	Nicotiana tabacum mRNA for chloroplast ribosomal protein L10, complete cds
4917	10024	15102	1.1	8.30E-01	U46916.1	NT	Fugu rubripes putative neurotransmitter receptors, YDR140w homolog, and glycamide
4917	10024	15103	1.1	8.30E-01	U46916.1	NT	ribonucleotide transferase (GART) genes, complete cds
5177	10024	15102	1.0	8.30E-01	U46916.1	NT	Canis familiaris MHC DLA Class II DRB pseudogene DRB2
5177	10024	15103	1.0	8.30E-01	U46916.1	NT	Canis familiaris MHC DLA Class II DRB pseudogene DRB2
2043	7156		0.5	8.20E-01	AF145589.1	NT	Canis familiaris MHC DLA Class II DRB pseudogene DRB2
2646	7735		1.1	8.20E-01	AW376990.1	EST_HUMAN	Mus musculus trophoblast (Tnm) gene, complete cds
4308	9431	14520	1.2	8.10E-01	7662285	NT	IL3-CTD219-181189-031-C08 CT0219 Homo sapiens cDNA
2731	7815		1.3	8.10E-01	AF191839.1	NT	Homo sapiens KIAA0769 gene product (KIAA0769), mRNA
3412	8554	13662	2.8	8.10E-01	AF055066.1	NT	Homo sapiens TANK binding kinase TBK1 (Tbk1) mRNA, complete cds
3412	8554	13663	2.8	8.10E-01	AF055066.1	NT	Mus musculus TANK binding kinase TBK1 (Tbk1) mRNA, complete cds
170	5364		1.0	8.00E-01	AJ271510.1	NT	Homo sapiens MHC class I region
285	5472	10602	1.3	8.00E-01	AJ132772.1	NT	Homo sapiens MHC class I region
763	5916	11063	1.1	8.00E-01	AF208153.1	NT	Staphylococcus aureus partial pla gene for phosphatase acyltransferase allele 15
1603	6730	11902	1.2	8.00E-01	Z54199.1	NT	Bos taurus tub and rtf genes
3039	8191	13293	2.7	8.00E-01	AF127897.1	NT	Drosophila americana texana strain LP97.09 transformer (tra) gene, tra-D_arn.01 allele, partial cds
3273	8418	13525	1.1	8.00E-01	AB006193.1	NT	L.esculentum DNA Alisa Craig encoding 1-aminocyclopropane-1-carboxylic acid oxidase
							Salmonella typhimurium olfactory receptor (SBO27) gene, partial cds
							Mus musculus gene for olfactory glycoprotein, complete cds

Table 4

3643	8782	1.8	8.00E-01	AL162758.2	NT	Neisseria meningitidis serogroup A strain Z2491 complete genome; segment 7/7
4432	9553	5.7	8.00E-01	X83739.2	NT	G.gallus mRNA for nicotinic acetylcholine receptor (nAChR) beta 3 subunit
446	5612	1.3	7.90E-01	D11476.1	NT	Lymantria dispar nuclear polyhedrosis virus gene for DNA polymerase, complete cds
698	5853	1.2	7.90E-01	AE002130.1	NT	Ureaplasma urealyticum section 31 of 59 of the complete genome
1587	6713	66.0	7.90E-01	AB040885.1	NT	Homo sapiens mRNA for KIAA1452 protein, partial cds
1634	6760	1.4	7.90E-01	U32739.1	NT	Haemophilus influenzae Rd section 54 of 163 of the complete genome
2216	7324	1.9	7.90E-01	AB004816.1	NT	Oryzias latipes cuticular mRNA for mitsugumin28, complete cds
2217	7325	0.8	7.90E-01	AF130459.1	NT	Danio rerio Trp-associated protein Tap1a (tap1a) mRNA, complete cds
3472	8613	2.8	7.90E-01	AF228664.1	NT	Gallus gallus SOX8 transcription factor (SOX8) mRNA, complete cds
4204	9329	0.9	7.90E-01	BE263612.1	EST_HUMAN	601192033F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3535785 5'
4508	9627	1.0	7.90E-01	6753745	NT	Mus musculus embigin (Emb), mRNA
4508	9627	1.0	7.90E-01	6753745	NT	Mus musculus embigin (Emb), mRNA
5075	10173	0.8	7.90E-01	Z47210.1	NT	S.pneumoniae dexB, cap3A, cap3B and cap3C genes and orfs
5075	10173	0.8	7.90E-01	Z47210.1	NT	S.pneumoniae dexB, cap3A, cap3B and cap3C genes and orfs
5084	10182	1.0	7.90E-01	M29930.1	NT	Human insulin receptor (allele 2) gene, exons 14, 15, 16 and 17
858	6006	0.6	7.80E-01	Z43785.1	EST_HUMAN	HSC1KH041 normalized infant brain cDNA Homo sapiens cDNA clone c-1kh04
2229	7336	1.2	7.80E-01	AW959567.1	EST_HUMAN	EST371637 MAGE resequences, MAGEF Homo sapiens cDNA
4803	9717	0.8	7.80E-01	U87305.1	NT	Rattus norvegicus transmembrane receptor Unc5h1 mRNA, complete cds
138	5334	2.2	7.70E-01	AF184345.1	NT	Lycopodium obscurum ADP-glucose pyrophosphorylase large subunit (AGP-L1) mRNA, complete cds
708	5863	0.6	7.70E-01	AF050157.1	NT	Mus musculus major histocompatibility locus class II region: major histocompatibility protein class II alpha chain (Iaalpha) and major histocompatibility protein class II beta chain (Ibbeta) genes, complete cds; butyrophilin-like (NG9), butyrophilin-1l>
772	5924	0.7	7.70E-01	P02921	SWISSPROT	MELIBIOSE CARRIER PROTEIN (THOMETHYL GALACTOSIDE PERMEASE II) (MELIBIOSE PERMEASE) (NA+ (L+)/MELIBIOSE SYMPORTER) (MELIBIOSE TRANSPORTER)
2680	7767	1.0	7.70E-01	O33915	SWISSPROT	CITRATE SYNTHASE
3313	8458	0.8	7.70E-01	8393408	NT	Homo sapiens UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylglucosaminyltransferase 7 (GALNAc-TT) (GALNAc-TT), mRNA
3549	8689	4.5	7.70E-01	AF118085.1	NT	Homo sapiens PRO1975 mRNA, complete cds
3722	8859	2.3	7.70E-01	6753425	NT	Mus musculus cytokine inducible SH2-containing protein (Cish), mRNA
4297	9421	2.9	7.70E-01	AF199488.1	NT	Coturnix coturnix japonica sub-species japonica beta-actin mRNA, partial cds
4297	9421	2.9	7.70E-01	AF199488.1	NT	Coturnix coturnix japonica sub-species japonica beta-actin mRNA, partial cds
502	5666	0.5	7.50E-01	AL163301.2	NT	Homo sapiens chromosome 21 segment HS21C101
569	5730	0.8	7.50E-01	AF020503.1	NT	Homo sapiens FFA3B common fragile region, diadenosine triphosphate hydrolase (FHTT) gene, exon 5
1972	7087	0.9	7.50E-01	4505834	NT	Homo sapiens polycystic kidney disease 2 (autosomal dominant) -NOTE: redefinition of symbol (PKD2) mRNA
3315	8460	0.9	7.50E-01	C14203.1	EST_HUMAN	C14203 Clontech human aorta polyA+ mRNA (#6572) Homo sapiens cDNA clone GEN-037E11 5'
4573	5305	13.9	7.50E-01	8922672	NT	Homo sapiens hypothetical protein FLJ10793 (FLJ10783), mRNA

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Table 4

1288	6418	11581	0.8	6.90E-01	AA593530.1	EST_HUMAN	m28a09.s1 NCI_CGAP_Gas1 Homo sapiens cDNA clone IMAGE:1085176.3
3182	8331	13443	1.6	6.90E-01	AE002271.2	NT	Chlamydia muridarum, section 3 of 85 of the complete genome
3341	8485	13599	2.6	6.90E-01	6677734	NT	Mus musculus rat guanine nucleotide dissociation stimulator (Rgds), mRNA
3399	8541	13649	0.9	6.90E-01	Y17373.1	NT	Mus musculus mRNA for immunoglobulin gamma heavy chain variable region, isolate PC 2811
941	6088	11245	1.0	6.80E-01	AF017784.1	NT	Giardia intestinalis carbamate kinase gene, complete cds
2789	6724	11894	0.6	6.80E-01	AA654475.1	EST_HUMAN	aJ75a05.s1 Soares_papillary_tumor_NbHPA Homo sapiens cDNA clone IMAGE:1402256.3 similar to gp:X56411_ma1 ALCOHOL DEHYDROGENASE CLASS II PI CHAIN (HUMAN);
4469	9589	14685	1.3	6.80E-01	J00762.1	NT	Rat(hooded) prolactin gene : exon III and flanks
4749	9860	14952	0.8	6.80E-01	4758521	NT	Homo sapiens hevN (HEVIN) mRNA
295	5481	10612	10.0	6.70E-01	AF213884.1	NT	Homo sapiens nuclear factor of kappa light polypeptide gene enhancer in B-cells 1 (NFKB1) gene, complete cds
336	5517	10642	6.7	6.70E-01	AF213884.1	NT	Homo sapiens nuclear factor of kappa light polypeptide gene enhancer in B-cells 1 (NFKB1) gene, complete cds
2100	7211	12419	0.6	6.70E-01	AA451864.1	EST_HUMAN	Zx12g12.s1 Soares_total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:786310.3 similar to contains element TAR1 repetitive element ;
2120	7835	12440	1.3	6.70E-01	AF186073.1	NT	Drosophila melanogaster Mst85C gene, complete cds; NMIMC isoform (Nmdmc) gene, complete cds, alternatively spliced; and transcription factor (Relish) gene, complete cds, alternatively spliced
2968	8117	13224	3.7	6.70E-01	6678580	NT	Mus musculus Wiskott-Aldrich syndrome protein (Wasp), mRNA
4350	9472	14564	1.0	6.70E-01	X74421.1	NT	S.tuberosum mRNA for glucose-6-phosphate dehydrogenase
4881	9889	15070	0.9	6.70E-01	AW079110.1	EST_HUMAN	xa9g12.x1 NCI_CGAP_Co17 Homo sapiens cDNA clone IMAGE:2574598.3
5182	10274	15343	0.9	6.70E-01	AJ252942.1	NT	Dendrobium fibroblast mRNA for phosphoenolpyruvate carboxylase, partial
2452	7551	12759	0.9	6.60E-01	AF075240.1	NT	Homo sapiens SLIT1 protein (SLIT2) mRNA, partial cds
2667	7754	12954	1.3	6.60E-01	AF199339.1	NT	Homo sapiens lens epithelium-derived growth factor gene, alternatively spliced, complete cds
3445	8587	13700	1.0	6.60E-01	4506880	NT	Homo sapiens sema domain, seven thrombospondin repeats (type 1 and type 1-like), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 5A (SEMA5A) mRNA
3484	8625	13737	1.1	6.60E-01	AB011536.1	NT	Homo sapiens mRNA for MEGF2, partial cds
3484	8625	13738	1.1	6.60E-01	AB011536.1	NT	Homo sapiens mRNA for MEGF2, partial cds
3608	8747	13842	3.1	6.60E-01	Y07689.1	NT	C.albicans random DNA marker, 282bp
4020	9149		0.9	6.60E-01	U91328.1	NT	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, RoRet gene, and sodium phosphate transporter (NPT3) gene, complete cds
608	5766	10884	1.4	6.50E-01	M75140.1	NT	H.vulgaris Na,K-ATPase alpha subunit mRNA, complete cds
608	5766	10885	1.4	6.50E-01	M75140.1	NT	H.vulgaris Na,K-ATPase alpha subunit mRNA, complete cds
3386	8529	13636	5.1	6.50E-01	AB041225.1	NT	Mus musculus gene for Tob2, complete cds
3951	9084	14165	1.1	6.50E-01	4504632	NT	Homo sapiens interleukin 10 receptor, alpha (IL10RA) mRNA
4165	9311	14392	4.2	6.50E-01	AJ272265.1	NT	Homo sapiens SPP2 gene for secreted phosphoprotein 24 precursor, exons 1-8

Table 4

4215	9339	14422	0.9	6.50E-01	AL161539.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 39
4894	10097	15164	2.3	6.50E-01	U28921.1	NT	Phaseolus vulgaris ATPase gamma subunit mRNA, nuclear gene encoding mitochondrial protein, partial cds
5031	10131	15207	1.0	6.50E-01	4826799	NT	Homo sapiens potassium inwardly-rectifying channel, subfamily J, member 5 (KCNJ5) mRNA
5175	10269		0.9	6.50E-01	U37258.1	NT	Acetabacter xylinum putative ATP binding protein delta-AceB gene, partial cds, and GDP-mannose:cellulobiosyl-diphosphopropylprenol alpha-mannosyltransferase gene, complete cds
252	5440	10567	1.8	6.40E-01	U48848.1	NT	Drosophila melanogaster Bld drayn light chain mRNA, complete cds
3410	8552	13660	2.5	6.40E-01	U48854.2	NT	Mus musculus dystroglycan 1 (DAG1) gene, exons 1 and 2 and complete cds
4389	9511	14598	0.8	6.40E-01	Y12488.1	NT	Musculus whn gene
4389	9511	14599	0.8	6.40E-01	Y12488.1	NT	Musculus whn gene
427	5594	10728	1.5	6.30E-01	P05228	SWISSPROT	HISTIDINE-RICH PROTEIN PRECURSOR (CLONE PEHRP-III)
524	5686	10809	0.7	6.30E-01	U32689.1	NT	Haemophilus influenzae Rd section 4 of 163 of the complete genome
							EST55935 Pineal gland II Homo sapiens cDNA 5' end similar to orthodenticle-related protein 1
1505	6831	11800	1.5	6.30E-01	AA365227.1	EST_HUMAN	Shigella flexneri multi-antibiotic resistance locus
2116	7227	12435	1.4	6.30E-01	U81136.1	NT	Gallus gallus bone morphogenetic protein 1 (BMP1) mRNA, partial cds
2534	7630	12832	1.4	6.30E-01	U75331.1	NT	Gallus gallus bone morphogenetic protein 1 (BMP1) mRNA, partial cds
2534	7630	12833	1.4	6.30E-01	U75331.1	NT	Gallus gallus bone morphogenetic protein 1 (BMP1) mRNA, partial cds
2983	8135		0.9	6.30E-01	Y17275.1	NT	Lycopodium obscurum p68a gene, complete CDS
3985	9117	14200	1.4	6.30E-01	X98675.1	NT	D.melanogaster mRNA for metabotropic glutamate receptor
4755	9866	14959	1.5	6.20E-01	4504402	NT	Homo sapiens major histocompatibility complex, class II, DO beta (HLA-DOB) mRNA
5002	10105	15173	1.0	6.20E-01	AI587039.1	EST_HUMAN	Homo sapiens major histocompatibility complex, class II, DO beta (HLA-DOB) mRNA
2345	7447		1.6	6.10E-01	6678076	NT	contains element MSR1 repetitive element
2856	8107		1.3	6.10E-01	AF153704.1	NT	Mus musculus secreted acidic cysteine rich glycoprotein (Sparc) mRNA
							Tetrahymena thermophila dynein heavy chain (DYH8) gene, partial cds
4931	10037	15109	1.0	6.10E-01	L20427.1	NT	Rattus norvegicus dihydroxyphenylbenzoate methyltransferase mRNA, complete cds
4931	10037	15110	1.0	6.10E-01	L20427.1	NT	Rattus norvegicus dihydroxyphenylbenzoate methyltransferase mRNA, complete cds
486	5651	10775	0.9	6.00E-01	D87675.1	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
549	5712		0.9	6.00E-01	5802999	NT	Homo sapiens adaptor-related protein complex 3, mu 2 subunit (CLAU20) mRNA
1339	6467	11635	0.6	6.00E-01	AF065253.1	NT	Human respiratory syncytial virus strain CH93-53b attachment protein (G) gene, complete cds
3744	8881	13970	1.0	6.00E-01	AJ233336.1	NT	Viral haemorrhagic septicaemia virus N, P, M, G, Nv, L genes, French strain 07-71
984	8129	11284	1.3	5.90E-01	U32701.1	NT	Haemophilus influenzae Rd section 16 of 163 of the complete genome
2354	7456	12663	2.3	5.90E-01	AI859966.1	EST_HUMAN	hm2201.x1 NCI CGAP U4 Homo sapiens cDNA clone IMAGE:2436697 3'
3232	8380	13486	4.9	5.90E-01	AL163267.2	NT	Homo sapiens chromosome 21 segment HS21C067
3232	8380	13487	4.9	5.90E-01	AL163267.2	NT	Homo sapiens chromosome 21 segment HS21C067
4129	9255		4.1	5.90E-01	AF162756.1	NT	Rattus norvegicus cennexin 2 mRNA, partial cds
1867	6885	12169	0.5	5.80E-01	P40472	SWISSPROT	SIM1 PROTEIN

Table 4

3401	8543	13651	2.0	5.80E-01	AF154923.1	NT	Mycoplasma arthritis strain H39 putative adhesin MAA1 (maa1) gene, complete cds
3900	9035	14127	1.0	5.80E-01	7662059	NT	Homo sapiens KIAA0335 gene product (KIAA0335), mRNA
4413	9533	14622	2.8	5.80E-01	AB009077.1	NT	Vigna radiata mRNA for proton pyrophosphatase, complete cds
4690	9802		1.0	5.80E-01	AF110846.1	NT	Megascelia scalaris sex-lethal homolog (Megsx) gene, partial cds, alternatively spliced products
764	5917	11064	2.0	5.70E-01	D83536.2	NT	Escherichia coli genomic DNA, (4.1 - 6.1 min)
1840	7928	12144	0.9	5.70E-01	AB024336.1	NT	Mus musculus mRNA for membrane-bound transferin-like protein p97, complete cds
1840	7928	12145	0.9	5.70E-01	AB024336.1	NT	Mus musculus mRNA for membrane-bound transferin-like protein p97, complete cds
3460	8601		2.4	5.70E-01	AB033503.1	NT	Populus euphratica peacs-2 mRNA for 1-aminocyclopropane-1-carboxylate synthase, complete cds
3829	8966	14065	1.7	5.70E-01	AF011581.1	NT	Homo sapiens T cell receptor beta chain (BV6S72-BJ1S1) mRNA, partial cds
5201	10292	15359	2.2	5.70E-01	U78517.1	NT	Rattus norvegicus cAMP-regulated guanine nucleotide exchange factor II (cAMP-GEFII) mRNA, partial cds
3318	8463	13575	1.2	5.60E-01	AB018283.2	NT	Homo sapiens mRNA for KIAA0740 protein, partial cds
3318	8463	13576	1.2	5.60E-01	AB018283.2	NT	Homo sapiens mRNA for KIAA0740 protein, partial cds
3808	8945	14041	0.8	5.60E-01	AL161501.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 13
4146	9272	14350	0.8	5.60E-01	D83135.1	NT	Chicken TBP gene, exon8, complete cds
4726	9838	14930	0.8	5.60E-01	7330334	NT	Homo sapiens chloride intracellular channel 4 like (CLIC4L), mRNA
1193	6325	11481	1.1	5.50E-01	8393912	NT	Rattus norvegicus Protonyl Coenzyme A carboxylase, beta polypeptide (Pccb), mRNA
2668	7755	12955	1.0	5.50E-01	P03341	SWISSPROT	GAG POLYPROTEIN (CONTAINS: INNER COAT PROTEIN P12; CORE PROTEIN P15; CORE SHELL PROTEIN P30; NUCLEOPROTEIN P10)
2668	7755	12956	1.0	5.50E-01	P03341	SWISSPROT	GAG POLYPROTEIN (CONTAINS: INNER COAT PROTEIN P12; CORE PROTEIN P15; CORE SHELL PROTEIN P30; NUCLEOPROTEIN P10)
2888	8039	13140	1.3	5.50E-01	5902085	NT	Homo sapiens superkiller virulicidic activity 2 (S. cerevisiae homolog)-like (SKIV2L), mRNA
3027	8179		1.4	5.50E-01	H46219.1	EST_HUMAN	yo18a10.s1 Soares adult brain N2b5HB55Y Homo sapiens cDNA clone IMAGE:178266 3'
3196	8345	13458	3.1	5.50E-01	AF227240.1	NT	Rabbit oral papillomavirus, complete genome
3634	8773	13867	1.3	5.50E-01	P48755	SWISSPROT	FOS-RELATED ANTIGEN-1
139	5335	10465	1.3	5.40E-01	7657286	NT	Homo sapiens KIAA0929 protein Msz2 interacting nuclear target (MINT) homolog (KIAA0929), mRNA
139	5335	10466	1.3	5.40E-01	7657266	NT	Homo sapiens KIAA0929 protein Msz2 interacting nuclear target (MINT) homolog (KIAA0929), mRNA
570	5731	10848	0.9	5.40E-01	AF232006.1	NT	Pseudomonas syringae pv. tomato strain DC3000 AvrE (avrE), HrpV (hrpV), and GsIA (gsIA) genes, complete cds; and unknown genes
570	5731	10849	0.9	5.40E-01	AF232006.1	NT	Pseudomonas syringae pv. tomato strain DC3000 AvrE (avrE), HrpV (hrpV), and GsIA (gsIA) genes, complete cds; and unknown genes
1250	6379	11538	0.8	5.40E-01	AW896087.1	EST_HUMAN	GVA-NN0040-070400-160-c04 NN0040 Homo sapiens cDNA
2059	7171		1.0	5.40E-01	AEO02247.2	NT	Chlamydia pneumoniae AR39, section 74 of 94 of the complete genome
2208	7317	12530	0.8	5.40E-01	AL276682.1	NT	Drosophila melanogaster mRNA for 15.15 beta carotene dioxygenase (beta-diox gene)

Table 4

505	5669	10792	0.7	5.30E-01	AF019413.1	NT	Homo sapiens HLA class III region containing tenascin X (tenascin-X) gene, partial cds: cytochrome P450 21-hydroxylase (CYP21B), complement component C4 (C4B) G11, helicase (SKIZW), RD, complement factor B (Bf), and complement component C2 (C2) genes, >
2093	7204	12409	0.9	5.30E-01	AF113919.1	NT	Brassica oleracea var. capitata phospholipase D2 (PLD2) gene, complete cds
2093	7204	12410	0.9	5.30E-01	AF113919.1	NT	Brassica oleracea var. capitata phospholipase D2 (PLD2) gene, complete cds
2332	7435	12643	0.9	5.30E-01	4506210	NT	Homo sapiens proteasome (prosome, macropain) 26S subunit, ATPase, 3 (PSM3) mRNA
2755	7839	13040	3.0	5.30E-01	4506328	NT	Homo sapiens protein tyrosine phosphatase, receptor-type, zeta polypeptide 1 (PTPRZ1) mRNA
2755	7839	13041	3.0	5.30E-01	4506328	NT	Homo sapiens protein tyrosine phosphatase, receptor-type, zeta polypeptide 1 (PTPRZ1) mRNA
2755	7839	13041	3.0	5.30E-01	4506328	NT	Homo sapiens secreted C-type lectin precursor (SLC) gene, complete cds
3205	8353	13463	2.9	5.30E-01	AF087658.1	NT	Xenopus laevis LDL receptor-1 gene, 5' flank
3919	9053		2.6	5.30E-01	M62977.1	NT	Mycoplasma genitalium section 9 of 51 of the complete genome
4117	9243		1.3	5.30E-01	U39687.1	NT	Drosophila melanogaster helix-loop-helix mRNA, complete cds
789	5950	11100	3.9	5.20E-01	L20770.1	NT	NUCLEAR FACTOR OF ACTIVATED T CELLS 5 (T CELL TRANSCRIPTION FACTOR NFAT5) (NF-A15) (REL DOMAIN-CONTAINING TRANSCRIPTION FACTOR NFAT5)
1148	6283	11436	2.6	5.20E-01	G9WV30	SWISSPROT	Homo sapiens phospholipid scramblase 1 gene, complete cds
1174	6308	11462	1.0	5.20E-01	AF224492.1	NT	Homo sapiens chromosome 21 segment HS21C085
1843	6961		1.8	5.20E-01	AL163285.2	NT	Homo sapiens mRNA for KIAA0740 protein, partial cds
2099	7210	12418	1.0	5.20E-01	AB016283.2	NT	Homo sapiens mRNA for KIAA0740 protein, partial cds
3081	8232	13330	1.9	5.20E-01	U65942.1	NT	Chlamydomonas reinhardtii lsd gene for isocitrate dehydrogenase, complete cds
3199	8348		1.2	5.20E-01	D73443.1	NT	Azotobacter vinelandii lsd gene for isocitrate dehydrogenase, complete cds
3359	8502		1.8	5.20E-01	AL116780.1	NT	Botrytis cinerea strain T4 cDNA library under conditions of nitrogen deprivation
3397	8539	13646	1.9	5.20E-01	AA984165.1	EST_HUMAN	ant77g05.s1 StrataGene schizo brain S11 Homo sapiens cDNA clone IMAGE:1616504.3'
3580	8719		1.1	5.20E-01	AF020269.1	NT	Medicago sativa chloroplast malate dehydrogenase precursor (p1mdh) mRNA, nuclear gene encoding chloroplast protein, complete cds
3582	8721	13819	1.1	5.20E-01	U82671.2	NT	Homo sapiens chromosome Xq28 melanoma antigen family A2a (MAGEA2A), melanoma antigen family A12 (MAGEA12), melanoma antigen family A2b (MAGEA2B), melanoma antigen family A3 (MAGEA3), calreticulin (CALT), NAD(P)H dehydrogenase-like protein (NSDHL), and L1>
4949	10054		1.3	5.20E-01	7106444	NT	Mus musculus vanilloid receptor-like protein 1 (Vr1), mRNA
601	5759	10879	0.6	5.10E-01	M58509.1	NT	Human adenodoxin reductase gene, exons 3 to 12
632	5791	10913	1.1	5.10E-01	AJ233944.1	NT	Polyangium vitellinum (strain P1 vt1) 16S rRNA gene
632	5791	10914	1.1	5.10E-01	AJ233944.1	NT	Polyangium vitellinum (strain P1 vt1) 16S rRNA gene
1632	6758		1.1	5.10E-01	X87685.1	NT	R. norvegicus mRNA for mammalian fusca protein
3984	9116	14199	3.8	5.10E-01	AB58495.1	EST_HUMAN	w39b12.x1 NC1 CGAP U11 Homo sapiens cDNA clone IMAGE:2427263.3'
4094	9220	14303	2.9	5.10E-01	P96380	SWISSPROT	TRANSCRIPTION-REPAIR COUPLING FACTOR (TRCF)
2087	7199	12403	1.4	5.00E-01	4885552	NT	Homo sapiens postmeiotic segregation increased 2-like 9 (PMS2L9), mRNA

Table 4

2087	7199	12404	1.4	5.00E-01	4885552	NT	Homo sapiens postmeiotic segregation increased 2-like 9 (PMS2L9) mRNA
2097	7208	12414	1.3	5.00E-01	AF008210.1	NT	Buchnera aphidicola genomic fragment containing (chaperone Hsp60) groEL, DNA biosynthesis initiating protein (dnaA), ATP operon (atpCDGAHFEb), and putative chromosome replication protein (gldA) genes, complete cds; and termination factor Rho (rho) gene>
2097	7208	12415	1.3	5.00E-01	AF008210.1	NT	Buchnera aphidicola genomic fragment containing (chaperone Hsp60) groEL, DNA biosynthesis initiating protein (dnaA), ATP operon (atpCDGAHFEb), and putative chromosome replication protein (gldA) genes, complete cds; and termination factor Rho (rho) gene>
2543	7639	12839	0.9	5.00E-01	U50730.2	NT	Human cyclin-dependent kinase 2 (cdk2) gene, 5' promoter region
2543	7639	12840	0.9	5.00E-01	U50730.2	NT	Human cyclin-dependent kinase 2 (cdk2) gene, 5' promoter region
3688	8826	13920	0.8	5.00E-01	U55574.1	NT	Mus musculus anti-DNA immunoglobulin light chain IgM mRNA, antibody 363p.138, partial cds
3797	8834	14027	3.4	5.00E-01	AB033010.1	NT	Homo sapiens mRNA for KIAA1184 protein, partial cds
1864	6982	12166	1.4	4.90E-01	U40869.1	NT	Cavia porcellus pulmonary surfactant protein A (SP-A) mRNA, complete cds
2111	7222	12431	1.1	4.80E-01	U01852.1	NT	Human ventricular myosin light chain 2 gene, seven exons
4577	9362		1.1	4.80E-01	4504850	NT	Homo sapiens potassium channel, subfamily K, member 5 (TASK-2) (KCNK5) mRNA, and translated products
1950	7067	12263	0.8	4.70E-01	X76636.1	NT	S. tuberosum L. (Desiree) PHA1 mRNA
3674	8813	13907	1.3	4.60E-01	AW818638.1	EST_HUMAN	RC1-ST0278-040400-018-b06 ST0278 Homo sapiens cDNA
5087	10185		1.0	4.50E-01	M11267.1	NT	Bovine steroid 21-hydroxylase gene (P-450-c21) gene, complete cds
965	6110	11266	1.0	4.50E-01	AA29416.1	EST_HUMAN	3550 seq. F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA 5'
1847	6965	12150	1.3	4.50E-01	AB033078.1	NT	Homo sapiens mRNA for KIAA1252 protein, partial cds
1847	6965	12151	1.3	4.50E-01	AB033078.1	NT	Homo sapiens mRNA for KIAA1252 protein, partial cds
1869	6987	12171	0.6	4.50E-01	AE001931.1	NT	Delnoccocus radiodurans R1 section 68 of 229 of the complete chromosome 1
1869	6987	12172	0.6	4.50E-01	AE001931.1	NT	Delnoccocus radiodurans R1 section 68 of 229 of the complete chromosome 1
2841	7992	13090	4.9	4.50E-01	AA677086.1	EST_HUMAN	z155d02.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:454179 3'
3275	8420	13528	4.0	4.50E-01	Q05793	SWISSPROT	BASEMENT MEMBRANE-SPECIFIC HEPARAN SULFATE PROTEOGLYCAN CORE PROTEIN PRECURSOR (HSPG) (PERLECAN) (PLC)
3331	8475	13588	1.1	4.50E-01	AF126378.1	NT	Mus musculus DNA polymerase epsilon catalytic subunit (Pole) gene, exons 2 through 12
3942	9075		1.4	4.50E-01	Q28247	SWISSPROT	COLLAGEN ALPHA 5(IV) CHAIN
3982	9114	14197	1.1	4.50E-01	A1708908.1	EST_HUMAN	as98609.x1 Bartsiad aorta HPLRB6 Homo sapiens cDNA clone IMAGE:2353480 3'
4085	9212		4.0	4.50E-01	AW873495.1	EST_HUMAN	h060902.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:3041810 3'
1991	7107		0.9	4.40E-01	6880503	NT	Mus musculus integral membrane-associated protein 1 (lmap1) mRNA
2340	7442	12650	1.3	4.40E-01	PA9765	SWISSPROT	VASCULAR ENDOTHELIAL GROWTH FACTOR B PRECURSOR (VEGF-B) (VEGF RELATED FACTOR)
3274	8419	13526	1.0	4.40E-01	AF058790.1	NT	Rattus norvegicus Syngap-5 mRNA, complete cds
3274	8419	13527	1.0	4.40E-01	AF058790.1	NT	Rattus norvegicus Syngap-5 mRNA, complete cds
4141	9267		1.3	4.40E-01	BE378707.1	EST_HUMAN	801237139F NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3609393 5'



Table 4

4464	9584	8.5	4.40E-01	AL115324.1	NT	Bovlytis chereia strain T4 cDNA library under conditions of nitrogen deprivation
4924	10031	0.9	4.40E-01	BE141398.1	EST_HUMAN	MR0-HT0078-131289-007-g05 HT0078 Homo sapiens cDNA
405	5573	0.7	4.30E-01	AF155218.1	NT	Caillitrix jacchus MW/LW opsin gene, upstream flanking region
405	5573	0.7	4.30E-01	AF155218.1	NT	Caillitrix jacchus MW/LW opsin gene, upstream flanking region
961	6106	0.7	4.30E-01	AI281909.1	EST_HUMAN	q182d03.x1 NCI CGAP Co14 Homo sapiens cDNA clone IMAGE:1961765 3' similar to contains Alu repetitive element
1585	6711	1.1	4.30E-01	AW866550.1	EST_HUMAN	GV4-SN0024-200400-183-b01 SN0024 Homo sapiens cDNA
2843	7994	1.0	4.30E-01	AW935268.1	EST_HUMAN	CM2-DT0003-010200-077-c01 DT0003 Homo sapiens cDNA
3022	8174	0.9	4.30E-01	AW998477.1	EST_HUMAN	MR0-BN0070-270300-008-g04 BN0070 Homo sapiens cDNA
3221	8369	1.5	4.30E-01	AE000698.1	NT	Aquilae aeolius section 30 of 109 of the complete genome
4059	9186	1.2	4.30E-01	J00306.1	NT	Human somatostatin 1 gene and flanks
4138	9284	1.1	4.30E-01	AB028026.1	NT	Nicotiana tabacum mRNA for granule-bound starch synthase, partial cds
4306	5673	1.0	4.30E-01	AF155218.1	NT	Caillitrix jacchus MW/LW opsin gene, upstream flanking region
4306	5673	1.0	4.30E-01	AF155218.1	NT	Caillitrix jacchus MW/LW opsin gene, upstream flanking region
4875	9982	1.1	4.30E-01	AL161502.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 14
5017	10119	2.1	4.30E-01	Y15839.1	NT	Coellobolus heterostrophus pkc1, fat1 genes
1335	7913	1.0	4.20E-01	Q39102	SWISSPROT	CELL DIVISION PROTEIN FTSH HOMOLOG PRECURSOR
1804	7022	0.9	4.20E-01	AA761653.1	EST_HUMAN	nc24a09.s1 NCI CGAP GCB1 Homo sapiens cDNA clone IMAGE:1288696 3'
3558	8697	4.8	4.20E-01	AE003947.1	NT	Xylella fastidiosa, section 83 of 228 of the complete genome
3585	8724	1.1	4.20E-01	AI280338.1	EST_HUMAN	q194070.x1 Soares NIH/NIHPU S1 Homo sapiens cDNA clone IMAGE:1879945 3'
3803	8940	1.0	4.20E-01	AW835527.1	EST_HUMAN	QV0-L-T0015-180200-127-h01 L-T0015 Homo sapiens cDNA
4545	8664	3.6	4.20E-01	BE073574.1	EST_HUMAN	RC5-BT0559-020300-013-E06 BT0559 Homo sapiens cDNA
4599	9713	5.0	4.20E-01	AA534093.1	EST_HUMAN	n169n01.s1 NCI CGAP P-110 Homo sapiens cDNA clone IMAGE:997777 similar to gb:M33600 HLA CLASS II HISTOCOMPATIBILITY ANTIGEN, DR-1 BETA CHAIN (HUMAN);
4671	9783	3.1	4.20E-01	R13467.1	EST_HUMAN	Y77601.r1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:28278 5'
1078	6216	0.6	4.10E-01	AI905481.1	EST_HUMAN	RC-BT091-210199-142 BT091 Homo sapiens cDNA
1592	6718	1.0	4.10E-01	AI905949.1	EST_HUMAN	PM-BT103-270499-584 BT103 Homo sapiens cDNA
2678	7765	0.6	4.10E-01	7705283	NT	Homo sapiens anaphase-promoting complex subunit 7 (APC7), mRNA
2910	8060	1.8	4.10E-01	AL161536.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 36
2910	8060	1.8	4.10E-01	AL161536.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 36
3263	8410	1.1	4.10E-01	AA908344.1	EST_HUMAN	q194008.s1 Soares NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1505943 3'
4177	9303	2.6	4.10E-01	AJ249207.1	NT	Rhodococcus sp. AD45 isoG, isoH, isoI, isoJ, isoK, isoL, isoM, isoN and isoP genes
4208	9333	1.1	4.10E-01	AA909257.1	EST_HUMAN	om333602.s1 Soares NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1542619 3'
4373	9495	0.8	4.10E-01	R41726.1	EST_HUMAN	Yg11b03.s1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:31814 3'
5185	10277	0.9	4.10E-01	Z99124.1	NT	Bacillus subtilis complete genome (section 21 of 21): from 3999281 to 4214814
1023	6162	1.3	4.00E-01	8404656	NT	Laqueus rubellus mitochondrion, complete genome
1316	6445	1.0	4.00E-01	AF203478.1	NT	Drosophila melanogaster Dalmatian (dm1) mRNA, complete cds
1469	6596	1.5	4.00E-01	6679258	NT	Mus musculus platelet derived growth factor receptor, beta polypeptide (Pdgfrb), mRNA

Table 4

1860	7831	12274	1.2	4.00E-01	Z96933.1	NT	<i>Ascobolus immersus</i> masc2 gene
1960	7931	12275	1.2	4.00E-01	Z96933.1	NT	<i>Ascobolus immersus</i> masc2 gene
2774	5332	10463	1.1	4.00E-01	6678490	NT	<i>Mus musculus</i> ubiquitin-protein ligase e3 component n-recoglin (Ubr1), mRNA
2839	8090	13197	2.2	4.00E-01	AL163280.2	NT	<i>Homo sapiens</i> chromosome 21 segment HS21C080
2939	8090	13198	2.2	4.00E-01	AL163280.2	NT	<i>Homo sapiens</i> chromosome 21 segment HS21C080
							<i>Streptococcus pneumoniae</i> YllC (YllC), YllD (YllD), penicillin-binding protein 2x (pbp2x), and undecaprenyl-phosphate-UDP-MurNAc-pentapeptide phospho-MurNAc-pentapeptide transferase (mtrA) genes, complete cds
3637	8776	13871	1.6	4.00E-01	AF068903.1	NT	Ovis aries partial JD2 gene for T cell receptor delta chain (TCRDJ2), exon 1
3755	8893	13983	3.2	4.00E-01	AJ277511.1	NT	Ovis aries partial JD2 gene for T cell receptor delta chain (TCRDJ2), exon 1
3755	8893	13984	3.2	4.00E-01	AJ277511.1	NT	NADH-PLASTOQUINONE OXIDOREDUCTASE CHAIN 5, CHLOROPLAST
4712	9824		7.3	4.00E-01	Q31849	SWISSPROT	CM4-HT0136-150999-014-09 HT0136 <i>Homo sapiens</i> cDNA
227	5418	10539	0.5	3.90E-01	AW352188.1	EST_HUMAN	Gorilla gorilla carboxy-ester lipase (CEL) gene, complete cds
1356	6484	11651	0.8	3.90E-01	AF206618.1	NT	<i>Homo sapiens</i> mRNA for KIAA1193 protein, partial cds
2605	7695	12899	1.3	3.90E-01	AB033019.1	NT	<i>H. sapiens</i> B-myb gene
2673	7760	12859	2.2	3.90E-01	X82032.1	NT	<i>H. sapiens</i> B-myb gene
2673	7760	12860	2.2	3.90E-01	X82032.1	NT	<i>Sinorhizobium meliloti</i> egf, syb2, cya3 genes and orf3
3058	8209	13308	3.6	3.90E-01	AJ225896.1	NT	<i>Homo sapiens</i> protein kinase PKNbeta (pknbeta), mRNA
154	5330		2.5	3.80E-01	7019486	NT	Olive latent ringspot virus genomic RNA for polyprotein gene
805	5956	11109	0.7	3.80E-01	AJ277435.1	NT	Olive latent ringspot virus genomic RNA for polyprotein gene
848	5997		0.7	3.80E-01	AJ277435.1	NT	<i>Xylella fastidiosa</i> , section 16 of 229 of the complete genome
1827	6946		1.2	3.80E-01	AE003870.1	NT	<i>Homo sapiens</i> DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)
2521	7617	12818	1.2	3.80E-01	AB026898.1	NT	<i>Arabidopsis thaliana</i> putative c-myc-like transcription factor (MYB3R-3) mRNA, complete cds
2524	7620	12821	0.9	3.80E-01	AF214117.1	NT	<i>Mus musculus</i> solute carrier family 1, member 6 (SLC1a6), mRNA
2591	7948	12884	1.6	3.80E-01	6678002	NT	Human immunodeficiency virus type 1 complete genome (isolate 98SE-MP1213)
2972	8123		0.9	3.80E-01	AJ251057.1	NT	<i>Pleurococcus americanus</i> aminopeptidase N (ampN) gene, partial cds
3010	8162	13264	2.0	3.80E-01	AF043383.1	NT	<i>Arabidopsis thaliana</i> DNA, chromosome 4, contig fragment No. 30
3494	8580	13692	7.8	3.80E-01	AL161518.2	NT	<i>wf38b12.x1</i> Soares NFL_T_GBC_S1 <i>Homo sapiens</i> cDNA clone IMAGE:2357855.3'
3494	8635		0.8	3.80E-01	AI807219.1	EST_HUMAN	<i>wf38b12.x1</i> Soares NFL_T_GBC_S1 <i>Homo sapiens</i> cDNA clone IMAGE:2357855.3'
3506	8635		0.9	3.80E-01	AI807219.1	EST_HUMAN	<i>wf38b12.x1</i> Soares NFL_T_GBC_S1 <i>Homo sapiens</i> cDNA clone IMAGE:2357855.3'
3841	8977	14077	0.9	3.80E-01	6754095	NT	<i>Mus musculus</i> general transcription factor II I (Gtf2i), mRNA
2131	7241	12449	1.2	3.70E-01	AF162061.1	NT	<i>Capnomyces stellatus</i> beta-tubulin (btub) gene, partial cds
2431	7530	12735	3.6	3.70E-01	AB037831.1	NT	<i>Homo sapiens</i> mRNA for KIAA1410 protein, partial cds
3414	8556	13665	9.5	3.70E-01	AF056336.1	NT	Danio rerio bone morphogenetic protein 4 precursor (BMP4) gene, complete cds
							OK33c07.x1 Soares_NSF_F8_9W_OT_PA_P_S1 <i>Homo sapiens</i> cDNA clone
4136	9262	14344	6.6	3.70E-01	AI218707.1	EST_HUMAN	IMAGE:1510188.3'
4225	9349	14430	1.5	3.70E-01	AW878037.1	EST_HUMAN	MR3-OT0007-080300-104-b02 OT0007 <i>Homo sapiens</i> cDNA
4292	9416	14506	3.3	3.70E-01	AE002408.1	NT	<i>Neisseria meningitidis</i> serogroup B strain MC58 section 50 of 206 of the complete genome
979	8124		2.4	3.60E-01	U89241.1	NT	Human mlbp gene, partial cds

Table 4

1292	6421	11586	0.9	3.60E-01	T60255.1	EST_HUMAN	Yd03ae05.r1 Soares infant brain 1N18 Homo sapiens cDNA clone IMAGE:24443 5'
1292	6421	11587	0.9	3.60E-01	T80255.1	EST_HUMAN	Yd03ae05.r1 Soares infant brain 1N18 Homo sapiens cDNA clone IMAGE:24443 5'
1874	6992	12177	2.2	3.60E-01	AW590184.1	EST_HUMAN	hg33102.x1 NCI CGAP GC6 Homo sapiens cDNA clone IMAGE:2947419 3'
1874	6992	12178	2.2	3.60E-01	AW590184.1	EST_HUMAN	hg33102.x1 NCI CGAP GC6 Homo sapiens cDNA clone IMAGE:2947419 3'
1908	7025	12214	2.2	3.60E-01	AF216207.1	NT	Mus musculus ribosomal protein S19 (Rps19) gene, complete cds
2007	7121		1.1	3.60E-01	AF056927.1	NT	Rattus norvegicus repeat element associated with the Rasgrt1 gene
2223	7330		1.0	3.60E-01	AB002321.1	NT	Human mRNA for KIAA0323 gene, partial cds
2341	7443		0.9	3.60E-01	X76725.1	NT	P. irregularis (P3804) gene for actin
2437	7536	12743	0.6	3.60E-01	AW812033.1	EST_HUMAN	RC5-ST0171-181099-011-g07 ST0171 Homo sapiens cDNA
							PROTEIN-L-ISOASPARTATE O-METHYLTRANSFERASE (PROTEIN-BETA-ASPARTATE METHYLTRANSFERASE) (PIMT) (PROTEIN L-ISOASPARTYL METHYLTRANSFERASE) (L-ISOASPARTYL PROTEIN CARBOXYL METHYLTRANSFERASE)
2589	7682	12882	0.8	3.60E-01	P24206	SWISSPROT	Drosophila melanogaster sugar transporter 3 (sui3) mRNA, complete cds
2869	8020		8.9	3.60E-01	AF199485.1	NT	H.sapiens serotonin transporter gene, exons 9 and 10
3424	8566	13677	1.9	3.60E-01	X76758.1	NT	H.sapiens serotonin transporter gene, exons 9 and 10
3424	8566	13678	1.9	3.60E-01	X76758.1	NT	H.sapiens serotonin transporter gene, exons 9 and 10
4192	9318	14402	0.9	3.60E-01	BE251129.1	EST_HUMAN	601107183F1 NIH MGC 16 Homo sapiens cDNA clone IMAGE:3343484 5'
4192	9318	14403	0.9	3.60E-01	BE251129.1	EST_HUMAN	601107183F1 NIH MGC 16 Homo sapiens cDNA clone IMAGE:3343484 5'
4635	9749	14844	0.9	3.60E-01	AL009809.1	NT	Brassica napus mRNA for MAPK4 alpha2 protein
4684	9786	14899	1.2	3.60E-01	AF229237.1	NT	Bacteria from anoxic bulk soil 16S rRNA gene (strain XB45)
4941	10047	15119	2.0	3.60E-01	AW339393.1	EST_HUMAN	hna2g04.x1 NCI CGAP Lu24 Homo sapiens cDNA clone IMAGE:2872566 3'
202	5396	10522	0.7	3.50E-01	6878933	NT	Mus musculus mannose receptor, C type 2 (Mrc2), mRNA
682	5818	10946	1.0	3.50E-01	AL161581.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 77
706	5862	10998	1.2	3.50E-01	7706136	NT	Homo sapiens GAP-like protein (LOC51306), mRNA
706	5862	10999	1.2	3.50E-01	7706136	NT	Homo sapiens GAP-like protein (LOC51306), mRNA
1622	6748	11916	1.1	3.50E-01	U35776.1	NT	Rattus norvegicus ADP-ribosylation factor-directed GTPase activating protein mRNA, complete cds
2663	7947	12859	0.7	3.50E-01	AA223252.1	EST_HUMAN	zr08a09.s1 Stratagene NT2 neuronal precursor 937230 Homo sapiens cDNA clone IMAGE:650872 3'
2672	7759		0.9	3.50E-01	U05897.1	NT	Fibrobacter succinogenes S85 endoglucanase E (celE) and endoglucanase D (celD) gene, complete cds
4165	9291	14371	1.9	3.50E-01	AF071253.1	NT	Danio rerio homeobox protein (hoxb5) gene, complete cds
4379	9501	14588	1.3	3.50E-01	BE146585.1	EST_HUMAN	RC5-HT0218-181099-011-g02 HT0218 Homo sapiens cDNA
4790	9901	14994	0.8	3.50E-01	N81203.1	EST_HUMAN	788IE1 fetal brain cDNA Homo sapiens cDNA clone 788IE1-K similar to R07879 240498
4849	9956	15045	3.8	3.50E-01	MT8349.1	NT	Rat leukocyte common antigen (L-CA) gene, exons 1 through 5
691	5846		0.7	3.40E-01	AJ242956.1	NT	Homo sapiens partial N-myc (exon 3), HPV45 L2, HPV45 L1, HPV45 E6, HPV45 E7 and HPV45 E1 genes isolated from IC4 cervical carcinoma cell line
980	6105	11263	1.5	3.40E-01	Y09798.2	NT	Pseudomonas fluorescens colR, colS genes, orf222 and partial inaA gene
1304	6433	11598	0.6	3.40E-01	Y00554.1	NT	Acetobacter vinelandii nifA gene for NifA protein (positive regulatory element)

Table 4

1321	6450	11615	0.6	3.40E-01	AF057083.1	NT	Emvilia carotovora subsp. carotovora aspartate aminotransferase (aat) gene, partial cds; HexA (hexA), NADH dehydrogenase chain A (nuoA), and NADH dehydrogenase chain B (nuoB) genes, complete cds; and NADH dehydrogenase chain C (nuoC) gene, partial cds
2352	7454	12661	1.0	3.40E-01	D90809.1	NT	Synechocystis sp. PCC6803 complete genome, 11/27, 1311235-1430418
2642	7731	12932	1.5	3.40E-01	AL161516.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 28
2679	7766	12967	1.1	3.40E-01	AJ251835.1	NT	Mus musculus Kcnq1, Ltrpc5, Mash2, Tapa-1, Tssc4 and Tssc6 genes, alternative transcripts
3124	8273	13378	5.4	3.40E-01	U83905.1	NT	Canis familiaris rod photoreceptor cGMP-gated channel alpha-subunit (CNGC1) mRNA, complete cds
3486	8629	13741	3.5	3.40E-01	AF106835.1	NT	Methylovorus sp. strain SSt1 putative GrpE (grpE), DnaK (dnaK), and putative DnaJ (dnaJ) genes, complete cds
3965	9097		1.2	3.40E-01	AA584186.1	EST_HUMAN	nc01b10.s1 NCI CGAP Phel Homo sapiens cDNA clone IMAGE:1100347 3'
4394	8516	14606	0.8	3.40E-01	AF166341.1	NT	Homo sapiens integrin alpha 6 (ITGA6) gene, exons 12 through 23
4544	9663	14753	1.8	3.40E-01	BE069912.1	EST_HUMAN	MR4-BT0403-230200-202-c01 BT0403 Homo sapiens cDNA
4645	7766	12967	2.2	3.40E-01	AJ251835.1	NT	Mus musculus Kcnq1, Ltrpc5, Mash2, Tapa-1, Tssc4 and Tssc6 genes, alternative transcripts
4828	9936	15026	0.9	3.40E-01	BE463761.1	EST_HUMAN	hy17d09.x1 NCI CGAP GC6 Homo sapiens cDNA clone IMAGE:3197585 3' similar to contains L1.13 L1 repetitive element;
4870	9977		3.6	3.40E-01	AI240973.1	EST_HUMAN	q95c05.x1 NCI CGAP_Kid3 Homo sapiens cDNA clone IMAGE:1867208 3' similar to contains Alu repetitive element;
4970	10073	15146	1.2	3.40E-01	X16544.1	NT	Sea urchin hsp70 gene II for heat shock protein 70
14	5222	10323	1.3	3.30E-01	X07990.1	NT	Rhizobium leguminosarum sym plasmid pRL511 nodX gene
100	5222	10323	2.7	3.30E-01	X07990.1	NT	Rhizobium leguminosarum sym plasmid pRL511 nodX gene
440	5606	10740	1.2	3.30E-01	AL161545.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 45
617	5776	10898	1.4	3.30E-01		NT	Homo sapiens KIAA1100 protein (KIAA1100), mRNA
1182	6315	11472	1.0	3.30E-01	Q12446	SWISSPROT	PROLINE-RICH PROTEIN LAS17
1588	6714	11884	1.1	3.30E-01	6753685	NT	Mus musculus disintegrin 5 (Dign5), mRNA
1704	6827		1.1	3.30E-01	AA332734.1	EST_HUMAN	EST38722 Embryo, 8 week 1 Homo sapiens cDNA 5' end
2355	7457		1.7	3.30E-01	4507834	NT	Homo sapiens uridine monophosphate synthetase (orotate phosphoribosyl transferase and orotidine-5'-decarboxylase) (UMPS) mRNA
2752	7836	13037	1.1	3.30E-01	AJ132478.1	NT	Chlamydomonas reinhardtii STF1 gene, partial
2760	7844	13046	3.1	3.30E-01	8923039	NT	Homo sapiens hypothetical protein FLJ20036 (FLJ20036), mRNA
2919	8070	13180	2.0	3.30E-01	AJ251805.1	NT	Bacteriophage phi-Y6O3-12 complete genome
2982	8134		1.1	3.30E-01	O02743	SWISSPROT	INTERLEUKIN-12 ALPHA CHAIN PRECURSOR (IL-12A) (CYTOTOXIC LYMPHOCYTE MATURATION FACTOR 35 KD SUBUNIT) (CLMF P35)
3016	8168	13269	1.0	3.30E-01	AJ007932.2	NT	Streptomyces argillaceus mitramycin biosynthetic genes
3450	8592	13705	1.1	3.30E-01	AB012822.1	NT	Homo sapiens MTA1-L1 gene, complete cds
3738	8875	13965	2.2	3.30E-01	084845	SWISSPROT	EXOEXOXYRIBONUCLEASE V BETA CHAIN
3884	9020	14114	1.6	3.30E-01	AL161498.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 10
3920	9064	14141	1.9	3.30E-01	AF200446.1	NT	Hypoxylon fragiforme chitin synthase gene, partial cds

Table 4

4271	9386	2.7	3.30E-01	D31682.1	NT	Rattus norvegicus DNA for regucalcin, partial cds
4569	9703	1.5	3.30E-01	A1539114.1	EST_HUMAN	U78b12.x1 NC1_CGAP_U3 Homo sapiens cDNA clone IMAGE:2205407.3 similar to gb:X57522 ANTIGEN PEPTIDE TRANSPORTER 1 (HUMAN);
5133	10228	1.0	3.30E-01	W30992.1	EST_HUMAN	285b03.r1 Soares_senescent_fibroblasts_NbHSF Homo sapiens cDNA clone IMAGE:310349.5
449	5615	0.7	3.20E-01	AF018261.1	NT	Rattus norvegicus EH domain binding protein Epsin mRNA, complete cds
701	5856	0.7	3.20E-01	AL161561.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 61
1146	6281	6.5	3.20E-01	AF047013.1	NT	Fusarium poae virus 1 RNA2 putative RNA dependent RNA polymerase gene, complete cds
1261	6390	1.0	3.20E-01	Z50202.1	NT	P. vulgaris ar5-1 gene
1366	6496	2.3	3.20E-01	Q46624	SWISSPROT	LACTOSE PERMEASE (LACTOSE-PROTON SYMPORT) (LACTOSE TRANSPORT PROTEIN)
1737	6860	1.2	3.20E-01	Z36041.1	NT	S.cerevisiae chromosome II reading frame ORF YBR172c
1744	6867	2.0	3.20E-01	AW957194.1	EST_HUMAN	EST369264 IMAGE resequences, MAGD Homo sapiens cDNA
1744	6867	2.0	3.20E-01	AW957194.1	EST_HUMAN	EST369264 IMAGE resequences, MAGD Homo sapiens cDNA
1800	6920	1.2	3.20E-01	AL111655.1	NT	Botrytis cinerea strain T4 cDNA library under conditions of nitrogen deprivation
2494	7590	1.1	3.20E-01	7710079	NT	Mus musculus Pdx/knotted 1 homeobox (Pknx1), mRNA
2677	7764	0.6	3.20E-01	AF060568.1	NT	Mus musculus promyelocytic leukemia zinc finger protein (PLZF) gene, complete cds
3556	8695	1.0	3.20E-01	D10872.1	NT	Human h NAT allele 3-2 gene for arylamine N-acetyltransferase
3866	9004	1.0	3.20E-01	AL161546.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 46
4295	9419	1.4	3.20E-01	M16818.1	NT	Rabbit beta-like globin gene cluster encoding the epsilon, gamma, delta (pseudogene) and beta globin polypeptides, complete cds
4375	9497	0.8	3.20E-01	AF111672	NT	Homo sapiens jun dimerization protein gene, partial cds; cds gene, complete cds; and unknown gene
4397	9519	1.3	3.20E-01	Q10268	SWISSPROT	HYPOTHETICAL 81.7 KD PROTEIN C13G7.0AC IN CHROMOSOME I PRECURSOR
4907	10014	1.2	3.20E-01	M32352.1	NT	Mouse retnin (Retn-1-d) gene, complete cds
2636	7725	1.4	3.10E-01	R18051.1	EST_HUMAN	ye90n06.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:125051.5 similar to gb:M64241 QM PROTEIN (HUMAN);
2665	7877	1.3	3.10E-01	7661971	NT	Homo sapiens KIAA0174 gene product (KIAA0174), mRNA
2665	7877	1.3	3.10E-01	7661971	NT	Homo sapiens KIAA0174 gene product (KIAA0174), mRNA
2827	7978	1.0	3.10E-01	AW629036.1	EST_HUMAN	Homo sapiens KIAA0174 gene product (KIAA0174), mRNA
3136	8285	2.8	3.10E-01	AB029089.1	NT	h146n08.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2975391.3
3832	8669	1.2	3.10E-01	AJ251566.1	NT	Mus musculus gene for Ser/Thr kinase KIAAMRE, exon 6
5073	10171	1.0	3.10E-01	AA576308.1	EST_HUMAN	Daucus carota mRNA for transcription factor E2F (E2F gene)
66	7857	0.5	3.00E-01	6755083	NT	mm61h05.s1 NC1_CGAP_813 Homo sapiens cDNA clone IMAGE:1072761.3
254	5442	3.8	3.00E-01	AJ271735.1	NT	Mus musculus protein kinase C, epsilon (Pkcε), mRNA
1204	6336	0.6	3.00E-01	AW300400.1	EST_HUMAN	Homo sapiens Xq pseudautosomal region, segment 1/2
1491	6618	2.3	3.00E-01	AJ006755.1	NT	xs33f08.x1 NC1_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2774343.3
1504	6630	0.9	3.00E-01	A1803369.1	EST_HUMAN	Balanophora physalis gene encoding atrial natriuretic peptide
						tc42c05.x1 Soares_totat_fetus_Nb2H-F8_9w Homo sapiens cDNA clone IMAGE:2067272.3

Table 4

2089	7200	12405	0.9	3.00E-01	AF237778.1	NT	Rattus norvegicus Gas2/calmodulin-dependent protein kinase II, alpha subunit mRNA, 3' untranslated region
3175	8324		1.0	3.00E-01	AB030481.1	NT	Corynebacterium sp. ALV-1 alyPG gene for polygluturonate lyase, complete cds
3709	8847	13937	1.1	3.00E-01	AF229122.1	NT	Homo sapiens acetylcholinesterase collagen-like tail subunit (COLC) gene, exons 11A and 12, and complete cds, alternatively spliced
3789	8926	14020	1.3	3.00E-01	AW817785.1	EST_HUMAN	PM1-ST0262-261199-001-901 ST0262 Homo sapiens cDNA
4104	9230		1.7	3.00E-01	L42123.1	NT	Mus musculus fibroblast growth factor receptor 3 (FGFR3) gene, intron 9
4412	9532	14621	1.9	3.00E-01	AJ006755.1	NT	Balaenoptera physalus gene encoding atrial natriuretic peptide
1038	6178	11331	0.5	2.90E-01	AA090216.1	EST_HUMAN	chp182.seq.f Human fetal heart, Lambda ZAP Express Homo sapiens cDNA, 5'
1100	6238	11390	0.9	2.90E-01	BE066156.1	EST_HUMAN	CMB-BT0320-261199-103-a06 BT0320 Homo sapiens cDNA
1878	7093	12294	0.6	2.90E-01	AE000736.1	NT	Aquilex aedule section 88 of 109 of the complete genome
2201	7310	12521	1.0	2.90E-01	AF222718.1	NT	Chrysodidymus synuroideus mitochondrion, complete genome
3147	8296	13405	1.0	2.90E-01	AF076111.1	NT	Xenopus laevis transcription factor E2F mRNA, complete cds
3213	8361	13471	2.3	2.90E-01	AW754239.1	EST_HUMAN	PM1-CT0326-171299-001-412 CT0326 Homo sapiens cDNA
3213	8361	13472	2.3	2.90E-01	AW754239.1	EST_HUMAN	PM1-CT0326-171299-001-412 CT0326 Homo sapiens cDNA
							lp21a11.x1 NCI CGAP Gas4 Homo sapiens cDNA clone IMAGE:2188412.3' similar to gb:D15050 NIL-2-A ZINC FINGER PROTEIN (HUMAN); contains element L1 repetitive element;
3821	8958	14054	1.3	2.90E-01	AF10836.1	EST_HUMAN	wf02110.x1 NCI CGAP GC6 Homo sapiens cDNA clone IMAGE:2480395.3'
3994	9126		0.8	2.90E-01	AW002902.1	EST_HUMAN	zs57d12.r1 NCI CGAP GC81 Homo sapiens cDNA clone IMAGE:701591.5' similar to contains Alu repetitive element;
4384	9506	14591	1.0	2.90E-01	AA284468.1	EST_HUMAN	Mus musculus SKD1 (Skd1) gene, complete cds
4388	9510	14596	0.8	2.90E-01	AF134119.1	NT	Mus musculus SKD1 (Skd1) gene, complete cds
4388	9510	14597	0.8	2.90E-01	AF134119.1	NT	Mus musculus SKD1 (Skd1) gene, complete cds
4729	9841	14933	0.9	2.90E-01	AB018029.1	NT	Mus musculus gene, complete cds, similar to EXLM1
4903	10010		0.9	2.90E-01	AF119676.1	NT	Mus musculus small GTP-binding protein RAB25 (Rab25) gene, complete cds
556	5719		0.6	2.80E-01	U67136.1	NT	Rattus norvegicus A-kinase anchoring protein AKAP150 mRNA, complete cds
1067	6205	11360	0.8	2.80E-01	AF168050.1	NT	Gulja gulja oocyte maturation factor Mos (C-mos) gene, partial cds
1197	6328	11484	1.1	2.80E-01	AF134404.1	NT	Homo sapiens delta-8 fatty acid desaturase (CYB5RP) mRNA, complete cds
1256	6385	11545	1.1	2.80E-01	BE313442.1	EST_HUMAN	601148733F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3163688.5'
1256	6385	11546	1.1	2.80E-01	BE313442.1	EST_HUMAN	601148733F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3163688.5'
1269	6398	11557	1.0	2.80E-01	D88550.1	NT	Human mRNA for serine/threonine protein kinase, complete cds
1696	6820	12002	0.6	2.80E-01	AW860020.1	EST_HUMAN	QV1-CT0364-120200-065-b05 CT0364 Homo sapiens cDNA
1968	7082	12282	0.6	2.80E-01	AL047620.1	EST_HUMAN	DKFZp586i2321 r1 586 (synonym: hule1) Homo sapiens cDNA clone DKFZp586i2321
2084	7196	12401	0.5	2.80E-01	AW511195.1	EST_HUMAN	h04403.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2912333.3'
							Drosophila melanogaster connector enhancer of KSR protein CNK mRNA, complete cds
2134	7244	12451	0.8	2.80E-01	AF100152.1	NT	CM1-CT0127-160899-005-d01 CT0127 Homo sapiens cDNA
2243	7349		0.9	2.80E-01	AW177111.1	EST_HUMAN	CM1-CT0127-160899-005-d01 CT0127 Homo sapiens cDNA
2423	7522	12729	1.1	2.80E-01	AE000494.1	NT	Escherichia coli K-12 MG1655 section 384 of 400 of the complete genome
2423	7522	12730	1.1	2.80E-01	AE000494.1	NT	Escherichia coli K-12 MG1655 section 384 of 400 of the complete genome
2500	7597		0.9	2.80E-01	AL161665.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 65
2630	7720	12920	1.4	2.80E-01	AB020975.1	NT	Arabidopsis thaliana mRNA for lipoyltransferase, complete cds

Table 4

2940	8091	1.5	2.80E-01	AF179480.1	NT	Toxoplasma gondii 90kDa heat-shock protein (HSP90) mRNA, partial cds
2941	8092	2.5	2.80E-01	Z14037.1	NT	B.taurus microsatellite (ETH121)
2941	8092	2.5	2.80E-01	Z14037.1	NT	B.taurus microsatellite (ETH121)
3095	8246	10.7	2.80E-01	Z73462.1	NT	A.chrysaeos mitochondrial cytochrome b gene
3332	8476	1.1	2.80E-01	AP000004.1	NT	Pyrococcus horikoshii OT3 genomic DNA, 777001-994000 nt. position (4/7)
3704	8842	0.9	2.80E-01	AL161593.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 89
3915	9049	1.8	2.80E-01	AE001180.1	NT	Borrelia burgdorferi (section 66 of 70) of the complete genome
4103	9229	2.2	2.80E-01	AI090866.1	EST_HUMAN	ov44g10.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1640226 3' similar to contains Alu repetitive element; contains element MER22 repetitive element;
4352	9474	1.0	2.80E-01	AL021127.2	NT	Mus musculus chromosome X contigA; putative Magea9 gene, Calitracin, NAD(P) steroid dehydrogenase and Zinc finger protein 185
4357	9479	2.2	2.80E-01	P13615	SWISSPROT	RNA POLYMERASE BETA SUBUNIT (LARGE STRUCTURAL PROTEIN) (L PROTEIN)
4421	9541	1.7	2.80E-01	U58881.1	NT	Mus musculus p53 binding protein 2 homolog (p53BP2), partial cDNA
4525	9644	0.8	2.80E-01	AF032870.1	NT	Drosophila melanogaster Shar pei/DRhogeF2 mRNA, complete cds
4673	9785	1.0	2.80E-01	D15050.1	NT	Human mRNA for transcription factor AREB6, complete cds
4673	9785	1.0	2.80E-01	D15050.1	NT	Human mRNA for transcription factor AREB6, complete cds
4722	9834	2.8	2.80E-01	AF030154.1	NT	Bovine adenovirus 3 complete genome
4771	10303	3.2	2.80E-01	Y10606.1	NT	M.musculus IgG2c gene for immunoglobulin constant heavy chain, allele Igh-1
4787	9898	1.7	2.80E-01	A1272669.1	EST_HUMAN	q15g11.x1 Soares_NbHMP_U_S1 Homo sapiens cDNA clone IMAGE:1876628 3' similar to contains Alu repetitive element; contains element L TR5 repetitive element;
5173	10267	0.9	2.80E-01	S69863.1	NT	mnp2=manganese peroxidase isozyme 2 (heat-shock elements, metal response elements)
5173	10267	0.9	2.80E-01	S69863.1	NT	[Phanerochaete chrysosporium, Genomic, 3297 nt]
5173	10267	0.9	2.80E-01	S69863.1	NT	mnp2=manganese peroxidase isozyme 2 (heat-shock elements, metal response elements)
468	5633	0.8	2.70E-01	Y17324.1	NT	[Phanerochaete chrysosporium, Genomic, 3297 nt]
597	5755	1.1	2.70E-01	AA450081.1	EST_HUMAN	Rattus norvegicus CDK104 mRNA
1240	6369	0.5	2.70E-01	AB004906.1	NT	zx39b10.s1 Soares_totat_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:788827 3' similar to contains Alu repetitive element;
1604	6731	0.6	2.70E-01	X79815.1	NT	Ipomoea purpurea transposable element Tip100 gene for transposase, complete cds
1698	6822	1.1	2.70E-01	W58067.1	EST_HUMAN	G.lambia SR2 gene
1738	6861	1.3	2.70E-01	P03341	SWISSPROT	zd42h10.r1 Soares_fetal_heart_NbHH19W Homo sapiens cDNA clone IMAGE:341443 5'
2088	7934	0.9	2.70E-01	AF047575.1	NT	GAG POLYPROTEIN [CONTAINS: INNER COAT PROTEIN P12; CORE PROTEIN P15; CORE SHELL PROTEIN P30; NUCLEOPROTEIN P10]
2316	7419	3.2	2.70E-01	Y13868.1	NT	Rattus norvegicus vesicular monoamine transporter type 2, promoter region and exon 1
2406	7505	1.3	2.70E-01	AI310858.1	EST_HUMAN	Feline immunodeficiency virus env gene, isolate ITTO088PU (M88), partial
2629	7719	1.5	2.70E-01	P22105	SWISSPROT	ta43c11.x2 NCI_CGAP_Lu25 Homo sapiens cDNA clone IMAGE:2046836 3' similar to contains element L1 repetitive element;
3929	9063	1.9	2.70E-01	AI928015.1	EST_HUMAN	TENASCIN-X-PRECURSOR (TN-X) (HEXABRACHION-LIKE)
3943	9076	2.3	2.70E-01	L77569.1	NT	w092a11.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2462828 3'
						Homo sapiens D1Ge01g1 syndrome critical region, telomeric end

Table 4

4286	9411	14498	5.1	2.70E-01	6680555	NT	Mus musculus corticosteroid binding globulin (Cbg), mRNA
4786	9907	15000	0.9	2.70E-01	L27516.1	NT	Triticum aestivum (Mc565) gene, complete cds
4973	10076		3.5	2.70E-01	AW856131.1	EST_HUMAN	RC1-CT0286-230200-016-e03 CT0286 Homo sapiens cDNA
5190	10281	15349	0.8	2.70E-01	BE182123.1	EST_HUMAN	PM3-HT0642-290300-001-b05 HT0642 Homo sapiens cDNA
462	7889	10756	0.5	2.60E-01	P78411	SWISSPROT	IROQUOIS-CLASS HOMEODOMAIN PROTEIN IRX-2
472	5638		1.4	2.60E-01	D16458.1	NT	Bos taurus mRNA for mb-1, complete cds
1355	6483	11649	1.0	2.60E-01	4557640	NT	Homo sapiens histone deacetylase 2 (HDAC2), mRNA
1355	6483	11650	1.0	2.60E-01	4557640	NT	Homo sapiens histone deacetylase 2 (HDAC2), mRNA
1418	6546	11720	1.0	2.60E-01	AB013290.1	NT	Glycine max pseudogene for Bd 30K
1854	6972	12156	3.1	2.60E-01	AL161472.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 2
1854	6972	12157	3.1	2.60E-01	AL161472.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 2
							bb04410.x1 NIH_MGC_14 Homo sapiens cDNA clone IMAGE:2958451 3' similar to gp:M36072 80S RIBOSOMAL PROTEIN L7A (HUMAN); gb:M14689_cds1 Mouse surfeit locus surfeit 3 protein gene (MOUSE);
2046	7159		3.6	2.60E-01	AW733152.1	EST_HUMAN	Human prealbumin gene, complete cds
2106	7217	12427	1.2	2.60E-01	M11844.1	NT	B.martinius tbc1 gene
2424	7523		1.0	2.60E-01	Y12996.1	NT	B.martinius tbc1 gene
2499	7596		3.5	2.60E-01	BE272440.1	EST_HUMAN	601126016F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:2990043 5'
3053	8204		1.0	2.60E-01	AW974531.1	EST_HUMAN	EST386635 MAGE resequences, MAGM Homo sapiens cDNA
							h30c02.x1 NCI CGAP L124 Homo sapiens cDNA clone IMAGE:3174914 3' similar to contains L1.13 L1 repetitive element ;
3485	8626		0.9	2.60E-01	BE217816.1	EST_HUMAN	Bacteriophage T2 DNA-(adenine-N6)methyltransferase (dam) gene, complete cds
3532	8673	13777	1.1	2.60E-01	M22342.1	NT	Homo sapiens acetylcholinesterase collagen-like tail subunit (COLQ) gene, exons 1A, 2, 3, 4, and 5
3591	8730	13827	1.7	2.60E-01	AF229118.1	NT	Rattus norvegicus mRNA for organic anion transporter 3, complete cds
3651	8790	13883	0.9	2.60E-01	AB017446.1	NT	EST371580 MAGE resequences, MAGF Homo sapiens cDNA
4010	9141	14223	1.0	2.60E-01	AW959510.1	EST_HUMAN	QV1-BT0630-040400-132-e03 BT0630 Homo sapiens cDNA
4062	9189	14274	13.1	2.60E-01	BE080598.1	EST_HUMAN	Enterococcus faecium strain N97-330 vand glycopeptide resistance gene cluster, complete cds; and unknown gene
4259	9384	14467	1.0	2.60E-01	AF175293.1	NT	Gallus gallus mRNA for skeletal myosin heavy chain, complete cds
4393	9515	14604	0.8	2.60E-01	AB021180.1	NT	Gallus gallus mRNA for skeletal myosin heavy chain, complete cds
4393	9515	14605	0.8	2.60E-01	AB021180.1	NT	Gallus gallus mRNA for skeletal myosin heavy chain, complete cds
4448	9566	14666	1.2	2.60E-01	AA457617.1	EST_HUMAN	aa89407.r1 Stratagene fetal retina 937202 Homo sapiens cDNA clone IMAGE:838477 5'
4548	9667	14756	1.6	2.60E-01	U01103.1	NT	Arabidopsis thaliana PSI type III chlorophyll a/b-binding protein (Lhca3*) mRNA, complete cds
4816	9730	14824	1.3	2.60E-01	AF142703.1	NT	Opiressia radicata maturase-like protein (mak) gene, complete cds; chloroplast gene for chloroplast product
4872	9784	14883	2.2	2.60E-01	AW027920.1	EST_HUMAN	ws52n11.x1 NCI CGAP Bm23 Homo sapiens cDNA clone IMAGE:2501829 3' similar to SW:ME13_MOUSE P97368 HOMEBOX PROTEIN MEIS3 ;
4896	10003	15086	3.6	2.60E-01	H04858.1	EST_HUMAN	y151e05.r1 Soares placenta N22HP Homo sapiens cDNA clone IMAGE:152288 5'
5051	10151	15228	0.9	2.60E-01	P08503	SWISSPROT	ACYL-CoA DEHYDROGENASE, MEDIUM-CHAIN SPECIFIC, MITOCHONDRIAL PRECURSOR (MCAD)

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Table 4

1282	6412	11574	5.9	2.40E-01	AJ289880.1	NT	Homo sapiens KIAA0851 gene (partial), XT3 gene and LZTFL1 gene
1362	6490	11655	1.0	2.40E-01	Y17293.1	NT	Homo sapiens FLI-1 gene, partial
1808	6927		8.7	2.40E-01	AF267753.1	NT	Mesembryanthemum crystallinum putative potassium channel protein Mktip mRNA, complete cds
1858	6976	12161	0.5	2.40E-01	AF251708.1	NT	Zoocys diimundes fructose-1,6-bisphosphatase mRNA, complete cds
							Homo sapiens serine palmitoyl transferase, subunit II gene, complete cds; and unknown genes
2091	7202	12407	0.9	2.40E-01	AF111168.2	NT	IMMUNOGLOBULIN A1 PROTEASE PRECURSOR (IGA1 PROTEASE)
2122	7232		1.2	2.40E-01	PA3384	SWISSPROT	
2215	7323	12537	0.7	2.40E-01	AE000680.1	NT	Aquilex aecilius section 12 of 109 of the complete genome
2491	7588	12792	0.6	2.40E-01	Z36534.1	NT	D.discoidium (Ax3-K) pona gene
2734	7818	13023	0.8	2.40E-01	X71783.1	NT	S.pombe swi6 gene
2756	7840	13042	2.4	2.40E-01	AF030154.1	NT	Bovine adenovirus 3 complete genome
							Oryza longistaminata receptor kinase-like protein, family member D, and retrofl. (gag/pol) genes, complete cds
3093	8244		2.8	2.40E-01	U72726.1	NT	
3109	8259	13363	1.9	2.40E-01	X74209.1	NT	H.sapiens AGT gene, PsiI fragment of intron 4
3871	9007	14106	2.4	2.40E-01	AJ009861.1	NT	Fugu rubripes PRGFR1 gene, exons 1-20
4594	9708	14800	78.8	2.40E-01	Y13183.1	NT	Herpesvirus salm1 C-488 DNA for ORF 12 to 25
							q986c07.s1 Soares_fetal_heart_NbhH19W Homo sapiens cDNA clone IMAGE:1693644 3'
4704	9816	14913	1.3	2.40E-01	AI123160.1	EST_HUMAN	
4817	9826	15018	0.9	2.40E-01	BE160080.1	EST_HUMAN	QV1-HT0412-020400-136-b10 HT0412 Homo sapiens cDNA
4981	10084	15154	50.2	2.40E-01	D00944.1	NT	Hepatitis C virus genomic RNA for polypeptide, complete cds
5101	10197	15277	1.0	2.40E-01	AI302019.1	EST_HUMAN	q02307.x1 NCJ CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1809369 3'
5188	10279	15347	1.4	2.40E-01	7657600	NT	Mus musculus small optic lobes homolog (Drosophila) (Solh), mRNA
383	5552	10685	0.9	2.30E-01	S75898.1	NT	aromatase [Poeophila guttata=zebra finches, ovary, mRNA, 3188 nt]
621	5780		1.5	2.30E-01	U39713.1	NT	Mycoplasma genitalium section 35 of 51 of the complete genome
651	5809	10935	6.8	2.30E-01	U67596.1	NT	Methanococcus jannaschii section 138 of 150 of the complete genome
792	5943	11094	4.4	2.30E-01	AE001708.1	NT	Thermotoga maritima section 20 of 136 of the complete genome
851	6000	11160	1.6	2.30E-01	AE001708.1	NT	Thermotoga maritima section 20 of 136 of the complete genome
918	6064	11219	1.1	2.30E-01	BE311883.1	EST_HUMAN	601142073F1 NIH_MGC_14 Homo sapiens cDNA clone IMAGE:3505818 5'
1494	6620	11790	0.5	2.30E-01	6677980	NT	Mus musculus vacuolar protein sorting 4b (yeast) (Vps4b), mRNA
							Yersinia pestis HmsH (hmsH), HmsF (hmsF), HmsR (hmsR), and HmsS (hmsS) genes, complete cds
1546	6673		0.9	2.30E-01	U22837.2	NT	
1586	6712	11883	1.4	2.30E-01	AJ245480.1	NT	Brassica napus slg gene for S-locus glycoprotein, cultivar T2
1614	6740	11910	1.0	2.30E-01	Y10887.2	NT	Mus musculus cdh5 gene, exon 1, partial
1999	7114		1.3	2.30E-01	AJ235353.1	NT	Homo sapiens partial intron 3 of the wild type AF-4/EL gene
2396	7496	12701	0.6	2.30E-01	BE297718.1	EST_HUMAN	601175562F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3531015 5'
2615	7705	12904	1.0	2.30E-01	M11319.1	NT	Human erythropoietin gene, complete cds
							Medicago sativa aquaporin-like transmembrane channel protein (pAF1 8-1) mRNA, complete cds
2757	7841	13043	0.5	2.30E-01	AF004708.1	NT	
2757	7841	13044	0.5	2.30E-01	AF004708.1	NT	Medicago sativa aquaporin-like transmembrane channel protein (pAF1 8-1) mRNA, complete cds

Table 4

2794	6493	11659	0.9	2.30E-01	AB015033.1	NT	Marrhabilla agarivorans gyrB gene for DNA gyrase subunit B, partial cds, strain JFO 14957
2934	8085	13193	1.3	2.30E-01	AA601379.1	EST_HUMAN	not6d08.s1 NCJ_CGAP Phe1 Homo sapiens cDNA clone IMAGE:1100843 3' similar to contains Alu repetitive element/contains element TH-R repetitive element :
2950	8101	13207	0.9	2.30E-01	AB005200.1	NT	Mus musculus DNA for DNA dependent protein kinase catalytic subunit, exon 69
3045	8196		5.7	2.30E-01	R21732.1	EST_HUMAN	yt21b07.s1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:130357 3'
3324	8466	13563	1.1	2.30E-01	H69836.1	EST_HUMAN	yr97h10.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:213283 5'
3766	8904	13993	1.1	2.30E-01	S82821.1	NT	GSTA5=glutathione S-transferase Yc2 subunit (5' region, intron 1) [rats, Morris hepatoma cell line, Genomic, 2212 nt, segment 1 of 3]
3856	8992		3.7	2.30E-01	7662133	NT	Homo sapiens KIAA0450 gene product (KIAA0450), mRNA
4253	9378	14458	0.9	2.30E-01	R82252.1	EST_HUMAN	y17f01.r1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:149017 5'
4300	9424		3.4	2.30E-01	L78789.1	NT	Mus musculus renin (Ren-1c) gene, promoter region
4349	9471	14563	1.0	2.30E-01	D80899.1	NT	Synechocystis sp. PCC6803 complete genome, 1127, 1-133859
4386	9508	14593	2.1	2.30E-01	AF092535.1	NT	Homo sapiens mitogen-activated protein kinase p38delta (PRKM13) mRNA, complete cds
4454	9574	14672	5.1	2.30E-01	5031984	NT	Homo sapiens nuclear transport factor 2 (placental protein 15) (PP15) mRNA
4582	9698	14792	22.6	2.30E-01	AB001995.1	NT	Schizosaccharomyces pombe gene for Tel1p, complete cds
4656	9894	14987	0.8	2.30E-01	J03280.1	NT	Human phenylethanolamine N-methyltransferase gene, complete cds
5020	10121	15193	3.7	2.30E-01	AE003995.1	NT	Xyella fastidiosa, section 141 of 229 of the complete genome
5146	10241	15315	27.0	2.30E-01	AE000240.1	NT	Escherichia coli K-12 MG1655 section 130 of 400 of the complete genome
84	5290	10417	1.0	2.20E-01	A052190.1	EST_HUMAN	oz14a10.x1 Soares fetal liver spleen, 1NFLS S1 Homo sapiens cDNA clone IMAGE:1675290 3' similar to TR:Q13040 Q13040 ATP-BINDING CASSETTE PROTEIN :
1545	6672	11843	1.1	2.20E-01	AF187850.1	NT	Homo sapiens PPAR delta gene, promoter region
2042	7155	12361	1.0	2.20E-01	M34640.1	NT	Fresh-water sponge Emr1 alpha collagen (COLF1) gene
2133	7243	12450	1.1	2.20E-01	AJ388469.1	NT	Cobitis taenia mitochondrial cyt b gene for cytochrome b
2653	8004	13102	4.0	2.20E-01	BE155625.1	EST_HUMAN	PM2-HT0353-281299-003-a12 HT0353 Homo sapiens cDNA
2653	8004	13103	4.0	2.20E-01	BE155625.1	EST_HUMAN	PM2-HT0353-281299-003-a12 HT0353 Homo sapiens cDNA
2690	8041		1.6	2.20E-01	AF020503.1	NT	Homo sapiens FRA3B common fragile region, diadenosine triphosphate hydrolase (FHL1) gene, exon 5
3176	8325	13437	1.9	2.20E-01	AI824368.1	EST_HUMAN	bx69c09.x1 NCJ_CGAP Utr Homo sapiens cDNA clone IMAGE:2274832 3'
3346	8490		2.7	2.20E-01	AI161562.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 62
3743	8880		1.1	2.20E-01	AF155728.1	NT	Xiphophorus maculatus truncated Rax1 retrotransposon reverse transcriptase (RT) pseudogene
4007	9136	14220	0.8	2.20E-01	AF213391.1	NT	Mus musculus ATP-binding cassette protein (Abcb8) mRNA, partial cds
4118	9244		1.2	2.20E-01	AF119102.1	NT	Drosophila melanogaster UNC-119 (unc-119) gene, complete cds
4125	9251	14332	5.1	2.20E-01	AF155142.1	NT	Mus musculus mixed lineage kinase 3 (Mlk3) and two pore domain K+ channel subunit (Kcnk6) genes, complete cds
4166	9292	14372	2.0	2.20E-01	AF117340.1	NT	Mus musculus MAP kinase kinase 1 (Meck1) mRNA, complete cds
4166	9292	14373	2.0	2.20E-01	AF117340.1	NT	Mus musculus MAP kinase kinase 1 (Meck1) mRNA, complete cds
4258	9383	14465	1.2	2.20E-01	U01307.1	NT	Human scRNA (BC200 beta) pseudogene

Table 4

4258	9383	14466	1.2	2.20E-01	U01307.1	NT	Human scRNA (BC200 beta) pseudogene
4399	9520	14610	1.1	2.20E-01	Z54148.1	NT	B.abortus pp26 gene
4719	9831		1.2	2.20E-01	D50604.1	NT	Human beta-cytoplasmic actin (ACTBP9) pseudogene
4724	9836	14928	2.5	2.20E-01	AA211216.1	EST_HUMAN	z687c05.r1 Stralagene hNT neuron (#937233) Homo sapiens cDNA clone IMAGE:648968 5'
4891	9898	15081	1.2	2.20E-01	M86524.1	NT	Human dystrophin gene
4975	10078		1.2	2.20E-01	L13299.1	NT	Mus musculus vinculin gene, exon 3
532	5696	10819	0.6	2.10E-01	AA827018.1	EST_HUMAN	gb:Z23090 HEAT SHOCK 27 KD PROTEIN (HUMAN);
532	5696	10820	0.6	2.10E-01	AA827018.1	EST_HUMAN	m89g09.s1 NCI CGAP_P125 Homo sapiens cDNA clone IMAGE:1175200 3' similar to
955	6101	11259	0.6	2.10E-01	AA569289.1	EST_HUMAN	gb:Z23090 HEAT SHOCK 27 KD PROTEIN (HUMAN);
956	6103	11261	0.9	2.10E-01	AL161504.2	NT	nm31611.s1 NCI CGAP_Lip2 Homo sapiens cDNA clone IMAGE:1061804
1108	6245		0.7	2.10E-01	AE002314.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 16
1180	6313	11468	1.2	2.10E-01	6754299	NT	Chlamydia muridarum, section 45 of 85 of the complete genome
1180	6313	11469	1.2	2.10E-01	6754299	NT	Mus musculus interferon (alpha and beta) receptor 2 (Imar2), mRNA
1467	6694	11771	1.3	2.10E-01	AE001988.1	NT	Mus musculus interferon (alpha and beta) receptor 2 (Imar2), mRNA
1792	6912	12097	1.4	2.10E-01	6961303	NT	Deinococcus radiodurans R1 section 125 of 229 of the complete chromosome 1
1871	6989	12174	0.7	2.10E-01	AA908824.1	EST_HUMAN	Rattus norvegicus Olfactory marker protein (Omp), mRNA
2894	8045	13145	1.7	2.10E-01	6912445	NT	ok38602.s1 NCI CGAP_G04 Homo sapiens cDNA clone IMAGE:1519610 3' similar to
3218	8366	13478	2.0	2.10E-01	AF069511.1	NT	gb:K02765 COMPLEMENT C3 PRECURSOR (HUMAN);
3967	9099	14183	1.0	2.10E-01	P11675	SWISSPROT	Homo sapiens potassium voltage-gated channel, subfamily H (eag-related), member 4 (KCNH4), mRNA
3967	9099	14184	1.0	2.10E-01	P11675	SWISSPROT	Rattus norvegicus putative sodium bicarbonate cotransporter (NBC), mRNA, complete cds
4279	9404		1.3	2.10E-01	AB033041.1	NT	IMMEDIATE-EARLY PROTEIN IE180
4474	9594	14689	1.2	2.10E-01	AB010273.1	NT	IMMEDIATE-EARLY PROTEIN IE180
4766	9877	14971	1.3	2.10E-01	AJ009794.1	NT	Homo sapiens mRNA for KIAA1215 protein, partial cds
5134	10229	15304	1.0	2.10E-01	M98261.1	NT	Homo sapiens pshp47 gene, complete cds
193	5387	10515	0.6	2.00E-01	AB017437.1	NT	Homo sapiens hox11 proto-oncogene, exons 1 to 3 and hug-1 gene
365	5543	10675	0.9	2.00E-01	A475599.1	EST_HUMAN	Saccharomyces cerevisiae Iku138 (TFIC3) gene, complete cds
365	5543	10676	0.9	2.00E-01	A475599.1	EST_HUMAN	Gallus gallus mRNA for avana, complete cds
523	5687	10676	0.8	2.00E-01	A475599.1	EST_HUMAN	tc92g12.y1 NCI CGAP_CLL1 Homo sapiens cDNA clone IMAGE:2073670 5' similar to
684	5639	10972	1.2	2.00E-01	M77085.1	NT	contains Alu repetitive element;
793	5944	11095	0.6	2.00E-01	AF027885.1	NT	tc92g12.y1 NCI CGAP_CLL1 Homo sapiens cDNA clone IMAGE:2073670 5' similar to
995	6137	11291	1.0	2.00E-01	D80905.1	NT	contains Alu repetitive element;
1082	6220	11371	1.3	2.00E-01	4826749	NT	Homio sapiens CGI-18 protein (LOC51008), mRNA
1109	6246	11398	0.9	2.00E-01	AL163213.2	NT	O.cuniculicus germinale Igh heavy chain V-H pseudogene, allotype VH2

Table 4

1234	6363	11525	1.4	2.00E-01	AJ132695.5	NT	Homo sapiens rac1 gene
1286	6416	11579	1.3	2.00E-01	AW384937.1	EST_HUMAN	PM1-HT0422-291299-002-c06 HT0422 Homo sapiens cDNA
1419	6547	11721	0.8	2.00E-01	M64239.1	NT	Mouse T-cell receptor alpha/delta chain locus
1419	6547	11722	0.8	2.00E-01	M64239.1	NT	Mouse T-cell receptor alpha/delta chain locus
1471	6598	11773	4.9	2.00E-01	4503408	NT	Homo sapiens dystrobrein, alpha (DTNA), mRNA
1534	6660	11827	0.9	2.00E-01	AB007974.1	NT	Homo sapiens mRNA, chromosome 1 specific transcript KIAA0505
1538	6664	11832	0.6	2.00E-01	AF260700.1	NT	Homo sapiens sodium/potassium symporter mRNA, partial cds
1688	6812		0.7	2.00E-01	AF111170.3	NT	Homo sapiens 14q32 jagged2 gene, complete cds; and unknown gene
1723	6846		0.6	2.00E-01	U67525.1	NT	Methanococcus jannaschii section 67 of 150 of the complete genome
2299	7403		0.6	2.00E-01	X82877.1	NT	H. sapiens Na+-D-glucose cotransport regulator gene
2861	8012		1.0	2.00E-01	AF074990.1	NT	Homo sapiens full length insert cDNA YH85A11
3442	8584	13698	0.8	2.00E-01	P46607	SWISSPROT	HOMEOBOX PROTEIN GLABRA2 (HOMEOBOX-LEUCINE ZIPPER PROTEIN ATHB-10)
3520	8661		0.9	2.00E-01	AW238005.1	EST_HUMAN	(HD-ZIP PROTEIN ATHB-10)
3646	8785	13878	0.8	2.00E-01	P34641	SWISSPROT	contains element MER21 repetitive element :
3945	9078	14160	0.8	2.00E-01	X83997.1	NT	C.parasilica eapC gene
4367	9489	14580	0.9	2.00E-01	AF060195.1	NT	Mus musculus proteasome regulator P28 beta subunit gene, complete cds
4859	9868	15051	1.1	2.00E-01	AF147083.1	NT	Homo sapiens gamma-glutamyl hydrolase gene, exons 8 and 9 and complete cds
4972	10075	15148	6.1	2.00E-01	8922080	NT	Homo sapiens hypothetical protein ASH1, mRNA
5041	10141	15219	1.1	2.00E-01	Y19216.1	NT	Homo sapiens putative psithBD pseudogene for hair keratin, exons 1 to 9
105	5308		3.5	1.90E-01	7549743	NT	Rattus norvegicus Aryl hydrocarbon receptor nuclear translocator 1 (Arlnt), mRNA
348	5530	10658	2.0	1.90E-01	AF004353.1	NT	Mus musculus pale ear (ep) gene, wild type allele, 3' region, partial cds
470	5635	10764	0.7	1.90E-01	O43474	SWISSPROT	KRUPPEL-LIKE FACTOR 4 (EPIITHELIAL ZINC-FINGER PROTEIN EZF)
640	5798	10924	1.3	1.90E-01	U32581.2	NT	Homo sapiens lambda/delta protein kinase C-interacting protein mRNA, complete cds
640	5799	10925	1.3	1.90E-01	U32581.2	NT	Homo sapiens lambda/delta protein kinase C-interacting protein mRNA, complete cds
647	5806	10932	1.8	1.90E-01	BE070801.1	EST_HUMAN	RC3-BT0502-251199-011-401 BT0502 Homo sapiens cDNA
648	5806	10932	2.5	1.90E-01	BE070801.1	EST_HUMAN	RC3-BT0502-251199-011-401 BT0502 Homo sapiens cDNA
870	6115		0.6	1.90E-01	7305180	NT	Mus musculus Interleukin 2 receptor, gamma chain (IL2rg), mRNA
1088	6228	11378	3.2	1.90E-01	AA358813.1	EST_HUMAN	EST167784 Fetal lung II Homo sapiens cDNA 5' end
1348	6476	11642	0.8	1.90E-01	AF061282.1	NT	Sorghum bicolor 22 kDa kafirin cluster
1416	6544		1.4	1.90E-01	AF184623.1	NT	Plasmodium vivax reticulocyte binding protein-2 (tbp-2) gene, complete cds
1873	6991	12176	0.6	1.90E-01	AW821631.1	EST_HUMAN	IL2-ST0311-270300-059-E04 ST0311 Homo sapiens cDNA
1928	7045	12236	0.9	1.90E-01	AF281940.1	NT	Spinacia oleracea Atwero ribosomal protein 5 precursor (Pp-5) mRNA, complete cds; nuclear gene for chloroplast product
2330	7433	12641	1.2	1.90E-01	8922533	NT	Homo sapiens hypothetical protein FLJ10581 (FLJ10581), mRNA
2892	8043	13143	3.9	1.90E-01	U66066.1	NT	Sigmodon hispidus p53 gene, partial cds
2908	8058		5.6	1.90E-01	J00922.1	NT	Gallus gallus ovalbumin (V) gene, complete cds
3348	8493	13604	3.4	1.90E-01	D13197.1	NT	Mouse gene for immunoglobulin diversity region D1
3434	8576	13688	4.6	1.90E-01	R16467.1	EST_HUMAN	y142r10.1 Scores fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:129547 5'

Table 4

3735	8872	13864	0.9	1.90E-01	AF264017.1	NT	Rattus norvegicus arylacetamidase deacetylase gene, complete cds	
3762	8900	13989	1.0	1.90E-01	P39768	SWISSPROT	PAIR-RULE PROTEIN ODD-PAIRED	
3910	9045	14132	3.0	1.90E-01	AB006784.1	NT	Schistosoma haematocytes pombe DNA for cytoplasmic dynein heavy chain, complete cds	
3992	9124	14208	1.9	1.90E-01	AW754106.1	EST_HUMAN	CM3-CT0315-271199-045-b11 CT0315 Homo sapiens cDNA	
4389	9491	14581	0.9	1.90E-01	AL161493.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 5	
4662	9774	14870	0.8	1.90E-01	Z93780.1	NT	Fugu rubripes genes encoding carbanomyl phosphate synthetase III, myosin light chain, MAP2	
4663	9775	14871	2.4	1.90E-01	AW821631.1	EST_HUMAN	IL2-ST0311-270300-059-E04 ST0311 Homo sapiens cDNA	
4857	9964	15049	2.1	1.90E-01	U31785.1	NT	Human papillomavirus type 36, complete genome	
4912	10019	15098	0.9	1.90E-01	AW849203.1	EST_HUMAN	IL3-CT0215-180200-087-D02 CT0215 Homo sapiens cDNA	
4943	10049		1.0	1.90E-01	AF223642.1	NT	Rattus norvegicus chemokine receptor CXCR3 mRNA, complete cds	
4982	10065	15137	1.1	1.90E-01	O95239	SWISSPROT	KINESIN-LIKE PROTEIN KIF4	
5113	10209	15287	1.0	1.90E-01	Z70296.1	NT	S.mansonii elastase HP1 gene	
							ts39g12.x1 NC1_CGAP_G06 Homo sapiens cDNA clone IMAGE:2238866 3' similar to gb:M21574 ALPHA PLATELET-DERIVED GROWTH FACTOR RECEPTOR PRECURSOR (HUMAN);	
5123	10219		1.2	1.90E-01	AI631199.1	EST_HUMAN	Mus musculus Notch gene homolog 3, (Drosophila) (Notch3), mRNA	
5153	10248	15321	1.0	1.90E-01	6678095	NT	Mus musculus p116Rip mRNA, complete cds	
17	5226	10327	0.7	1.80E-01	X79037.1	NT	H.sapiens Y315 gene	
29	5238	10343	0.8	1.80E-01	U73200.1	NT	Mus musculus Cdcg gene for chaperonin containing TCP-1 gamma subunit, partial cds	
260	7885	10573	1.2	1.80E-01	AB022090.1	NT	Mus musculus calcium channel, voltage-dependent, beta 2 subunit (CACNB2) mRNA, and translated products	
366	5544	10677	0.8	1.80E-01		4502532	NT	Oryzias latipes gene for membrane guanylyl cyclase OIGC1, complete cds
729	5883	11025	0.7	1.80E-01	AB021490.2	NT	wc71102.x1 NC1_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2337051 3'	
966	6111	11267	0.9	1.80E-01	AI912212.1	EST_HUMAN	Dicystostellum discoidium plasmid Ddp5, complete genome	
1075	6212	11364	1.2	1.80E-01	AF000580.1	NT	Yersinia pestis plasmid pCD1	
1267	6396	11556	1.8	1.80E-01	AL117189.1	NT	Mus musculus guanylate nucleotide binding protein 1 (Gbp1), mRNA	
1487	6614	11784	1.3	1.80E-01		6753947	NT	Mus musculus guanylate nucleotide binding protein 1 (Gbp1), mRNA
1487	6614	11785	1.3	1.80E-01		6753947	NT	Mus musculus guanylate nucleotide binding protein 1 (Gbp1), mRNA
1803	6922		0.9	1.80E-01		4505036	NT	Homo sapiens latent transforming growth factor beta binding protein 4 (LTBP4) mRNA
1823	6942		0.7	1.80E-01	AI733708.1	EST_HUMAN	qg22d10.x5 NC1_CGAP_Kid3 Homo sapiens cDNA clone IMAGE:1761811 3' similar to TR:O75936 O75936 GAMMA BUTYROBETALINE HYDROXYLASE ;	
2421	7520		1.5	1.80E-01	J03216.1	NT	TT plasmid virB operon encoding twelve virulence genes, complete cds	
2660	7749		1.1	1.80E-01	AW935728.1	EST_HUMAN	QV3-DT0018-081299-036-g04 DT0018 Homo sapiens cDNA	
2868	8019		1.6	1.80E-01	AF184589.1	NT	Jonopsidium aculea LEAFY protein (LEAFY2) gene, partial cds	
2873	8024	13127	1.1	1.80E-01	AW182300.1	EST_HUMAN	x41a03.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2659756 3'	
3006	8158		4.9	1.80E-01	P13983	SWISSPROT	EXTENSIN PRECURSOR (CELL WALL HYDROXYPROLINE-RICH GLYCOPROTEIN)	
3040	8226	10327	2.0	1.80E-01	X79037.1	NT	H.sapiens Y315 gene	
3065	8236	13335	1.3	1.80E-01	AW995178.1	EST_HUMAN	QV0-BN0041-070300-147-c04 BN0041 Homo sapiens cDNA	
3570	8709	13807	1.1	1.80E-01	H03389.1	EST_HUMAN	y45e01.s1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:151704 3' similar to contains Alu repetitive element;	

Table 4

3570	8709	13808	1.1	1.80E-01	H03369.1	EST_HUMAN	Y45607.s1 Scores placenta NB2HP Homo sapiens cDNA clone IMAGE:151704 3' similar to contains Alu repetitive element;
4154	9280	14360	0.8	1.80E-01	AJ271735.1	NT	Homo sapiens Xq pseudautosomal region; segment 1/2
4238	9363		1.1	1.80E-01	D37954.1	NT	Bovine NB25 mRNA for MHC class II (BoLA-DQB), complete cds
4436	9576	14673	5.1	1.80E-01	AL161556.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 55
4595	9709	14801	1.1	1.80E-01	U17755.1	NT	Human laminin S B3 chain (LAMB3) gene, exon 13
4700	9812	14909	0.9	1.80E-01	X92179.1	NT	S. tuberosum mRNA for alcohol dehydrogenase
4977	10080	15150	1.8	1.80E-01	AW814270.1	EST_HUMAN	MR3-ST0203-151299-112-g08 ST0203 Homo sapiens cDNA
5027	10128	15202	4.2	1.80E-01	AF181258.1	NT	Mesocricetus auratus Na-taurocholate cotransporting polypeptide mRNA, partial cds
5053	10153	15228	1.3	1.80E-01	A43988.1	EST_HUMAN	U57604.X1 NCI CGAP_Lym12 Homo sapiens cDNA clone IMAGE:2134590 3'
5117	10213		1.0	1.80E-01	AJ000742.1	NT	Homo Sapiens HsH1 gene, 5' UTR
563	5725	10841	0.6	1.70E-01	BE385184.1	EST_HUMAN	601274604F1 NIH MGC_20 Homo sapiens cDNA clone IMAGE:3615768 5'
788	5839	11091	0.7	1.70E-01	X53330.1	NT	P.dumerilli histone gene cluster for core histones H2A, H2B, H3 and H4
945	6092		0.6	1.70E-01	P35616	SWISSPROT	NEUROFILAMENT TRIPLET L PROTEIN (NEUROFILAMENT LIGHT POLYPEPTIDE) (NF-L)
1042	6182	11334	0.6	1.70E-01	AF081810.1	NT	Lymantria dispar nucleopolydnavirus, complete genome
1042	6182	11335	0.6	1.70E-01	AF081810.1	NT	Lymantria dispar nucleopolydnavirus, complete genome
1938	7055		1.4	1.70E-01	AF255051.1	NT	Homo sapiens BINP3H (BINP3H) gene, complete cds; nuclear gene for mitochondrial product
2829	7980	13080	1.9	1.70E-01	AF000716.1	NT	Vibrio cholerae hypoxanthine phosphoribosyltransferase (hpr) gene, partial cds, hemagglutinin/protease regulatory protein (hprP) gene, complete cds, and YRAL VIBCO gene, partial cds
2829	7980		1.9	1.70E-01	AF000716.1	NT	Vibrio cholerae hypoxanthine phosphoribosyltransferase (hpr) gene, partial cds, hemagglutinin/protease regulatory protein (hprP) gene, complete cds, and YRAL VIBCO gene, partial cds
2829	7980	13081	1.9	1.70E-01	AF000716.1	NT	EST41651 Endometrial tumor Homo sapiens cDNA 5' end
2896	8047	13148	1.7	1.70E-01	AA336909.1	EST_HUMAN	EST41651 Endometrial tumor Homo sapiens cDNA 5' end
2967	8118	13225	1.4	1.70E-01	AJ238736.1	NT	Naja naja atra cx-1 gene, exons 1-3
2967	8118	13226	1.4	1.70E-01	AJ238736.1	NT	Naja naja atra cx-1 gene, exons 1-3
3067	8218	13317	1.9	1.70E-01	AF081514.1	NT	Taxus canadensis geranylgeranyl diphosphate synthase mRNA, complete cds
3076	8227	13325	2.3	1.70E-01	AB015873.1	NT	Orizias latipes mRNA for guanylate cyclase OIGC-R1, complete cds
3076	8227	13326	2.3	1.70E-01	AB015873.1	NT	Orizias latipes mRNA for guanylate cyclase OIGC-R1, complete cds
3557	8696	13794	1.0	1.70E-01	AJ224877.1	NT	Homo sapiens hsp1 gene, complete CDS
3859	8995	14094	4.4	1.70E-01	AJ235377.1	NT	Homo sapiens derivative 11 breakpoint fragment; partial intron 10 of the ALL-1/MLL/HRX gene fused to intron 5 of the AF-4/FEL gene
4459	9579		1.9	1.70E-01	X52936.1	NT	Schistosoma gregaria alpha repetitive DNA
4732	9843	14935	1.4	1.70E-01	AJ247635.1	EST_HUMAN	q157609.x1 Scores_fetal_liver_spleen_1NF.LS S1 Homo sapiens cDNA clone IMAGE:184808 3' similar to contains ORF.b1 ORF repetitive element;
4986	10089		1.2	1.70E-01	U28376.1	NT	IMAGE:184808 3' similar to contains ORF.b1 ORF repetitive element;
5067	10165		1.2	1.70E-01	AF072725.1	NT	Zea mays calcium-dependent protein kinase (MZCDPK2) mRNA, complete cds
120	5319	10449	0.6	1.60E-01	AF217532.1	NT	Zea mays starch branching enzyme IIb (ae) gene, complete cds
664	7863	10948	0.5	1.60E-01	R31497.1	EST_HUMAN	Homo sapiens neuronal kinase gene, exon 6 and 7
670	5826	10953	1.1	1.60E-01	DB4224.1	NT	Y17512.1 Scores placenta NB2HP Homo sapiens cDNA clone IMAGE:135595 5'
							Homo sapiens mRNA for methionyl tRNA synthetase, complete cds

Table 4

1882	7000	12185	0.9	1.60E-01	P22063	SWISSPROT	AXONIN-1 PRECURSOR (AXONAL GLYCOPROTEIN TAG-1)
1941	7058		1.0	1.60E-01	U10334.1	NT	Crassostrea gigas RNA polymerase II largest subunit mRNA, partial cds
2247	7353	12560	1.8	1.60E-01	AF109907.1	NT	Homo sapiens S164 gene, partial cds; PS1 and hypothetical protein genes, complete cds; and S171 gene, partial cds
2335	7941	12647	1.0	1.60E-01	X64232.1	NT	H. sapiens mRNA for novel T-cell activation protein
2443	7542	12750	0.8	1.60E-01	AB037729.1	NT	Homo sapiens mRNA for KIAA1308 protein, partial cds
2863	8014	13115	8.9	1.60E-01	AF185589.1	NT	Homo sapiens cytochrome P450 3A4 (CYP3A4) gene, promoter region
2863	8014	13116	8.9	1.60E-01	AF185589.1	NT	Homo sapiens cytochrome P450 3A4 (CYP3A4) gene, promoter region
3581	8720	13817	1.3	1.60E-01	AJ003165.1	NT	Populus trichocarpa cv. Trichobel ABI3 gene
3581	8720	13818	1.3	1.60E-01	AJ003165.1	NT	Populus trichocarpa cv. Trichobel ABI3 gene
3583	8722		0.9	1.60E-01	AI810954.1	EST_HUMAN	U09709.x1 NCI_CGAP_P28 Homo sapiens cDNA clone IMAGE:2250569.3'
4234	9358	14440	7.9	1.60E-01	AF179680.1	NT	Homo sapiens apelin gene, complete cds
4249	9374	14454	4.0	1.60E-01	AL163279.2	NT	Homo sapiens chromosome 21 segment HS21C079
4353	9475		2.4	1.60E-01	AW968601.1	EST_HUMAN	EST380677 MAGE resequences, MAGEJ Homo sapiens cDNA
4361	9483		4.0	1.60E-01	6753319	NT	Mus musculus chaperonin subunit 3 (gamma) (Cct3), mRNA
4781	9891	14983	0.9	1.60E-01	Z28330.1	NT	S. cerevisiae chromosome XI reading frame ORF YKR105c
4781	9891	14984	0.9	1.60E-01	Z28330.1	NT	S. cerevisiae chromosome XI reading frame ORF YKR105c
4846	9953	15042	7.1	1.60E-01	AF187881.1	NT	Homo sapiens leukiniegtr alpha d gene, promoter and partial cds
4865	9972	15056	1.1	1.60E-01	AA088343.1	EST_HUMAN	z184h09.s1 Striatagene colon (#937204) Homo sapiens cDNA clone IMAGE:511361.3' similar to TR.E221955 E221965 38,685 BP SEGMENT OF CHROMOSOME XIV.;
4869	9996	15078	1.9	1.60E-01	AJ006356.1	NT	Lycopodium obscurum Resal fragment 2, satellite region
4889	9996	15079	1.9	1.60E-01	AJ006356.1	NT	Lycopodium obscurum Resal fragment 2, satellite region
							bb83h08.y1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3049023.5' similar to gb:M61715 TRYPTOPHANYL-TRNA SYNTHETASE (HUMAN); gb:X69657 M.musculus (MOUSE);
4958	10061	15133	1.1	1.60E-01	BE018707.1	EST_HUMAN	Citellus griseus 170 kDa glucose regulated protein (grp170) mRNA, complete cds
567	5728	10845	0.7	1.50E-01	U34206.1	NT	Homo sapiens chromosome 21 segment HS21C084
766	5919	11066	1.4	1.50E-01	AL163284.2	NT	Homo sapiens cDNA for EGG522 myosin heavy chain, 3'UTR
1076	6214	11366	0.9	1.50E-01	AJ009735.1	NT	Cyprinus carpio mRNA for EGG522 myosin heavy chain, 3'UTR
1081	6219	11370	0.6	1.50E-01	AJ251885.1	NT	Homo sapiens partial SLG22A2 gene for organic cation transporter (OCT2), exon 1
1097	6235		0.6	1.50E-01	L36125.1	NT	Rattus norvegicus insulin-responsive glucose transporter (GLUT4) gene, 5' end
1104	6242	11395	1.0	1.50E-01	Q12697	SWISSPROT	PROBABLE CATION-TRANSPORTING ATPASE 9
1198	6330	11485	1.4	1.50E-01	AW195516.1	EST_HUMAN	h339411.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2696085.3'
1254	6383	11542	1.0	1.50E-01	D26535.1	NT	Human gene for dihydrofolate succinyltransferase, complete cds (exon 1-15)
1254	6383	11543	1.0	1.50E-01	D26535.1	NT	Human gene for dihydrofolate succinyltransferase, complete cds (exon 1-15)
1466	6593	11770	0.5	1.50E-01	AF117340.1	NT	Mus musculus MAP kinase kinase 1 (Mek1) mRNA, complete cds
1866	6984	12168	0.6	1.50E-01	AW444451.1	EST_HUMAN	U1-H-B13-akb-b-09-q-U.s1 NCI_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:2733641.3'
2999	8151	13251	0.9	1.50E-01	M81441.1	NT	Bos laurus factor V variant 2 (factor V) mRNA, complete cds
3013	8165	13266	3.5	1.50E-01	P01138	SWISSPROT	BETA-NERVE GROWTH FACTOR PRECURSOR (BETANGF)
3308	8453	13566	4.2	1.50E-01	AA935049.1	EST_HUMAN	0068605.s1 NCI_CGAP_GC4 Homo sapiens cDNA clone IMAGE:1571337.3' similar to gb:M11433 RETINOL-BINDING PROTEIN I, CELLULAR (HUMAN);



Table 4

3322	8466	13560	0.9	1.50E-01	Z23104.1	NT	L.stegnalis mRNA for G protein-coupled receptor
3322	8466	13561	0.9	1.50E-01	Z23104.1	NT	L.stegnalis mRNA for G protein-coupled receptor
3380	8523	13629	1.0	1.50E-01	AW612237.1	EST_HUMAN	h129102.x1 NC1_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2956539 3' similar to contains element MER16 repetitive element;
3696	8635	13926	1.3	1.50E-01	U09964.1	NT	Mus musculus ICR/Swiss glyceroldehyde 3-phosphate dehydrogenase (Gapd-S) gene, complete cds
3706	8644	13935	185.3	1.50E-01	7108358	NT	Homo sapiens pyruvate dehydrogenase kinase, isoenzyme 1 (PDK1), nuclear gene encoding mitochondrial protein, mRNA
3791	8628	14022	2.4	1.50E-01	AW665983.1	EST_HUMAN	h101016.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2981411 3'
3806	8643	14038	0.8	1.50E-01	AJ003165.1	NT	Populus trichocarpa cv. Trichobel ABI3 gene
3806	8643	14039	0.8	1.50E-01	AJ003165.1	NT	Populus trichocarpa cv. Trichobel ABI3 gene
3964	8096	14161	1.0	1.50E-01	AW366659.1	EST_HUMAN	RC2-HT0149-191099-012-c09 HT0149 Homo sapiens cDNA
4006	9137	14219	1.0	1.50E-01	Z12628.1	NT	B.napus mitochondrion DNA for ORF158
4091	9217	14300	8.4	1.50E-01	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
4680	9792	14893	1.1	1.50E-01	BE173786.1	EST_HUMAN	CM0-HT0565-280200-245-b10 HT0565 Homo sapiens cDNA
4680	9792	14894	1.1	1.50E-01	BE173786.1	EST_HUMAN	CM0-HT0565-280200-245-b10 HT0565 Homo sapiens cDNA
4829	10036	15108	1.3	1.50E-01	AL161560.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 60
5072	10170	15246	0.9	1.50E-01	AF003105.1	NT	Arabidopsis thaliana AP2 domain containing protein RAP2.12 mRNA, partial cds
298	5482		0.7	1.40E-01	AF009663.1	NT	Homo sapiens T cell receptor beta locus, TCRBV85SP to TCRBV21S2A2 region
892	6040		0.9	1.40E-01	D78638.1	NT	Xenopus laevis mRNA for DNA (cytosine 5'-methyltransferase, complete cds
1238	6367		0.6	1.40E-01	T91864.1	EST_HUMAN	Yd54cd1.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:112032 3'
1714	6837		0.5	1.40E-01	6679980	NT	Mus musculus growth differentiation factor 5 (Gdf5), mRNA
1717	6840	12019	0.6	1.40E-01	AE001710.1	NT	Thermotoga maritima section 22 of 136 of the complete genome
1863	6981		0.9	1.40E-01	AW135741.1	EST_HUMAN	U1-H-B11-act-a-09-0-U1.s1 NC1_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2714009 3'
1942	7059		3.7	1.40E-01	AA720615.1	EST_HUMAN	py72d07.s1 NC1_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1283821 3'
2426	7525	12731	1.0	1.40E-01	P30706	SWISSPROT	GLYCEROL-3-PHOSPHATE ACYLTRANSFERASE PRECURSOR (GPAT)
2762	7846	13049	1.1	1.40E-01	AU933496.1	EST_HUMAN	wn17401.x1 NC1_CGAP_U12 Homo sapiens cDNA clone IMAGE:2441665 3'
3823	8960	14056	1.0	1.40E-01	R59232.1	EST_HUMAN	yg97a03.t1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:41467 5'
3823	8960	14057	1.0	1.40E-01	R59232.1	EST_HUMAN	yg97a03.t1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:41467 5'
4083	9210	14284	8.4	1.40E-01	AI699094.1	EST_HUMAN	b55cd2.x1 NC1_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2273570 3'
4083	9210	14285	8.4	1.40E-01	AI699094.1	EST_HUMAN	b55cd2.x1 NC1_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2273570 3'
4144	9270	14349	3.2	1.40E-01	AE001710.1	NT	Thermotoga maritima section 22 of 136 of the complete genome
4313	9436		0.8	1.40E-01	AA776287.1	EST_HUMAN	z150b01.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:453673
4803	9913		1.2	1.40E-01	AL049866.2	NT	z150b01.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:453673
5032	10132		0.9	1.40E-01	AW866022.1	EST_HUMAN	z150b01.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:453673
5116	10212	15291	1.0	1.40E-01	AL163284.2	NT	(HUMAN):contains Alu repetitive element;
							Mus musculus chromosome X contigB; X-linked lymphocyte regulated 5 gene, Zinc finger protein 275, Zinc finger protein 92, mnx28orf
							CV3-SN0022-100500-166-h09 SN0022 Homo sapiens cDNA
							Homo sapiens chromosome 21 segment HS21C084

Table 4

5147	10242	15316	0.8	1.40E-01	ALJ005180.1	NT	Lyopercicon esculentum genomic RAPD band 26
319	5503	10630	0.9	1.30E-01	4758467	NT	Homo sapiens G protein-coupled receptor 50 (GPR50) mRNA
319	5503	10631	0.9	1.30E-01	4758467	NT	Homo sapiens G protein-coupled receptor 50 (GPR50) mRNA
518	5682	10803	0.6	1.30E-01	AB013139.1	NT	Homo sapiens gene for NBS1, complete cds
620	5779	10901	0.9	1.30E-01	AL277606.1	NT	Human calicivirus HUJNLV/Girlington/83/UK RNA for capsid protein (ORF2), strain HUJNLV/Girlington/83/UK
620	5779	10902	0.9	1.30E-01	AL277606.1	NT	Human calicivirus HUJNLV/Girlington/83/UK RNA for capsid protein (ORF2), strain HUJNLV/Girlington/83/UK
826	5975	11135	1.1	1.30E-01	X63330.1	NT	P. dumerilii histone gene cluster for core histones H2A, H2B, H3 and H4
876	6024	11184	0.6	1.30E-01	AF139518.1	NT	Rattus norvegicus A-kinase anchor protein mRNA, complete cds
1010	6150	11303	0.5	1.30E-01	AL117078.1	NT	Bolovitis cinerea strain T4 cDNA library under conditions of nitrogen deprivation
1111	6248		0.8	1.30E-01	AL115265.1	NT	Bolovitis cinerea strain T4 cDNA library under conditions of nitrogen deprivation
1426	6553		1.4	1.30E-01	AF146277.1	NT	Homo sapiens adapter protein CMS mRNA, complete cds
1916	7033	12221	0.9	1.30E-01	AL117078.1	NT	Bolovitis cinerea strain T4 cDNA library under conditions of nitrogen deprivation
2124	7234		1.3	1.30E-01	AL243578.1	NT	Rhodopseudomonas acidophila pucB5, pucA5, pucB6, pucA6, pucB7, pucA7, pucB8, pucA8 and pucC genes and ORF151
2245	7351		1.2	1.30E-01	AW812104.1	EST_HUMAN	RCA-ST0173-191089-032-d12 ST0173 Homo sapiens cDNA
2329	7432		1.1	1.30E-01	AE001016.1	NT	Archaeoglobus fulgidus section 91 of 172 of the complete genome
2542	7638	12838	1.3	1.30E-01	M86918.1	NT	Carassius auratus keratin type I mRNA, complete cds
3404	8546	13654	1.0	1.30E-01	M21572.1	NT	Bovine branched chain alpha-keto acid dihydrolipoyl transacylase mRNA, complete cds
3661	8600	13894	1.2	1.30E-01	AP000001.1	NT	Pyrococcus horikoshii OT3 genomic DNA, 1-287000 nt, position (1/7)
3661	8600	13895	1.2	1.30E-01	AP000001.1	NT	Pyrococcus horikoshii OT3 genomic DNA, 1-287000 nt, position (1/7)
3667	8606	13900	0.8	1.30E-01	AB032159.1	NT	Homo sapiens DD4 gene for dihydrolipoyl dehydrogenase 4 [AKR1C4], exon 2
3714	8800	13894	0.9	1.30E-01	AP000001.1	NT	Pyrococcus horikoshii OT3 genomic DNA, 1-287000 nt, position (1/7)
3714	8800	13895	0.9	1.30E-01	AP000001.1	NT	Pyrococcus horikoshii OT3 genomic DNA, 1-287000 nt, position (1/7)
3734	8871	13963	0.9	1.30E-01	6976840	NT	Rattus norvegicus Fibrinogen, gamma polypeptide (Fgg), mRNA
3906	9041		1.7	1.30E-01	AL161581.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 77
4046	9173		1.2	1.30E-01	AF020713.1	NT	Bacteriophage SPBc2 complete genome
4066	9193		3.4	1.30E-01	AW36434.1	EST_HUMAN	QV3-DT0018-081289-036-a03 DT0018 Homo sapiens cDNA
4075	9202	14288	1.9	1.30E-01	AF026805.1	NT	Schistosoma mansoni fructose biphosphate aldolase mRNA, complete cds
4093	9219	14302	16.4	1.30E-01	AW278741.1	EST_HUMAN	xv2310.x1 Soares NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2813995.3
4218	9342		1.7	1.30E-01	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080
4433	9554	14648	2.2	1.30E-01	BE272339.1	EST_HUMAN	601126098F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:2990063.5
5074	10172	15250	1.2	1.30E-01	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
5074	10172	15251	1.2	1.30E-01	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
5103	10199	15279	0.9	1.30E-01	Z73419.1	NT	Mycobacterium tuberculosis H37Rv complete genome; segment 57/162
378	5584	10717	2.5	1.20E-01	AA421744.1	EST_HUMAN	tf3902.x1 NCI_CGAP_Brn23 Homo sapiens cDNA clone IMAGE:2098539.3 similar to gb:U05760.mat ANNEXIN V (HUMAN);
418	5207		0.5	1.20E-01	U6612.1	NT	Dicystostellum discalaeum ORF DG1016 gene, partial cds
535	5698		0.9	1.20E-01	AF039442.1	NT	Homo sapiens colon cancer antigen NY-CO-45 mRNA, partial cds

Table 4

1490	6617	1.1	1.20E-01	AA897474.1	EST_HUMAN	a448609.s1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1460584 3' similar to TR:Q16671 Q16671 ANTI-MULLERIAN HORMONE TYPE II RECEPTOR PRECURSOR. ;
1613	6739	1.2	1.20E-01	Q14934	SWISSPROT	NUCLEAR FACTOR OF ACTIVATED T-CELLS, CYTOPLASMIC 4 (T CELL
1631	6757	1.0	1.20E-01	A1285402.1	EST_HUMAN	TRANSCRIPTION FACTOR NFAT3 (NF-ATC4) (NF-AT3)
1730	6853	11.0	1.20E-01	X89211.1	NT	q69709.x1 NCI CGAP_Eso2 Homo sapiens cDNA clone IMAGE:1860553 3'
1739	6862	0.6	1.20E-01	U41418.1	NT	H.sapiens DNA for endogenous retroviral like element
1877	6995	0.5	1.20E-01	AW449368.1	EST_HUMAN	Vibrio furnissii chitinase gene, complete cds
2240	7346	1.0	1.20E-01	AL163213.2	NT	U1-H-B13-ak-e-10-0-U1.s1 NCI CGAP_Sub5 Homo sapiens cDNA clone IMAGE:2734554 3'
2346	7642	0.7	1.20E-01	AW996556.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C013
						QV3-BN0046-220300-129-110 BND046 Homo sapiens cDNA
						ts18607.x1 NCI CGAP_Pant1 Homo sapiens cDNA clone IMAGE:2228988 3' similar to
						TR:Q14048 Q14048 COLLAGEN VI ALPHA-2 ALTERNATIVE C-TERMINAL DOMAIN. (1)
						:contains element PTR5 repetitive element ;
2697	7783	0.9	1.20E-01	A1623388.1	EST_HUMAN	Human E1A enhancer binding protein (E1A-F) mRNA, partial cds
2812	7963	1.5	1.20E-01	U18018.1	NT	as80c08.x1 Barstead colon HPLR87 Homo sapiens cDNA clone IMAGE:2335024 3' similar to
2872	8023	2.0	1.20E-01	A1720470.1	EST_HUMAN	gp1.105095 60S RIBOSOMAL PROTEIN L30 (HUMAN);
2904	8055	2.9	1.20E-01	M16364.1	NT	Human creatine kinase-B mRNA, complete cds
2974	8125	1.0	1.20E-01	X56882.1	NT	Wheat mRNA for a group 3 late embryogenesis abundant protein (LEA)
3177	8326	2.0	1.20E-01	M86376.1	NT	Rat topoisomerase gene, exon 28-36
3177	8326	2.0	1.20E-01	M86376.1	NT	Rat topoisomerase gene, exon 28-36
3192	8341	2.0	1.20E-01	AW370686.1	EST_HUMAN	QV1-BT0259-261099-021-405 BT0259 Homo sapiens cDNA
3219	8367	1.0	1.20E-01	U67600.1	NT	Methanococcus jannaschii section 142 of 150 of the complete genome
3433	8575	0.8	1.20E-01	Z99118.1	NT	Bacillus subtilis complete genome (section 15 of 21): from 2795131 to 3013540
3477	8618	1.1	1.20E-01	X56882.1	NT	Wheat mRNA for a group 3 late embryogenesis abundant protein (LEA)
3477	8618	1.1	1.20E-01	X56882.1	NT	Wheat mRNA for a group 3 late embryogenesis abundant protein (LEA)
3554	8575	1.2	1.20E-01	Z99118.1	NT	Bacillus subtilis complete genome (section 15 of 21): from 2795131 to 3013540
4090	8216	2.2	1.20E-01	Z54255.1	NT	P. clarkei mRNA; repeat region (ID 2MR17)
4090	8216	2.2	1.20E-01	Z54255.1	NT	P. clarkei mRNA; repeat region (ID 2MR17)
						much [rats, Sprague-Dawley, sulfur-dioxide-treated tracheal epithelium, mRNA Partial, 390
						nt]
4745	9856	7.1	1.20E-01	S65019.1	NT	H.sapiens gene for N-methyl-D-aspartate receptor R1 exons 6-21
4775	9865	6.7	1.20E-01	Z32774.1	NT	H.sapiens gene for N-methyl-D-aspartate receptor R1 exons 6-21
4775	9865	6.7	1.20E-01	Z32774.1	NT	H.sapiens gene for N-methyl-D-aspartate receptor R1 exons 6-21
5012	10114	1.0	1.20E-01	P16466	SWISSPROT	HEMOLYSIN PRECURSOR
5174	10268	1.5	1.20E-01	Q10441	SWISSPROT	HYPOTHETICAL 52.4 KD PROTEIN C12B10.08C IN CHROMOSOME 1
5174	10268	1.5	1.20E-01	Q10441	SWISSPROT	HYPOTHETICAL 52.4 KD PROTEIN C12B10.08C IN CHROMOSOME 1
5199	10290	2.5	1.20E-01	AW401836.1	EST_HUMAN	U1-H-F-BK0-aah-d-01-0-U1.1 NIH_MGC_36 Homo sapiens cDNA clone IMAGE:3053617 5'
552	5715	1.0	1.10E-01	A1561003.1	EST_HUMAN	nt18d08.x1 NCI CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2187983 3'

Table 4

599	5757	10876	1.2	1.10E-01	AA569006.1	EST_HUMAN	nm00811.1 st NCI CGAP Co10 Homo sapiens cDNA clone IMAGE:1059620 3' similar to gb:X05985 mat HEME OXYGENASE 1 (HUMAN);
1069	6207		1.3	1.10E-01	AL161560.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 60
1143	7908	11431	1.4	1.10E-01	AV972158.1	EST_HUMAN	EST384142 MAGE resequences, MAGL Homo sapiens cDNA
1229	6359	11522	0.6	1.10E-01	D64004.1	NT	Synchocystis sp. PCC6803 complete genome, 23/27, 2868767-3002865
1821	6940		0.9	1.10E-01	AF051784.1	NT	Xenopus laevis 14S cohesin SMC1 subunit mRNA, complete cds
2268	7312		0.8	1.10E-01	6755215	NT	Mus musculus pre T-cell antigen receptor alpha (Ptcra), mRNA
2492	7875		1.2	1.10E-01	6976676	NT	Rattus norvegicus Procollagen II alpha 1 (Col2a1), mRNA
2520	7616		1.2	1.10E-01	AW821909.1	EST_HUMAN	RCO-ST0379-210100-032-g04 ST0379 Homo sapiens cDNA
2825	7976	13078	1.8	1.10E-01	S62418.1	NT	interleukin-12 p35 subunit [mice, Genomic, 700 nt, segment 4 of 5]
2997	8149	13249	0.8	1.10E-01	F03265.1	EST_HUMAN	HSC1RF022 normalized infant brain cDNA Homo sapiens cDNA clone c-1rf02 3'
							Mus musculus calcium channel, voltage-dependent, T type, alpha 1G subunit (Caena10), mRNA
3299	8445		1.4	1.10E-01	6753231	NT	
3374	8517	13624	3.0	1.10E-01	BE393186.1	EST_HUMAN	601308679F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3627066 5'
3405	8547	13655	1.5	1.10E-01	X62135.1	NT	C.reinhardtii nuclear gene on linkage group XIX
3534	8675	13778	0.9	1.10E-01	Y07695.1	NT	Alimurus gene for transposase
3648	8787	13880	1.2	1.10E-01	X62708.1	NT	G.gallus gene encoding non-histone chromosomal protein HMG-14b, exons 4 and 5
4021	9150	14230	1.3	1.10E-01	AW819412.1	EST_HUMAN	MR3-ST0290-290100-025-g07 ST0290 Homo sapiens cDNA
4021	9150	14231	1.3	1.10E-01	AW819412.1	EST_HUMAN	MR3-ST0290-290100-025-g07 ST0290 Homo sapiens cDNA
							Mus musculus major histocompatibility locus class III region; butyrophilin-like protein gene, partial cds; Notch4, PBX2, RAGE, lysophosphatidic acid acyl transferase-alpha, palmitoyl-protein thioesterase 2 (PPT2), CREB-RP, and tenascin X (TNX) genes, complete>
4027	9155		0.9	1.10E-01	AF030001.1	NT	Drosophila melanogaster Karsicht protein (kar) mRNA, complete cds
4159	9285		7.9	1.10E-01	AF157066.1	NT	IL5-UM0070-020500-068-a08 UM0070 Homo sapiens cDNA
4189	9315	14399	0.8	1.10E-01	AW802056.1	EST_HUMAN	HYPOTHETICAL 82 KD AVIRULENCE PROTEIN IN AVRBS3 REGION
4341	9464		5.9	1.10E-01	P14728	SWISSPROT	Fugu rubripes neurofibromatosis type 1 (NF1), A-kinase anchor protein (AKAP84), BAW
4466	9586	14682	0.9	1.10E-01	AF064564.2	NT	protein (BAW), and WSB1 protein (WSB1) genes, complete cds
4539	9658	14746	2.0	1.10E-01	S44957.1	NT	Tapa-1=Integral membrane protein TAPA-1 [mice, B cell lymphoma line 38C13, Genomic, 1973 nt, segment 1 of 7]
4725	9837	14929	1.3	1.10E-01	Y07695.1	NT	Alimurus gene for transposase
4819	9928	15019	1.3	1.10E-01	D90908.1	NT	Synchocystis sp. PCC6803 complete genome, 10/27, 1188886-1311234
4979	10082	15152	1.1	1.10E-01	Z83335.1	NT	S.pneumoniae dexB, cap1[A,B,C,D,E,F,G,H,I,J,K] genes, dTDP-ribose biosynthesis genes and alla gene
							DEOXYRIBONUCLEASE II PRECURSOR (DNASE II) (ACID DNASE) (LYSOSOMAL DNASE II)
1183	6316		1.4	1.00E-01	O62655	SWISSPROT	ws08601.x1 NCI CGAP Kid11 Homo sapiens cDNA clone IMAGE:249657 3' similar to contains MERT.13 MERT repetitive element;
1251	6380	11539	0.6	1.00E-01	A1985499.1	EST_HUMAN	Helicobacter pylori, strain J99 section 53 of 132 of the complete genome
1336	6464	11632	1.0	1.00E-01	AE001492.1	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 16
1370	6498	11664	1.0	1.00E-01	AL161504.2	NT	
1809	7026	12215	0.9	1.00E-01	AW862179.1	EST_HUMAN	MR1-CT0355-180200-007-g07 CT0355 Homo sapiens cDNA

Table 4

2439	7538	12745	1.0	1.00E-01	AW451385.1	EST_HUMAN	U1-H-B13-alc-d-07-0-U1.s1 NCI CGAP_Sub5 Homo sapiens cDNA clone IMAGE:2736420 3'
3130	8278	13386	4.7	1.00E-01	AA314107.1	EST_HUMAN	EST185938 Colon carcinoma (HCC) cell line II Homo sapiens cDNA 5' end
3130	8279	13387	4.7	1.00E-01	AA314107.1	EST_HUMAN	EST185938 Colon carcinoma (HCC) cell line II Homo sapiens cDNA 5' end
3603	8742	13837	2.6	1.00E-01	U76890.1	NT	Human amelogenin (AMELX) gene on X chromosome, partial promoter region
4307	9430	14519	1.5	1.00E-01	AE002265.2	NT	Chlamydia pneumoniae AR39, section 91 of 94 of the complete genome
4455	8575		1.2	1.00E-01	A1792349.1	EST_HUMAN	an3204.y5 Gessler Wilms tumor Homo sapiens cDNA clone IMAGE:1700358 5'
4613	9727	14821	1.3	1.00E-01	U50450.1	NT	Drosophila melanogaster tyrosine kinase p45 isoform (ter) mRNA, complete cds
4838	9945	15034	2.1	1.00E-01	AW952344.1	EST_HUMAN	EST364414 MAGE resequences, MAGEB Homo sapiens cDNA
4883	10086	15156	6.0	1.00E-01	U50133.1	NT	Human ankyrin (ANK1) gene, exon 42 and complete cds
4983	10086	15157	6.0	1.00E-01	U50133.1	NT	Human ankyrin (ANK1) gene, exon 42 and complete cds
5149	10244		0.8	1.00E-01	BE157114.1	EST_HUMAN	RC3-HT0371-180200-015-c01 HT0371 Homo sapiens cDNA
5158	10253	15324	0.9	1.00E-01	D49683.1	NT	Mouse FTZ-F1 gene
213	5406		1.6	9.90E-02	AF136389.1	NT	Bacillus cereus strain H6 gyrase B subunit (gyrB) gene, partial cds
3229	8377	13484	1.2	9.90E-02	AF099810.1	NT	Homo sapiens neuroxin III-alpha gene, partial cds
551	5714		0.5	9.80E-02	X56338.1	NT	O.saliva RAmv3C gene for alpha-amylase
1711	8834	12014	0.6	9.80E-02		NT	Homo sapiens cytochrome P450, subfamily 1F, polypeptide 1 (CYP2E1) mRNA
3106	8256	13359	3.3	9.80E-02	AF184274.1	NT	Homo sapiens fibroblast growth factor receptor 3 (achondroplasia, thanatophoric dwarfism) (FGFR3) mRNA
4131	9257	14337	6.7	9.80E-02	AF257329.1	NT	Leptospira maculans beta-tubulin mRNA, complete cds
4131	9257	14338	6.7	9.80E-02	AF257329.1	NT	Leptospira maculans beta-tubulin mRNA, complete cds
1328	6457	11624	1.2	9.70E-02	AB005808.1	NT	Aloe arborescens mRNA for NADP-malic enzyme, complete cds
1567	6693		1.0	9.70E-02		NT	Homo sapiens fibroblast growth factor receptor 3 (achondroplasia, thanatophoric dwarfism) (FGFR3) mRNA
2214	7322	12536	0.9	9.70E-02	BE168660.1	EST_HUMAN	QV1-HT0516-070300-095-a04 HT0516 Homo sapiens cDNA
3901	9036		3.6	9.70E-02	Q99795	SWISSPROT	CELL SURFACE A33 ANTIGEN PRECURSOR (GLYCOPROTEIN A33)
1969	7084	12285	1.3	9.60E-02	A1080721.1	EST_HUMAN	oz47d11.x1 Soares NIHMPU S1 Homo sapiens cDNA clone IMAGE:1678485 3'
1969	7084	12286	1.3	9.60E-02	A1080721.1	EST_HUMAN	oz47d11.x1 Soares NIHMPU S1 Homo sapiens cDNA clone IMAGE:1678485 3'
2250	7356	12563	1.0	9.60E-02	AW836565.1	EST_HUMAN	PM3-LT0032-030100-004-b01 LT0032 Homo sapiens cDNA
2250	7356	12564	1.0	9.60E-02	AW836565.1	EST_HUMAN	PM3-LT0032-030100-004-b01 LT0032 Homo sapiens cDNA
4248	9373	14453	6.0	9.60E-02	Z32686.2	NT	Proteus mirabilis fimbrial operon, strain HI4320
4932	10038	15111	0.9	9.60E-02	AW966230.1	EST_HUMAN	EST378303 MAGE resequences, MAGEI Homo sapiens cDNA
5093	10191	15270	0.8	9.60E-02	BE061729.1	EST_HUMAN	RC5-BT0254-031099-011-a03 BT0254 Homo sapiens cDNA
4012	9143	14226	2.3	9.50E-02	AW992395.1	EST_HUMAN	CM2-BN0023-050200-007-f12 BN0023 Homo sapiens cDNA
5062	10160	15236	0.9	9.50E-02	U63374.1	NT	Lycopodium obscurum polygalacturonase isoenzyme 1 beta subunit gene, complete cds
1820	6939	12129	0.9	9.40E-02	U55944.1	NT	Cavia porcellus 3beta-hydroxysteroid sulfotransferase mRNA, complete cds
1820	6939	12130	0.9	9.40E-02	U55944.1	NT	Cavia porcellus 3beta-hydroxysteroid sulfotransferase mRNA, complete cds
3604	8941	14036	4.3	9.40E-02	Z33059.1	NT	M.capricolum DNA for CONTIG MC073
4980	10083	15153	0.9	9.40E-02	6753517	NT	Mus musculus coding region determinant-binding protein (Crdp), mRNA
2960	8111		1.8	9.30E-02		NT	Homo sapiens BAI1-associated protein 3 (BAIAP3) mRNA

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Table 4

3828	8965	14064	1.0	8.80E-02	AA299128.1	EST_HUMAN	EST11595 Uterus Homo sapiens cDNA 5' end
3948	9081		3.2	8.80E-02	O00268	SWISSPROT	TRANSCRIPTION INITIATION FACTOR TFIID 135 KDA SUBUNIT (TAFII-135) (TAFII-130) (TAFII130)
4205	9330		1.1	8.80E-02	4580423	NT	Homo sapiens paired box gene 6 (anhidra, keratilis) (PAX6), isoform b, mRNA
							Homo sapiens zinc finger protein 92 (ZFP92), expressed-Xq28STS protein (XQ28ORF), and biglycan (BGN) genes, complete cds; and plasma membrane calcium ATPase isoform 3 (PMCA3) gene, partial cds
3636	8775	13869	3.0	8.70E-02	U82695.2	NT	Homo sapiens zinc finger protein 92 (ZFP92), expressed-Xq28STS protein (XQ28ORF), and biglycan (BGN) genes, complete cds; and plasma membrane calcium ATPase isoform 3 (PMCA3) gene, partial cds
3636	8775	13870	3.0	8.70E-02	U82695.2	NT	Homo sapiens zinc finger protein 92 (ZFP92), expressed-Xq28STS protein (XQ28ORF), and biglycan (BGN) genes, complete cds; and plasma membrane calcium ATPase isoform 3 (PMCA3) gene, partial cds
3879	9015	14110	0.8	8.70E-02	W87841.1	EST_HUMAN	zh6802.1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:417194.5' similar to contains element MER12 repetitive element ;
4609	9723	14818	1.2	8.70E-02	AF178636.1	NT	Mus musculus JNK interacting protein-3a (Jip3) mRNA, complete cds
							Methanobacterium thermocautotrophicum from bases 1176181 to 1189406 (section 101 of 148) of the complete genome
5034	10134		1.1	8.70E-02	AEO00895.1	NT	Homo sapiens Xq pseudautosomal region: segment 2/2
1232	6361	11523	2.4	8.60E-02	AL271736.1	NT	801304016F1 NIH MGC 21 Homo sapiens cDNA clone IMAGE:3638643.5'
2197	7306	12518	0.8	8.60E-02	BE408667.1	EST_HUMAN	Trichomonas vaginalis beta-tubulin (tub1) gene, complete cds
3151	8300	13408	2.9	8.60E-02	L05486.1	NT	Dicystostellum discoideum jplA gene for inositol 1,4,5-trisphosphate receptor-like protein (jplA), exons 1-4
3264	8411		0.8	8.60E-02	AL277590.1	NT	Dicystostellum discoideum adenylyl cyclase (accA) gene, complete cds
3593	8732		3.1	8.60E-02	AF153362.1	NT	Oryctolagus cuniculus galeactin-3 gene, untranslated exon and 5' flanking region
4385	9507	14592	0.9	8.60E-02	U68179.1	NT	Homo sapiens KIAA0395 mRNA, partial cds
1330	6459	11625	0.6	8.50E-02	AB007855.1	NT	Helicobacter pylori 26695 section 130 of 134 of the complete genome
2347	7449	12856	1.0	8.50E-02	AE000652.1	NT	zdd4e11.1 Soares_fetal_heart_NbHH18W Homo sapiens cDNA clone IMAGE:343532.5'
2632	7950	12923	1.5	8.40E-02	W69330.1	EST_HUMAN	oe09b09.81 NCI CGAP_OV2 Homo sapiens cDNA clone IMAGE:1385369 similar to contains Alu repetitive element; contains element L1 repetitive element ;
4152	9278		0.8	8.40E-02	AA847045.1	EST_HUMAN	Ixodes hexagonus mitochondrion, complete genome
1985	7081	12280	0.9	8.30E-02	5835680	NT	Ixodes hexagonus mitochondrion, complete genome
1985	7081	12281	0.9	8.30E-02	5835680	NT	Ixodes hexagonus mitochondrion, complete genome
3544	8685	13786	6.2	8.30E-02	P75334	SWISSPROT	HYPOTHETICAL LIPOPROTEIN MG309 HOMOLOG PRECURSOR
3567	8706	13803	0.9	8.30E-02	AA36797.1	EST_HUMAN	th62g06.x1 Soares_NhhMPu_S1 Homo sapiens cDNA clone IMAGE:2125210.3'
3567	8706	13804	0.9	8.30E-02	AA36797.1	EST_HUMAN	th62g06.x1 Soares_NhhMPu_S1 Homo sapiens cDNA clone IMAGE:2125210.3'
1243	6372		0.7	8.20E-02	6881050	NT	Mus musculus colony stimulating factor 3 receptor (granulocyte) (Csfr3), mRNA
1357	6485		2.8	8.20E-02	Y08170.2	NT	Gallus gallus mRNA for for OBCAM protein gamma isoform
1480	6607	11780	1.2	8.20E-02	AF167077.2	NT	Canis familiaris glutamate transporter (EAAT4) mRNA, complete cds
3036	8188		1.8	8.20E-02	AL163206.2	NT	Homo sapiens chromosome 21 segment HS21C006
3733	8870		1.3	8.20E-02	AL161498.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 10
3926	9060	14147	1.1	8.20E-02	AL163206.2	NT	Homo sapiens chromosome 21 segment HS21C006
4187	9313	14394	5.4	8.20E-02	P48960	SWISSPROT	LEUCOCYTE ANTIGEN CD97 PRECURSOR
4187	9313	14395	5.4	8.20E-02	P48960	SWISSPROT	LEUCOCYTE ANTIGEN CD97 PRECURSOR



Table 4

4187	9313	14396	5.4	8.20E-02	P48960	SWISSPROT	LEUCOCYTE ANTIGEN CD97 PRECURSOR
5014	10116	15187	2.8	8.20E-02	U76009.1	NT	Mus musculus zinc transporter (ZnT-3) gene, complete cds
1479	6606	11779	1.7	8.10E-02	AB017138.1	NT	Pseudomonas putida malonate decarboxylase gene cluster (mdcA, mdcB, mdcC, mdcD, mdcE, mdcG, mdcH, mdcI, and mdcM genes), complete cds
5	7879	10316	1.1	8.00E-02	AW934653.1	EST_HUMAN	EST366723 MAGE resequences, MAGC Homo sapiens cDNA
920	6066	11222	1.3	8.00E-02	U60315.1	NT	Molluscum contagiosum virus subtype 1, complete genome
1353	6481	11647	4.6	8.00E-02	D63881.1	NT	Homo sapiens DNA for cyclophilin 40, complete cds
1671	7923	11972	3.8	8.00E-02	D26535.1	NT	Human gene for dihydrodipicolinate succinyltransferase, complete cds (exon 1-15)
1671	7923	11973	3.8	8.00E-02	D26535.1	NT	Human gene for dihydrodipicolinate succinyltransferase, complete cds (exon 1-15)
1861	6979	12164	1.4	8.00E-02	BE067219.1	EST_HUMAN	PM3-BT0347-170200-001-508 BT0347 Homo sapiens cDNA
2323	7426	12835	1.0	8.00E-02	D90915.1	NT	Synechocystis sp. PCC6803 complete genome, 17/27, 2137259-2267259
2323	7426	12836	1.0	8.00E-02	D90915.1	NT	Synechocystis sp. PCC6803 complete genome, 17/27, 2137259-2267259
2790	6213	11365	0.8	8.00E-02	M23449.1	NT	Dicystosium discoideum cyclic nucleotide phosphodiesterase gene, complete cds
3745	8863	13972	0.8	8.00E-02	AW986118.1	EST_HUMAN	EST378191 MAGE resequences, MAGI Homo sapiens cDNA
3980	9112		1.1	8.00E-02	4503034	NT	Homo sapiens cAMP responsive element binding protein-like 2 (CREBL2) mRNA
4709	9821		5.6	8.00E-02	X72794.1	NT	M. musculus gene for gelatinase B
4834	9942	15031	0.9	8.00E-02	M28071.1	NT	Herpesvirus salmifit transformation-associated protein (STP), and dihydrodipicolate reductase (DHFR) gene, s complete cds, and small nuclear RNAs (uRNAs)
1544	6671	11841	0.5	7.90E-02	AE001501.1	NT	Helicobacter pylori, strain J99 section 62 of 132 of the complete genome
1544	6671	11842	0.5	7.90E-02	AE001501.1	NT	Helicobacter pylori, strain J99 section 62 of 132 of the complete genome
2127	7237	12445	1.4	7.90E-02	BE250008.1	EST_HUMAN	600943191F NIH_MGC_15 Homo sapiens cDNA clone IMAGE:2969510 5'
2948	8099	13205	6.4	7.90E-02	A1582029.1	EST_HUMAN	ar86c08.x1 Barstead colon HPLRB7 Homo sapiens cDNA clone IMAGE:2173646 3' similar to gb:226876 60S RIBOSOMAL PROTEIN L38 (HUMAN):
3255	8402	13508	1.2	7.90E-02	A457925.1	EST_HUMAN	ij55q03.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2145460 3'
3776	8913	14003	3.3	7.90E-02	6681044	NT	Mus musculus colony stimulating factor 1 receptor (Csf1r), mRNA
3776	8913	14004	3.3	7.90E-02	6681044	NT	Mus musculus colony stimulating factor 1 receptor (Csf1r), mRNA
4706	9818		1.2	7.90E-02	AB008019.1	NT	Arabidopsis thaliana RXW24L mRNA, partial cds
1192	6324	11479	1.4	7.80E-02	A1793275.1	EST_HUMAN	0059402.y5 NCL_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1570467 5' similar to contains L1.13 L1 repetitive element:
1192	6324	11480	1.4	7.80E-02	A1793275.1	EST_HUMAN	0059402.y5 NCL_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1570467 5' similar to contains L1.13 L1 repetitive element:
1378	7915	11671	1.0	7.80E-02	AW868884.1	EST_HUMAN	CM3-SNU032-010400-137-107 SNU032 Homo sapiens cDNA
5019	8826		2.7	7.80E-02	BE250048.1	EST_HUMAN	600943055F NIH_MGC_15 Homo sapiens cDNA clone IMAGE:2959693 5'
5197	10288	15357	1.0	7.80E-02	A418520.1	EST_HUMAN	ig48g12.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2112070 3' similar to contains MER10.13 MER10 repetitive element:
3538	8679		2.1	7.70E-02	AJ238093.1	NT	Homo sapiens partial AF-4 gene, exons 2 to 7 and Alu repeat elements
3362	8505	13613	0.9	7.60E-02	AA296447.1	EST_HUMAN	EST112214 Cerebellum II Homo sapiens cDNA 5' end similar to similar to protocadherin 43
3512	8653	13761	0.9	7.60E-02	A4400877.1	NT	Homo sapiens ASCL3 gene, CEGP1 gene, C11orf14 gene, C11orf15 gene, C11orf16 gene and C11orf17 gene



Table 4

4765	9876	1.0	7.60E-02	AW85844.1	EST_HUMAN	RC3-CT0347-110300-014-205 CT0347 Homo sapiens cDNA
767	5920	1.1	7.50E-02	5602093	NT	Homo sapiens solute carrier family 6 (neurotransmitter transporter, glycine), member 9 (SLC6A9), mRNA
767	5920	1.1	7.50E-02	5602093	NT	Homo sapiens solute carrier family 6 (neurotransmitter transporter, glycine), member 9 (SLC6A9), mRNA
767	5920	1.1	7.50E-02	5602093	NT	Homo sapiens chromosome 21 segment HS21C078
1878	6996	0.9	7.50E-02	AL163276.2	NT	Homo sapiens IL-18 gene for interleukin-18, intron 1 and exon 2
4407	9527	0.8	7.50E-02	AB015981.1	NT	Homo sapiens IL-18 gene for interleukin-18, intron 1 and exon 2
469	5634	1.2	7.40E-02	AW838547.1	EST_HUMAN	RC5-LT0054-260100-011-H09 LT0054 Homo sapiens cDNA
1444	6571	1.1	7.40E-02	AF030027.1	NT	Equine herpesvirus 4 strain NS80567, complete genome
2536	7632	0.9	7.40E-02	675069	NT	Mus musculus paired-like homeodomain transcription factor 1 (Pbx1), mRNA
3545	8686	0.9	7.40E-02	AI807885.1	EST_HUMAN	Mus musculus ADP/ATP carrier protein (ANT-2) gene, complete cds
4806	9720	3.4	7.40E-02	L78810.1	NT	Homo sapiens ADP/ATP carrier protein (ANT-2) gene, complete cds
4687	9799	2.7	7.40E-02	6978442	NT	Rattus norvegicus Activin receptor like kinase 1 (Acvrl), mRNA
4858	9965	1.7	7.40E-02	6878492	NT	Mus musculus ubiquitin C-terminal hydrolase related polypeptide (Uchmp), mRNA
669	5625	0.9	7.30E-02	AE001789.1	NT	Thermotoga maritima section 101 of 136 of the complete genome
1465	7917	1.1	7.30E-02	AW900281.1	EST_HUMAN	CM0-NN1004-130300-284-808 NN1004 Homo sapiens cDNA
1801	7927	5.4	7.30E-02	AL163302.2	NT	Homo sapiens chromosome 21 segment HS21C102
4927	10034	1.0	7.30E-02	U12283.1	NT	Mus musculus transcription factor USF2 (USF2) gene, exons 8-10 and complete cds
114	5315	0.9	7.20E-02	AE000882.1	NT	Methanobacterium thermoautotrophicum from bases 1029155 to 1039934 (section 88 of 148) of the complete genome
114	5315	0.9	7.20E-02	AE000882.1	NT	Methanobacterium thermoautotrophicum from bases 1029155 to 1039934 (section 88 of 148) of the complete genome
114	5315	0.9	7.20E-02	AE000882.1	NT	Methanobacterium thermoautotrophicum from bases 1029155 to 1039934 (section 88 of 148) of the complete genome
1460	6587	0.8	7.20E-02	AL163301.2	NT	Homo sapiens chromosome 21 segment HS21C101
1460	6587	0.8	7.20E-02	AL163301.2	NT	Homo sapiens chromosome 21 segment HS21C101
2502	7599	0.9	7.20E-02	U14794.1	NT	Human immunodeficiency virus type 1 isolate 26 reverse transcriptase (pol) gene, internal fragment, partial cds
3810	8947	0.8	7.20E-02	AW298322.1	EST_HUMAN	U1-H-BW0-ajl-a-05-0-UI.s1 NC1_CGAP_Sub6 Homo sapiens cDNA clone IMAGE:2732049 3'
4997	10100	0.9	7.20E-02	AB001562.1	NT	Streptococcus mutans gene for glucose-1-phosphate uridylyltransferase, complete cds
1091	6229	1.3	7.10E-02	AB010711.1	NT	Mus sp. mRNA for MB20, complete cds
1862	6980	0.6	7.10E-02	L02290.1	NT	Human immunodeficiency virus type 1 (D9) proviral structural capsid protein (gag) gene, partial cds
517	5681	1.2	7.00E-02	Q07092	SWISSPROT	COLLAGEN ALPHA 1(XV) CHAIN PRECURSOR
1484	6611	0.5	7.00E-02	X86677.1	NT	Matrilinea Mitcu-1 gene
1725	6848	1.4	7.00E-02	AA056343.1	EST_HUMAN	Zf6604.s1 Stralagene colon (#937204) Homo sapiens cDNA clone IMAGE:505599 3'
2994	8146	1.7	7.00E-02	AW138152.1	EST_HUMAN	U1-H-B1-acy-c-07-0-UI.s1 NC1_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2716020 3'
3822	8959	1.0	7.00E-02	AA815438.1	EST_HUMAN	ai85a12.s1 Soares_testis_NHT Homo sapiens cDNA clone 1375678 3' similar to gb:K03002
3956	9091	1.2	7.00E-02	BE070264.1	EST_HUMAN	60S RIBOSOMAL PROTEIN L32 (HUMAN);
						QV4-BT0407-280100-090-e10 BT0407 Homo sapiens cDNA

Table 4

4047	9174	1.1	7.00E-02	AW792862.1	EST_HUMAN	GM0-UM0001-060300-270-e12 UM0001 Homo sapiens cDNA
4121	9247	1.3	7.00E-02	AF077821.1	NT	Carls familiaris inducible nitric oxide synthase mRNA, complete cds
503	5667	1.8	6.90E-02	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
503	5667	1.8	6.90E-02	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
						Homo sapiens regulator of Gz-selective protein signaling (ZGAP1) mRNA, and translated products
1311	6439	1.3	6.90E-02	4507968	NT	
3724	8661	1.4	6.90E-02	Q06364	SWISSPROT	265 PROTEASOME REGULATORY SUBUNIT S3 (NUCLEAR ANTIGEN 21D7)
3724	8661	1.4	6.90E-02	Q06364	SWISSPROT	265 PROTEASOME REGULATORY SUBUNIT S3 (NUCLEAR ANTIGEN 21D7)
5100	10196	1.1	6.90E-02	AF079906.1	NT	Rabies virus isolate b615 glycoprotein gene, partial cds
						ae3002.r1 Gessler Wilms tumor Homo sapiens cDNA clone IMAGE:897339 5' similar to
						gb:M22382 MITOCHONDRIAL MATRIX PROTEIN P1 PRECURSOR (HUMAN);
1839	6658	1.1	6.80E-02	AA496759.1	EST_HUMAN	ae3002.r1 Gessler Wilms tumor Homo sapiens cDNA clone IMAGE:897339 5' similar to
						gb:M22382 MITOCHONDRIAL MATRIX PROTEIN P1 PRECURSOR (HUMAN);
1839	6658	1.1	6.80E-02	AA496759.1	EST_HUMAN	ae3002.r1 Gessler Wilms tumor Homo sapiens cDNA clone IMAGE:897339 5' similar to
1865	6683	1.4	6.80E-02	AF156673.1	NT	gb:M22382 MITOCHONDRIAL MATRIX PROTEIN P1 PRECURSOR (HUMAN);
3062	8213	1.2	6.80E-02	AA781986.1	EST_HUMAN	Homo sapiens putative hepatic transcription factor (WBSOR14) gene, complete cds
3062	8213	1.2	6.80E-02	AA781986.1	EST_HUMAN	ai75606.s1 Soares testis_NHT Homo sapiens cDNA clone 1376626 3'
3062	8213	1.2	6.80E-02	AA781986.1	EST_HUMAN	ai75606.s1 Soares testis_NHT Homo sapiens cDNA clone 1376626 3'
4453	9573	0.9	6.80E-02	BE141076.1	EST_HUMAN	MR0-HT0069-071099-001-c05 HT0069 Homo sapiens cDNA
4773	9883	0.9	6.80E-02	M86150.1	NT	Caenorhabditis elegans LDL receptor-related protein (lpr-1) gene, complete cds
						Oncorhynchus mykiss TAP1 protein (OnmyTAP1) mRNA, OnmyTAP1*01 allele, complete cds
1511	6638	0.8	6.70E-02	AF15536.1	NT	
1511	6638	0.9	6.70E-02	AI220285.1	EST_HUMAN	qg79e04.x1 Soares NFL_T GBC S1 Homo sapiens cDNA clone IMAGE:1841406 3'
2982	8113	1.1	6.70E-02	M13156.1	NT	Yeast (S.pombe) cdc25+ gene (mitosis initiation), complete cds
2982	8113	1.1	6.70E-02	M13156.1	NT	Yeast (S.pombe) cdc25+ gene (mitosis initiation), complete cds
						x65101.x1 NCI CGAP Lu26 Homo sapiens cDNA clone IMAGE:2766961 3' similar to
3316	8461	0.8	6.70E-02	AW301973.1	EST_HUMAN	contains element TAR1 repetitive element;
3656	8795	3.5	6.70E-02	P17278	SWISSPROT	HOMEOBOX PROTEIN HOX-D4 (HOX-A)
1326	6455	1.1	6.60E-02	AF735509.1	EST_HUMAN	ai12609.x1 Barstead aorta HPLRB6 Homo sapiens cDNA clone IMAGE:2354920 3' similar to
1347	6475	0.5	6.60E-02	AF245116.1	NT	SW:LIN1_NYCCO P08548 LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.;
3133	8282	1.3	6.60E-02	Q13585	SWISSPROT	Drosophila melanogaster cactin mRNA, complete cds
3418	8560	8.6	6.60E-02	R64306.1	EST_HUMAN	MELATONIN-RELATED RECEPTOR (H9)
3432	8574	2.2	6.60E-02	7108357	NT	y18b10.s1 Soares placenta NB2HP Homo sapiens cDNA clone IMAGE:139579 3'
3432	8574	2.2	6.60E-02	7108357	NT	Homo sapiens mesothelin (MSLN) transcript variant 1, mRNA
						Homo sapiens mesothelin (MSLN) transcript variant 1, mRNA
						INTER-ALPHA-TRYPsin INHIBITOR HEAVY CHAIN H2 PRECURSOR (ITI HEAVY CHAIN H2)
4904	10011	8.4	6.60E-02	Q61703	SWISSPROT	INTER-ALPHA-TRYPsin INHIBITOR HEAVY CHAIN H2 PRECURSOR (ITI HEAVY CHAIN H2)
4904	10011	8.4	6.60E-02	Q61703	SWISSPROT	INTER-ALPHA-TRYPsin INHIBITOR HEAVY CHAIN H2 PRECURSOR (ITI HEAVY CHAIN H2)
5167	10261	1.3	6.60E-02	AF204882.1	NT	Amnacta albigata nucleopolydnavirus AcORF17 homolog gene, complete cds
971	6117	0.6	6.50E-02	7708068	NT	Homo sapiens E2F-like protein (LOC51270). mRNA
1369	6497	1.5	6.50E-02	U47624.1	NT	Xenopus laevis alpha(E)-catenin mRNA, complete cds

Table 4

1702	6625	12006	0.8	6.50E-02	AE000764.1	NT	Aquifex aeolicus section 96 of 109 of the complete genome
561	5723	10839	0.5	6.40E-02	X9549.1	NT	A. carterae precursor of peritrophin-chitroplyla-protein (PCP) gene
4802	8133	13240	1.4	6.40E-02	6996923	NT	Mus musculus histone deacetylase 5 (Hdac5), mRNA
5180	10272		8.8	6.40E-02	6996923	NT	Mus musculus histone deacetylase 5 (Hdac5), mRNA
							Mus musculus major histocompatibility locus class III regions Hsc70t gene, partial cds; smRNP, G7A, NG23, Muls homolog, CLCP, NG24, NG25, and NG26 genes, complete cds; and unknown genes
1720	6843	12022	0.9	6.30E-02	AF109905.1	NT	HEAT SHOCK PROTEIN 70 HOMOLOG.
3552	8692		2.1	6.30E-02	P37092	SWISSPROT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 68
4157	9283	14363	3.4	6.20E-02	AL161572.2	NT	Rattus norvegicus differentiation-associated Na-dependent inorganic phosphate cotransporter
4243	9368		1.1	6.20E-02	AF271235.1	NT	(ONP) mRNA, complete cds
4347	9470	14559	0.8	6.20E-02	AW951243.1	EST_HUMAN	EST363313 MAGE resequences, MAGA Homo sapiens cDNA
4347	9470	14560	0.8	6.20E-02	AW951243.1	EST_HUMAN	EST363313 MAGE resequences, MAGA Homo sapiens cDNA
							52 KD RO PROTEIN (SJOGEREN SYNDROME TYPE A ANTIGEN (SS-A)) (RO(SS-A)) (RO52)
4479	9599		5.4	6.20E-02	Q62191	SWISSPROT	Human mRNA, Xq terminal portion
256	5444	10570	1.5	6.10E-02	D16471.1	NT	Arabidopsis thaliana K+ inward rectifying channel protein (AKC1) gene, complete cds
3909	9044		2.7	6.10E-02	U73325.1	NT	Homo sapiens mRNA for KIAA1464 protein, partial cds
5150	10245	15317	1.0	6.10E-02	AB040897.1	NT	Thermoplasma maritima section 89 of 136 of the complete genome
1241	6370	11529	1.4	6.00E-02	AE001777.1	NT	MR3-ST0220-120100-025-d04 ST0220 Homo sapiens cDNA
2547	7643		1.5	6.00E-02	AW816119.1	EST_HUMAN	EST380924 MAGE resequences, MAGI Homo sapiens cDNA
2641	7730	12931	0.6	6.00E-02	AW968848.1	EST_HUMAN	Mesocostoides cori mitochondrial DNA, NADH dehydrogenase subunit 4, tRNA-Gln, tRNA-Phe, tRNA-Met, ATPase subunit 6, and NADH dehydrogenase subunit 2
2745	7829		0.6	6.00E-02	AB031289.1	NT	zp78c04.r1 Stralagene HeLa cell s3 937216 Homo sapiens cDNA clone IMAGE:626310 5'
2906	5296	10424	1.2	6.00E-02	AA188730.1	EST_HUMAN	zp78c04.r1 Stralagene HeLa cell s3 937216 Homo sapiens cDNA clone IMAGE:626310 5'
2906	5298	10425	1.2	6.00E-02	AA188730.1	EST_HUMAN	EST184268 Colon adenocarcinoma IV Homo sapiens cDNA 5' and similar to tissue-specific protein
3191	8340	13453	1.2	6.00E-02	AA372376.1	EST_HUMAN	EST184268 Colon adenocarcinoma IV Homo sapiens cDNA 5' and similar to tissue-specific protein
3191	8340	13454	1.2	6.00E-02	AA372376.1	EST_HUMAN	EST184268 Colon adenocarcinoma IV Homo sapiens cDNA 5' and similar to tissue-specific protein
4893	10000	15083	1.2	6.00E-02	Z67739.2	NT	Streptococcus pneumoniae parC, parE and transposase genes and ORF DNA
229	5420	10543	1.2	5.90E-02	AW934719.1	EST_HUMAN	RC1-DT0001-290100-012-e10 DT0001 Homo sapiens cDNA
2955	8106	13213	2.6	5.90E-02	AF190269.1	NT	Mus musculus p53 tumor suppressor gene, exon 10 and 11, partial cds; alternatively spliced
4517	9636		1.1	5.90E-02	4506466	NT	Homo sapiens radixin (RDX) mRNA
4770	9681	14975	0.9	5.90E-02	AF006304.1	NT	Saccharomyces cerevisiae protein tyrosine phosphatase (PTP3) gene, complete cds
917	6063		1.5	5.80E-02	D90110.1	NT	Thiobacillus ferrooxidans merC, merA genes and URF-1
2830	7981		1.1	5.80E-02	AJ223621.1	NT	Populus trichocarpa CCoAOMT1 gene, exon 1 to exon 5
3813	8752	13846	1.4	5.80E-02	AE001775.1	NT	Thermoplasma maritima section 87 of 136 of the complete genome
4257	9382	14463	4.4	5.80E-02	AW051927.1	EST_HUMAN	wc24c02.x1 NCI CGAP Kid11 Homo sapiens cDNA clone IMAGE:2544578 3'

Table 4

4257	8382	14464	4.4	5.80E-02	AW051927.1	EST_HUMAN	w24c02.x1 NCI CGAP Kid11 Homo sapiens cDNA clone IMAGE:2544578.3'
4447	9567	14664	4.2	5.80E-02	AI247505.1	EST_HUMAN	qb5601.x1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1848697.3 similar to gb:M13142 COAGULATION FACTOR XI PRECURSOR (HUMAN);
4447	9567	14665	4.2	5.80E-02	AI247505.1	EST_HUMAN	qb5601.x1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1848697.3 similar to gb:M13142 COAGULATION FACTOR XI PRECURSOR (HUMAN);
4471	9591		2.0	5.80E-02	AF098264.1	NT	Gallus gallus tyrosine kinase JAK1 (JAK1) mRNA, complete cds
2659	7748	12946	1.0	5.70E-02	AI708246.1	EST_HUMAN	as24f06.x1 Barstead aorta HPLRB6 Homo sapiens cDNA clone IMAGE:2318147.3 similar to gb:X14850.cds1 HISTONE H2A.X (HUMAN);
2659	7748	12947	1.0	5.70E-02	AI708246.1	EST_HUMAN	as24f06.x1 Barstead aorta HPLRB6 Homo sapiens cDNA clone IMAGE:2318147.3 similar to gb:X14850.cds1 HISTONE H2A.X (HUMAN);
3018	8170	13270	1.3	5.70E-02	AI081644.1	EST_HUMAN	WP-C37A2.2 CE08611.1
3033	8185	13286	1.3	5.70E-02	AF119117.1	NT	Homo sapiens dopamine transporter (SLC6A3) gene, complete cds
3731	8868	13960	1.8	5.70E-02	AW966791.1	EST_HUMAN	EST378865 MAGE resequences, MAGE Homo sapiens cDNA
1510	6637	11806	0.9	5.60E-02	AF094455.1	NT	Hydroxycylo rotundifolia ribosomal protein L16 (p116) gene, intron; chloroplast gene for chloroplast product
4217	9341	14425	0.9	5.60E-02	AI390487.1	NT	Candida albicans mitochondrial mRNA for NADH dehydrogenase (nde1 gene)
4540	9659	14747	1.3	5.60E-02	AB013100.1	NT	Lycepericon esculentum LE-ACS6 mRNA for 1-aminocyclopropane-1-carboxylate synthase, complete cds
4598	9712	14804	1.1	5.60E-02	AA290599.1	EST_HUMAN	z545c01.s1 NCI CGAP GCB1 Homo sapiens cDNA clone IMAGE:700416.3'
2618	7708	12907	3.0	5.50E-02	X97869.1	NT	H.sapiens gene encoding La autoantigen
3179	8328	13441	3.6	5.50E-02	6755501	NT	Mus musculus SH3 domain protein 1B (Sh3d1B), mRNA
4777	9887	14980	0.8	5.50E-02	AF161266.1	NT	Murray Valley encephalitis virus strain MVE-1-51, complete genome
2986	8138		1.0	5.40E-02	AI277468.1	NT	Oryza sativa rbb13-1 gene for putative Bowman Birk trypsin inhibitor
3375	8518		6.3	5.40E-02	BE073468.1	EST_HUMAN	RC3-BT0559-140200-012-C03 BT0559 Homo sapiens cDNA
4908	10015	15095	0.9	5.40E-02	U53528.1	NT	Xenopus laevis homeobox protein (Xox-1) mRNA, complete cds
5108	10204	15283	1.0	5.40E-02	M96781.1	NT	Mus musculus p-glycoprotein (mdr1a) gene, exons 1 and 2
1037	6177	11329	0.6	5.30E-02	AW391248.1	EST_HUMAN	QVO-ST0213-021299-062-a09 ST0213 Homo sapiens cDNA
1037	6177	11330	0.6	5.30E-02	AW391248.1	EST_HUMAN	QVO-ST0213-021299-082-a09 ST0213 Homo sapiens cDNA
							ye37T12.r1 Stratiagene lung (#937210) Homo sapiens cDNA clone IMAGE:119951.5' similar to gb:K01506 HLA CLASS II HISTOCOMPATIBILITY ANTIGEN, DP(1) ALPHA CHAIN (HUMAN);
1489	6616	11787	6.6	5.30E-02	T94759.1	EST_HUMAN	Pseudomonas putida tigs gene
2447	7546	12754	1.1	5.30E-02	AI276408.1	NT	Drosophila melanogaster lamnlin B2 gene, complete cds
2912	8063	13170	3.9	5.30E-02	M58417.1	NT	Drosophila melanogaster lamnlin B2 gene, complete cds
2912	8063	13171	3.9	5.30E-02	M58417.1	NT	Pseudomonas putida tigs gene
3113	8262	13366	4.6	5.30E-02	AI276408.1	NT	Arabidopsis thaliana ell5 gene, exons 1-11
4506	9625	14717	1.2	5.30E-02	AI011048.1	NT	Mus musculus caudal type homeobox-1 (Cdx-1) gene, complete cds
5021	10122	15194	7.3	5.30E-02	M80463.1	NT	Mus musculus caudal type homeobox-1 (Cdx-1) gene, complete cds
2239	7345		160.0	5.20E-02	5031908	NT	Homo sapiens meprin A, alpha (PABA peptide hydrolase) (MEP1A) mRNA

Table 4

4181	9307	14386	3.4	5.20E-02	U07132.1	NT	Human steroid hormone receptor Nr1 mRNA, complete cds
4490	9610	14703	2.4	5.20E-02	X58743.1	NT	H.sapiens HCK gene for tyrosine kinase (PTK), exon 12
4490	9610	14704	2.4	5.20E-02	X58743.1	NT	H.sapiens HCK gene for tyrosine kinase (PTK), exon 12
4633	9747	14843	1.0	5.20E-02	L33246.1	NT	Drosophila melanogaster filament protein homolog (sep1) gene, complete cds
2313	7416		1.0	5.10E-02	AL134071.1	EST_HUMAN	DKFZps47D073_t1 547 (synonym: hbr1) Homo sapiens cDNA clone DKFZps47D073.5'
3610	8749	13843	3.6	5.10E-02	AF094269.1	NT	HIV-1 isolate 2001-4-37 from USA, envelope glycoprotein (env) gene, partial cds
3644	8783		5.8	5.10E-02	AA652287.1	EST_HUMAN	nas69d01.s1 NCI CGAP_P12 Homo sapiens cDNA clone IMAGE:118865 similar to contains Alu repetitive element; contains element PTR5 repetitive element ;
474	5640	10766	0.7	5.00E-02	AF098004.1	NT	Mus musculus fatty acid amide hydrolase gene, exon 10
1186	6318	11474	2.4	5.00E-02	Z99104.1	NT	Bacillus subtilis complete genome (section 1 of 21): from 1 to 213080
1847	7064	12258	1.5	5.00E-02	P02810	SWISSPROT	SALIVARY ACIDIC PROLINE-RICH PHOSPHOPROTEIN 1/2 PRECURSOR (PRP-1/PRP-3) (PRP-2/PRP-4) (PIF-F/PIF-S) (PROTEIN A/PROTEIN C) [CONTAINS: PEPTIDE P-C]
2788	6116	11274	0.6	5.00E-02	U72742.1	NT	Oryctolagus cuniculus UDP-glucuronosyltransferase (UGT2B13) mRNA, complete cds
3295	8441		1.2	5.00E-02	7305610	NT	Mus musculus Unc-51 like kinase 2 (C. elegans) (Ulk2), mRNA
3629	8768	13862	5.5	5.00E-02	U12769.2	NT	Antheraea pernyi period clock protein homolog mRNA, complete cds
4890	9997	15080	0.9	5.00E-02	AF188530.1	NT	Homo sapiens ubiquitous tetrapeptide containing protein RoXan mRNA, partial cds
218	5410		9.9	4.90E-02	M14230.1	NT	Chicken 28-kDa vitamin D-dependent calcium-binding protein (CaBP-28) mRNA, complete cds
413	5581		1.9	4.90E-02	D26607.1	NT	Homo sapiens endothelial nitric oxide synthase gene, complete cds
3251	8398	13504	1.9	4.90E-02	PS4258	SWISSPROT	ATROPHIN-1 (DENTATORUBRAL-PALLIDOLYSIAN ATROPHY PROTEIN)
3522	8663		0.9	4.90E-02	AA188940.1	EST_HUMAN	zq48a12.s1 Strata gene nNT neuron (#937233) Homo sapiens cDNA clone IMAGE:632826 3' similar to contains Alu repetitive element; contains element MSR1 repetitive element ;
3543	8684	13784	1.2	4.90E-02	AA400914.1	EST_HUMAN	z178a03.s1 Soares testis nNT Homo sapiens cDNA clone IMAGE:728428 3'
3543	8684	13785	1.2	4.90E-02	AA400914.1	EST_HUMAN	z178a03.s1 Soares testis nNT Homo sapiens cDNA clone IMAGE:728428 3'
4733	9844	14936	1.9	4.90E-02	AW167821.1	EST_HUMAN	xg56g10.x1 NCI CGAP U14 Homo sapiens cDNA clone IMAGE:2632386 3'
4733	9844	14937	1.9	4.90E-02	AW167821.1	EST_HUMAN	xg56g10.x1 NCI CGAP U14 Homo sapiens cDNA clone IMAGE:2632386 3'
327	5509	10836	1.5	4.80E-02	D16471.1	NT	Human mRNA, Xq terminal portion
328	5509	10836	0.7	4.80E-02	D16471.1	NT	Human mRNA, Xq terminal portion
480	5646	10771	2.6	4.80E-02	AF003100.1	NT	Arabidopsis thaliana AP2 domain containing protein RAP2.7 mRNA, partial cds
2227	7334	12546	0.7	4.80E-02	W51983.1	EST_HUMAN	zcd9b02.s1 Soares senescent fibroblasts NbHSF Homo sapiens cDNA clone IMAGE:325611 3' similar to gb:IM0938 LUPUS KU AUTOANTIGEN PROTEIN P86 (HUMAN);
3172	8321	13435	2.1	4.80E-02	X17144.1	NT	Tetrahymena rostrata histone H3II and histone H4II intergenic DNA
4572	9690		1.7	4.80E-02	Z54280.1	NT	S.scrota gene for skeletal muscle ryanodine receptor
5076	10174	15254	1.3	4.80E-02	U91914.1	NT	Streptococcus constellatus D-alanine:D-alanine ligase gene, partial cds
4940	10046	15118	0.8	4.70E-02	6981261	NT	Rattus norvegicus Nestin (Nes), mRNA
722	5876	11016	0.9	4.60E-02	AE000445.1	NT	Escherichia coli K-12 MG1655 section 335 of 400 of the complete genome
1270	6399		1.1	4.60E-02	A014235.1	EST_HUMAN	bm50d02.s1 Johnston frontal cortex Homo sapiens cDNA clone IMAGE:1538979 3 similar to TRP:P90533 P90533 LIMA ; contains element LTR1 repetitive element ;

Table 4

2438	7537	12744	0.9	4.60E-02	AW236023.1	EST_HUMAN	hm24f03.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2694653 3' similar to SW:GRF1_HUMAN Q12849 G-RICH SEQUENCE FACTOR-1 :
2777	5457	10584	0.5	4.60E-02	BE153583.1	EST_HUMAN	PMO-HT0339-251198-003-g05 HT0339 Homo sapiens cDNA
2977	8128	13235	1.0	4.60E-02	BE153583.1	EST_HUMAN	PMO-HT0339-251199-003-g05 HT0339 Homo sapiens cDNA
3451	8128	13235	1.0	4.60E-02	BE153583.1	EST_HUMAN	PMO-HT0339-251199-003-g05 HT0339 Homo sapiens cDNA
4033	9161		1.2	4.60E-02	AF220365.1	NT	Mus musculus nuclear RNA helicase I/IGu (ddx21) gene, complete cds
439	5605	10739	0.6	4.50E-02	P22448	SWISSPROT	RETINOIC ACID RECEPTOR BETA (RAR-BETA)
1200	6332	11487	0.9	4.50E-02	AF005730.1	NT	Marburg virus strain WIS_Africa/Johannesburg/1975/Ozolin VP35 gene, complete cds
1200	6332	11488	0.9	4.50E-02	AF005730.1	NT	Marburg virus strain WIS_Africa/Johannesburg/1975/Ozolin VP35 gene, complete cds
1763	6884	12067	1.3		P32182	SWISSPROT	HEPATOCYTE NUCLEAR FACTOR 3-BETA (HNF-3B)
2063	7175	12382	0.7	4.50E-02	AE003964.1	NT	Xyella fastidiosa, section 110 of 229 of the complete genome
3662	8801	13896	3.8	4.50E-02	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C078
1008	6148	11302	1.3	4.40E-02	L19295.1	NT	Drosophila melanogaster extracellular (EXD) mRNA, complete cds
2049	7162		2.2	4.40E-02	P31568	SWISSPROT	HYPOTHETICAL PROTEIN (ORF 2280)
2440	7539	12746	1.3	4.40E-02	AW875475.1	EST_HUMAN	QV2-PT0012-010300-070-g02 PT0012 Homo sapiens cDNA
3303	8448	13558	1.0	4.40E-02	M64798.1	NT	Methanobacterium formicicum fdhC gene, complete cds
3588	8727	13823	1.9	4.40E-02	AF159160.1	NT	Mycobacterium xenopus serine/threonine kinase Pkn10 (pkn10) gene, complete cds
4527	9846	14735	1.1	4.40E-02	AF109907.1	NT	Homo sapiens S164 gene, partial cds; PS1 and hypothetical protein genes, complete cds; and S171 gene, partial cds
4527	9846	14735	1.1	4.40E-02	AF109907.1	NT	Homo sapiens S164 gene, partial cds; PS1 and hypothetical protein genes, complete cds; and S171 gene, partial cds
4637	9751		3.1	4.40E-02	ALJ222689.1	NT	Ovis aries CCAAT-enhancer binding protein epsilon gene
1690	6814		1.2	4.30E-02	T67911.1	EST_HUMAN	yc28a09.s1 Stragene liver (#937224) Homo sapiens cDNA clone IMAGE:81976 3' similar to contains Alu repetitive element;
3383	8526	13633	7.0	4.30E-02	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
3608	8748		1.1	4.30E-02	AF060568.1	NT	Homo sapiens promyelocytic leukemia zinc finger protein (PLZF) gene, complete cds
4334	9457	14545	3.5	4.30E-02	F17181.2	EST_HUMAN	HSP001704 HM1 Homo sapiens cDNA clone NOTAVALL0704
5141	10236	15311	0.9	4.30E-02	X51594.1	NT	Pea P4 organ specific gene
878	6026	11186	0.8	4.20E-02	AW003645.1	EST_HUMAN	wx34g01.x1 NCI_CGAP_Pit1 Homo sapiens cDNA clone IMAGE:2545584 3' similar to TR:Q63291 Q63291 L1 RETROPOSON, ORF2 mRNA; contains L1.13 L1 L1 L1 repetitive element :
3117	8266	13370	0.9	4.20E-02	AI493472.1	EST_HUMAN	qy95f10.x1 NCI_CGAP_Bim25 Homo sapiens cDNA clone IMAGE:2019787 3' similar to gb:M35718 FIBROBLAST GROWTH FACTOR RECEPTOR BFR-2 PRECURSOR (HUMAN);
5172	10266		1.1	4.20E-02	D63484.1	NT	Human mRNA for KIAA0150 gene, partial cds
2643	7732	12933	1.0	4.10E-02	AE002330.2	NT	Chlamydia muridarum, section 60 of 85 of the complete genome
3824	8961	14058	0.9	4.10E-02	BE297236.1	EST_HUMAN	601177907F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3533353 5'
3824	8961	14059	0.9	4.10E-02	BE297236.1	EST_HUMAN	601177907F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3533353 5'
4372	9494		7.4	4.10E-02	AW693484.1	EST_HUMAN	QV1-NN0012-180400-164-08 NN0012 Homo sapiens cDNA
2816	7967	13071	1.4	4.00E-02	U18667.2	NT	Mus musculus uroporphyrinogen III synthase mRNA, complete cds
3206	8354	13464	2.7	4.00E-02	AB040904.1	NT	Homo sapiens mRNA for KIAA1471 protein, partial cds
1322	6451	11616	1.3	3.90E-02	P41047	SWISSPROT	FAS ANTIGEN LIGAND

Table 4

1918	7035	12223	1.1	3.90E-02	ALJ03386.1	NT	M.musculus DNA for desmin-binding fragment Desd7
2671	7758		0.8	3.90E-02	4506862	NT	Homo sapiens succinate dehydrogenase complex, subunit C, integral membrane protein, 15kD (SDHC) mRNA
5105	10201	15280	1.0	3.90E-02	8924019	NT	Homo sapiens hypothetical protein PRO1163 (PRO1163), mRNA
5105	10201	15281	1.0	3.90E-02	8924019	NT	Homo sapiens hypothetical protein PRO1163 (PRO1163), mRNA
1568	6694		1.3	3.80E-02	AJ229042.1	NT	Homo sapiens 959 kb contig between AML1 and CBR1 on chromosome 21q22, segment 2/3
976	6121	11278	1.6	3.70E-02	P19137	SWISSPROT	LAMININ ALPHA-1 CHAIN PRECURSOR (LAMININ A CHAIN)
1366	6494	11660	0.9	3.70E-02	L14561.1	NT	Homo sapiens plasma membrane calcium ATPase isoform 1 (ATP2B1) gene, alternative splice products, partial cds
2190	7299	12514	2.3	3.70E-02	A1894806.1	EST_HUMAN	wf85608.x1 NCI CGAP Kid11 Homo sapiens cDNA clone IMAGE:2494502.3
2533	7829	12831	0.9	3.70E-02	AB018261.1	NT	Homo sapiens mRNA for KIAA0718 protein, partial cds
3012	8164	13265	0.8	3.70E-02	P79944	SWISSPROT	ECMESODERMIN
3408	8550		1.1	3.70E-02	6680541	NT	Mus musculus poliovirus large conductance pH-sensitive channel, subfamily M, alpha member 3 (Kcma3), mRNA
3604	8743	13838	0.9	3.60E-02	X73221.1	NT	H. vulgare Sst1 gene for sucrose synthase
3612	8751	13845	0.8	3.60E-02	AL096806.1	NT	Homo sapiens genomic region containing hypervariable minisatellites chromosome 10(10q26.3) of Homo sapiens
5135	10230	15305	0.8	3.60E-02	AL096810.1	NT	Homo sapiens genomic region containing hypervariable minisatellites chromosome 10(10q26.3) of Homo sapiens
877	6025	11165	1.2	3.50E-02	U09506.1	NT	Drosophila melanogaster Uppin mRNA, complete cds
992	6135	11290	0.5	3.50E-02	AF23417.1	NT	Homo sapiens microsomal epoxide hydrolase (EPHX1) gene, complete cds
1188	6320		3.5	3.50E-02	AW772365.1	EST_HUMAN	hnt2c08.x1 NCI CGAP Kid11 Homo sapiens cDNA clone IMAGE:3033422.3
3271	8416		1.5	3.50E-02	T29124.1	EST_HUMAN	EST69851 Human White blood cells Homo sapiens cDNA 5' end similar to T-cell receptor, alpha chain, V region (HT-3229)
3663	8802	13897	0.9	3.50E-02	X61109.1	NT	G. gorilla beta-globin gene
4120	9246	14330	2.0	3.50E-02	AE001773.1	NT	Thermotoga maritima section 85 of 136 of the complete genome
4220	9344	14427	1.4	3.50E-02	P53780	SWISSPROT	CYSTATHIONINE BETA-L YASE PRECURSOR (CBL) (BETA-CYSTATHIONASE) (CYSTEINE LYASE)
4538	9655		1.0	3.50E-02	AW958469.1	EST_HUMAN	EST370539 IMAGE ressequences, IMAGE Homo sapiens cDNA
5154	10249		0.8	3.50E-02	P47144	SWISSPROT	HYPOTHETICAL 80.7 KD PROTEIN IN SOD1-CPA2 INTERGENIC REGION
							xy26d07.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2814253.3 similar to SW:0211_HUMAN P53801 PUTATIVE SURFACE GLYCOPROTEIN C21ORF1 PRECURSOR
1035	6175	11327	1.3	3.40E-02	AW274020.1	EST_HUMAN	zif508.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:728199.3'
1817	6936	12126	0.6	3.40E-02	AA398742.1	EST_HUMAN	yc20606.r1 Stralagene lung (#937210) Homo sapiens cDNA clone IMAGE:81250.5 similar to contains MER29 repetitive element
2343	7445	12652	0.8	3.40E-02	T57180.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C008
3384	8527	13634	1.3	3.40E-02	AL163208.2	NT	Homo sapiens chromosome 21 segment HS21C008
3845	8981	14082	3.2	3.40E-02	AW794952.1	EST_HUMAN	RC6-UM0015-210200-021-A10 UM0015 Homo sapiens cDNA
4494	9614	14706	2.4	3.40E-02	X59199.1	NT	M.musculus S-antigen gene promoter region
4992	10095		3.4	3.40E-02	Q26457	SWISSPROT	LA PROTEIN HOMOLOG (LA RIBONUCLEOPROTEIN) (LA AUTOANTIGEN HOMOLOG)

Table 4

5010	10112	15182	1.3	3.40E-02	AJ012469.1	NT	<i>Caenorhabditis elegans</i> mRNA for DYS-1 protein, partial
368	5546		4.5	3.30E-02	AA398735.1	EST_HUMAN	z175608.s1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:728198.3'
1151	6266	11439	4.5	3.30E-02	AB035867.1	NT	<i>Cricetulus griseus</i> CYP2A17 mRNA for cytochrome P450 2A17, complete cds
1621	6747	11915	1.1	3.30E-02	AF110763.1	NT	Homo sapiens skeletal muscle LIM-protein 1 (FHL1) gene, complete cds
1705	6828		1.3	3.30E-02	AEO00700.1	NT	<i>Aquifex aeolicus</i> section 32 of 109 of the complete genome
2038	7151		1.0	3.30E-02	RO9112.1	EST_HUMAN	y25c09.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:127888.5'
2448	7547	12755	1.1	3.30E-02	T02847.1	EST_HUMAN	FB12A2 Fetal brain, Stralagene Homo sapiens cDNA clone FB12A2.3'end
2448	7547	12756	1.1	3.30E-02	T02847.1	EST_HUMAN	FB12A2 Fetal brain, Stralagene Homo sapiens cDNA clone FB12A2.3'end
4088	6747	11915	2.2	3.30E-02	AF110763.1	NT	Homo sapiens skeletal muscle LIM-protein 1 (FHL1) gene, complete cds
4366	9488	14579	1.9	3.30E-02	6755862	NT	<i>Mus musculus</i> tumor rejection antigen gp96 (Tra1) mRNA
127	5323	10455	1.1	3.20E-02	AJ002005.1	NT	<i>Oryctolagus cuniculus</i> gene encoding ileal sodium-dependent bile acid transporter
1110	6247	11399	4.3	3.20E-02	AF096275.1	NT	<i>Drosophila melanogaster</i> heat shock protein 68 (hsp68) gene, hsp68d allele, complete cds
1110	6247	11400	4.3	3.20E-02	AF096275.1	NT	<i>Drosophila melanogaster</i> heat shock protein 68 (hsp68) gene, hsp68d allele, complete cds
1734	6857	12035	1.1	3.20E-02	AF128894.1	NT	Homo sapiens telomerase reverse transcriptase (TERT) gene, exons 7-16 and complete cds
2072	7184		0.9	3.20E-02	P28955	SWISSPROT	LARGE TEGUMENT PROTEIN
2809	5323	10455	1.2	3.20E-02	AJ002005.1	NT	<i>Oryctolagus cuniculus</i> gene encoding ileal sodium-dependent bile acid transporter
3653	8792	13886	1.1	3.20E-02	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
4124	9250		12.4	3.20E-02	X04768.1	NT	H.sapiens RP3 gene (XLRP gene 3)
4658	9770	14865	2.9	3.20E-02	AF114182.1	NT	<i>Saxifraga nidifica</i> maturase (matk) gene, chloroplast gene encoding chloroplast protein, partial cds
1239	6368		0.7	3.10E-02	4503416	NT	Homo sapiens dual specificity phosphatase 4 (DUSP4) mRNA
1283	6413	11575	1.3	3.10E-02	P18845	SWISSPROT	NEURONAL ACETYLCHOLINE RECEPTOR PROTEIN, ALPHA-3 CHAIN PRECURSOR (GF-ALPHA-3)
1501	6627		1.0	3.10E-02	AF200465.1	NT	Homo sapiens coxsackievirus and adenovirus receptor (CXADR) gene, complete cds; and ANA gene, partial cds
1650	6968	12153	1.4	3.10E-02	6671564	NT	<i>Mus musculus</i> adaptor-related protein complex AP-3, delta subunit (Ap3d), mRNA
1931	7048		1.1	3.10E-02	Z50097.1	NT	<i>Drosophila melanogaster</i> mRNA for headcase protein
4767	9878	14972	1.0	3.10E-02	AW635313.1	EST_HUMAN	QV0.LT0014+250200-129-h09 LT0014 Homo sapiens cDNA
1606	6733		1.0	3.00E-02	AF187125.1	NT	<i>Physokleines minutus</i> cytochrome oxidase I gene, partial cds; mitochondrial gene for mitochondrial product
2541	7637	12837	1.1	3.00E-02	AA402242.1	EST_HUMAN	z165103.r1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:727253.5'
3518	8659	13766	1.1	3.00E-02	M84176.1	NT	<i>Saccharomyces cerevisiae</i> stem-loop mutation suppressor SCL2 gene, complete cds
3665	8823		1.0	3.00E-02	AW620223.1	EST_HUMAN	QV2.ST0296-150200-040-409 ST0296 Homo sapiens cDNA
3666	9002		1.2	3.00E-02	AA364003.1	EST_HUMAN	ESTT4530 Pineal gland II Homo sapiens cDNA 5' end
2385	7942	12689	1.1	2.90E-02	AF228703.1	NT	Homo sapiens mitochondrial glutathione reductase and cytosolic glutathione reductase (GRD1) gene, complete cds, alternatively spliced
2449	7548	12757	0.5	2.90E-02	4502272	NT	Homo sapiens ATPase, Na+/K+-transporting, alpha 3 polypeptide (ATP1A3), mRNA



Table 4

3651	8987	14087	0.9	2.90E-02	H72805.1	EST_HUMAN	yu07e10.1 Soares fetal liver spleen 11NFLS Homo sapiens cDNA clone IMAGE:233130 5'
4950	10055	15125	1.3	2.80E-02	X65137.1	NT	S.vulgate pepC gene for PEP carboxylase
4950	10055	15126	1.3	2.80E-02	X65137.1	NT	S.vulgate pepC gene for PEP carboxylase
553	5716		0.9	2.80E-02	AW670153.1	EST_HUMAN	EST1382234 MAGe resequences, MAGk Homo sapiens cDNA
3321	8465	13576	1.3	2.80E-02	AF066063.1	NT	Homo sapiens retinal fascic (FSCN2) gene, exon 2
3321	8465	13579	1.3	2.80E-02	AF066063.1	NT	Homo sapiens retinal fascic (FSCN2) gene, exon 2
4214	9338		1.0	2.80E-02	8393751	NT	Rattus norvegicus microtubule-associated protein tau (Mapt), mRNA
1473	6600	11774	1.3	2.70E-02	U66059.1	NT	Human germline T-cell receptor beta chain Dopamine-beta-hydroxylase-like, TRY1, TRY2, TRY3, TCRBV27S1P, TCRBV22S1A2N1T, TCRBV9S1A1T, TCRBV7S1A1N2T, TCRBV5S1A1T, TCRBV13S3, TCRBV6S7P, TCRBV7S3A2T, TCRBV13S2A1T, TCRBV9S2A2PT, TCRBV7S2A1N4T, TCRBV13S9/13S>
3385	8528	13835	2.0	2.70E-02	AL161494.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 6
4107	9233	14315	2.1	2.70E-02	NA7258.1	EST_HUMAN	yy86h12.1 Soares, multiple_sclerosis_2NBHMSP Homo sapiens cDNA clone IMAGE:280487 5'
4107	9233	14316	2.1	2.70E-02	NA7258.1	EST_HUMAN	yy86h12.1 Soares, multiple_sclerosis_2NBHMSP Homo sapiens cDNA clone IMAGE:280487 5'
5194	10285	15352	1.0	2.70E-02	AI825422.1	EST_HUMAN	wo18a04.x1 NCI_CGAP GC6 Homo sapiens cDNA clone IMAGE:2306048 3'
5194	10285	15353	1.0	2.70E-02	AI825422.1	EST_HUMAN	wo18a04.x1 NCI_CGAP GC6 Homo sapiens cDNA clone IMAGE:2306046 3'
559	5721	10837	1.1	2.60E-02	AL163282.2	NT	Homo sapiens chromosome 21 segment HS21C082
1345	6473		1.0	2.60E-02	AW850515.1	EST_HUMAN	IL3-CT0219-280100-062-C09 CT0219 Homo sapiens cDNA
2315	7418	12625	1.1	2.60E-02	AA490021.1	EST_HUMAN	ab02002.s1 Striatogene fetal retina 937202 Homo sapiens cDNA clone IMAGE:839595 3'
2317	7420	12627	1.0	2.60E-02	6754241	NT	Mus musculus histidine rich calcium binding protein (Hrc), mRNA
2317	7420	12628	1.0	2.60E-02	6754241	NT	Mus musculus histidine rich calcium binding protein (Hrc), mRNA
							Mus musculus MHC class III region RD gene, partial cds; B1, C2, G9A, NG22, G9, HSP70, HSP70, HSC70, and snRNP genes, complete cds; G7A gene, partial cds; and unknown genes
2865	8036		1.6	2.60E-02	AF109906.1	NT	Citrus unshiu ADP-glucose pyrophosphorylase small subunit (agps) mRNA, complete cds
3285	8430	13538	1.0	2.60E-02	AF184597.1	NT	XJ68109.x1 Soares, NFL T GBC ST Homo sapiens cDNA clone IMAGE:2662409 3'
3883	9019		1.1	2.60E-02	AW181945.1	EST_HUMAN	XJ68109.x1 Soares, NFL T GBC ST Homo sapiens cDNA clone IMAGE:2662409 3'
4811	9921	15013	3.7	2.60E-02	L12032.1	NT	Chicken dorsalis-1 mRNA, complete cds
4898	10101	15169	1.7	2.60E-02	AE002014.1	NT	Deinococcus radiodurans R1 section 151 of 229 of the complete chromosome 1
5025	10126	15189	2.1	2.60E-02	AW241154.1	EST_HUMAN	xs52004.x1 NCI_CGAP Sa14 Homo sapiens cDNA clone IMAGE:1557827 5'
521	5685	10806	1.5	2.50E-02	AI793130.1	EST_HUMAN	SW-Y089_HUMAN Q15041 HYPOTHETICAL PROTEIN KIAA0069
521	5685	10807	1.5	2.50E-02	AI793130.1	EST_HUMAN	on26r06.05 NCI_CGAP Lu5 Homo sapiens cDNA clone IMAGE:1557827 5'
1992	7108	12310	1.6	2.50E-02	6660967	NT	on26r06.05 NCI_CGAP Lu5 Homo sapiens cDNA clone IMAGE:1557827 5'
2735	7819		0.9	2.50E-02	U12571.1	NT	Mus musculus procollagen, type IV, alpha 3 (Col4a3), mRNA
2926	8077	13184	4.4	2.50E-02	X99697.1	NT	Rattus norvegicus rabphilin-3A mRNA, complete cds
2926	8077	13184	4.4	2.50E-02	X99697.1	NT	H. cantareae mRNA for fucoxanthin chlorophyll a/c binding protein, Fcp1
2926	8077	13185	4.4	2.50E-02	X99697.1	NT	H. cantareae mRNA for fucoxanthin chlorophyll a/c binding protein, Fcp1

Table 4

3376	8619	13625	1.0	2.50E-02	BE464190.1	EST_HUMAN	hxb6d10.x1 NCI CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3194611 3' similar to gb:M16838 HOMEDBOX PROTEIN HOXC6 (HUMAN);
4111	9237	14320	5.1	2.50E-02	AW592114.1	EST_HUMAN	h36n08.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2934015 3'
167	5361	10488	1.0	2.40E-02	AI378582.1	EST_HUMAN	tc22c07.x1 Soares_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:2070156 3'
1580	6706	11876	0.7	2.40E-02	H65884.1	EST_HUMAN	y75t11.11 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:211149 5'
1998	7932	12316	0.8	2.40E-02	P01901	SWISSPROT	H-2 CLASS I HISTOCOMPATIBILITY ANTIGEN, K-B ALPHA CHAIN PRECURSOR (H-2K(B))
1998	7932	12317	0.8	2.40E-02	P01901	SWISSPROT	H-2 CLASS I HISTOCOMPATIBILITY ANTIGEN, K-B ALPHA CHAIN PRECURSOR (H-2K(B))
4272	9397	14480	1.4	2.40E-02	J05110.1	NT	T.thermophila calcium-binding 25 kDa (TCBP 25) protein mRNA, complete cds
4420	9540	14631	1.4	2.40E-02	P01901	SWISSPROT	H-2 CLASS I HISTOCOMPATIBILITY ANTIGEN, K-B ALPHA CHAIN PRECURSOR (H-2K(B))
4420	9540	14632	1.4	2.40E-02	P01901	SWISSPROT	H-2 CLASS I HISTOCOMPATIBILITY ANTIGEN, K-B ALPHA CHAIN PRECURSOR (H-2K(B))
5119	10215		11.5	2.40E-02	AL161595.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 91
1829	6948		2.1	2.30E-02	W05340.1	EST_HUMAN	zab4g08.r1 Soares_fetal_lung_NbHL19W Homo sapiens cDNA clone IMAGE:299294 5'
1844	6962		2.9	2.30E-02	U94165.1	NT	4 Homo sapiens mammary tumor-associated protein INT6 (INT6) gene, exon 4
2302	7405	12613	0.9	2.30E-02	Z74283.1	NT	S.cerevisiae chromosome IV reading frame ORF YDL245c
3628	8767	13861	4.8	2.30E-02	Z20377.1	EST_HUMAN	HSAACACDH.P_Human foetal Brain Whole tissue Homo sapiens cDNA
4057	9184	14267	1.2	2.30E-02	L24799.1	NT	Gallus gallus connexin 45.6 (Cx45.6) gene, complete cds
4057	9184	14268	1.2	2.30E-02	L24799.1	NT	Gallus gallus connexin 45.6 (Cx45.6) gene, complete cds
4323	9446	14534	1.3	2.30E-02	AW699107.1	EST_HUMAN	CMA-NN0080-290400-160-004 NN0080 Homo sapiens cDNA
4348	10300	14561	0.9	2.30E-02	AW693693.1	EST_HUMAN	xs25cd08.x1 NCI CGAP_U2 Homo sapiens cDNA clone IMAGE:2770671 3'
4348	10300	14562	0.9	2.30E-02	AW693693.1	EST_HUMAN	xs25cd08.x1 NCI CGAP_U2 Homo sapiens cDNA clone IMAGE:2770671 3'
4402	9523	14613	5.2	2.30E-02	Z83867.1	NT	Mycobacterium tuberculosis H37Rv complete genome; segment 138/162
4472	9592	14687	1.8	2.30E-02	BE143150.1	EST_HUMAN	MRO-HT0159-151099-001-e03 HT0159 Homo sapiens cDNA
4948	10053	15123	1.0	2.30E-02	AT793177.1	EST_HUMAN	qz35c03.x5 NCI CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2028868 3'
4948	10053	15124	1.0	2.30E-02	AT793177.1	EST_HUMAN	qz35c03.x5 NCI CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2028868 3'
720	5874	11014	1.1	2.20E-02	AF018267.1	NT	Columbia llyla nucleoside diphosphate kinase (NDPK) gene, nuclear gene encoding mitochondrial protein, complete cds
1713	6836		0.6	2.20E-02	4557448	NT	Homo sapiens chromodomain helicase DNA binding protein 2 (CHD2) mRNA
1968	7083	12284	0.6	2.20E-02	Z82001.1	NT	S.pneumoniae pcps gene and open reading frames
2695	7952	12980	0.5	2.20E-02	AF108633.1	NT	Mus musculus ets variant protein ER81 gene, exons 1 through 4
3388	8531		1.9	2.20E-02	AA577785.1	EST_HUMAN	nm24a04.s1 NCI CGAP_Gas1 Homo sapiens cDNA clone IMAGE:1084782 3'
3595	8734		3.3	2.20E-02	AF083094.1	NT	Infectious bursal disease virus segment B strain IL4 VP1 gene, complete cds
3779	8916	14009	1.1	2.20E-02	AW601317.1	EST_HUMAN	PMO-BT0340-170100-004-503 BT0340 Homo sapiens cDNA
3844	8980	14081	1.0	2.20E-02	Z74293.1	NT	S.cerevisiae chromosome IV reading frame ORF YDL245c
441	5607		2.7	2.10E-02	AF029726.1	NT	Dicotyledonous discoidium histidine kinase C (dhkc) mRNA, complete cds
1242	6371	11530	2.5	2.10E-02	UT2073.1	NT	Bacillus subtilis colKLM cluster, ColK (colK), ColL (colL), and spore coat protein ColM (colM) genes, complete cds

Table 4

1365	6492	11657	0.7	2.10E-02	AF204395.1	NT	Mus musculus macrophage migration inhibitory factor (MIF) gene, 5' flanking region and partial cds
1365	6492	11658	0.7	2.10E-02	AF204395.1	NT	Mus musculus macrophage migration inhibitory factor (MIF) gene, 5' flanking region and partial cds
1920	7037	12228	1.0	2.10E-02	AF190899.1	NT	Tegula aureoflucta major acrosomal protein precursor (TMAP) mRNA, complete cds
2785	5915	11062	1.4	2.10E-02	N29286.1	EST_HUMAN	h4307.1 Soares melanocyte 2bHhM Homo sapiens cDNA clone IMAGE:264541 5'
3110	7105	12308	0.9	2.10E-02	BE072546.1	EST_HUMAN	PM2-BT0546-120100-001-11 BT0546 Homo sapiens cDNA
3110	7105	12309	0.9	2.10E-02	BE072546.1	EST_HUMAN	PM2-BT0546-120100-001-11 BT0546 Homo sapiens cDNA
3535	8676	13779	1.2	2.10E-02	AA461271.1	EST_HUMAN	z63609.1 Soares_telus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:796121 5'
4036	8166	14251	0.9	2.10E-02	Z74293.1	NT	S. cerevisiae chromosome IV reading frame ORF YDL245c
4342	9465	14554	1.6	2.10E-02	U44914.1	NT	Borrelia burgdorferi plasmid cp32-2, erpC and erpD genes, complete cds; and unknown genes
4351	9473	14565	1.0	2.10E-02	A1768127.1	EST_HUMAN	wg81d11.x1 Soares_NSF_F8_9w_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2371509 3'
4611	9725	14820	4.7	2.10E-02	Y08501.1	NT	A. thaliana mitochondrial genome, part A
4714	9826	14918	0.9	2.10E-02	A1823432.1	EST_HUMAN	wf54a05.x1 NCI_CGAP_Kid1 Homo sapiens cDNA clone IMAGE:2384528 3'
18	5227	10328	2.7	2.00E-02	AW895565.1	EST_HUMAN	QV44NN0038-270400-187-405 NN0038 Homo sapiens cDNA
259	5447	10572	0.9	2.00E-02	6733635	NT	Mus musculus D1b1 homolog 1 (E. coli) (D1b1), mRNA
292	5478	10609	0.9	2.00E-02	AA456538.1	EST_HUMAN	aa15b10.1 Soares_NhhMPu_S1 Homo sapiens cDNA clone IMAGE:813307 5'
781	5933	11062	0.6	2.00E-02	6753835	NT	Mus musculus D1b1 homolog 1 (E. coli) (D1b1), mRNA
1071	6209	11362	1.0	2.00E-02	AL096805.1	NT	Mus musculus genomic region containing hypervariable minisatellites chromosome 11p36.33 of Homo sapiens
1181	6314	11470	0.6	2.00E-02	8922391	NT	Homo sapiens hypothetical protein FLJ10379 (FLJ10379), mRNA
1181	6314	11471	0.6	2.00E-02	8922391	NT	Homo sapiens hypothetical protein FLJ10379 (FLJ10379), mRNA
1830	6949	12132	0.8	2.00E-02	8922453	NT	Homo sapiens hypothetical protein FLJ10486 (FLJ10486), mRNA
1830	6949	12133	0.8	2.00E-02	8922453	NT	Homo sapiens hypothetical protein FLJ10486 (FLJ10486), mRNA
2768	7852		0.6	2.00E-02	AL161532.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 32
3105	8255		1.2	2.00E-02	7305474	NT	Mus musculus sema domain, transmembrane domain (TM), and cytoplasmic domain, (semaphorin) 6B (Sema6b), mRNA
3189	8338		3.3	2.00E-02	AF095588.1	NT	Arabidopsis thaliana C2H2 zinc finger protein FZF mRNA, complete cds
3925	9059	14146	1.5	2.00E-02	M18096.1	NT	P. vulgaris hydroxyproline-rich glycoprotein (HRGP) mRNA, 3' end
5079	10177	15257	1.0	2.00E-02	AL163276.2	NT	Homo sapiens chromosome 21 segment HS21C078
5085	10163	15262	1.0	2.00E-02	AA456538.1	EST_HUMAN	aa15b10.1 Soares_NhhMPu_S1 Homo sapiens cDNA clone IMAGE:813307 5'
678	5833	10964	0.6	1.90E-02	AA572764.1	EST_HUMAN	nt19a07.s1 NCI_CGAP_P1 Homo sapiens cDNA clone IMAGE:914196 similar to contains 1.111 L1 repetitive element;
1589	6726	11898	0.8	1.90E-02	P18488	SWISSPROT	EMPTY SPIRACLES HOMEOTIC PROTEIN
1993	7109	12311	0.9	1.90E-02	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103
1993	7109	12312	0.9	1.90E-02	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103
2458	7557	12762	0.9	1.90E-02	AL161550.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 50
2875	8026	13128	7.1	1.90E-02	AA713856.1	EST_HUMAN	hw0405.s1 NCI_CGAP_SS1 Homo sapiens cDNA clone IMAGE:1236337 3'

Table 4

3222	8370		0.8	1.90E-02	AB033611.1	NT	Utrichius talpoides mitochondrial gene for cytochrome b, complete cds
3560	8699		1.3	1.90E-02	N52250.1	EST_HUMAN	y228b02.s1 Soares, multiple_sclerosis_2NbhMSP Homo sapiens cDNA clone IMAGE:284331.3
3654	8793	13887	1.0	1.90E-02	AI301183.1	EST_HUMAN	gn4cd7.x1 NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1897260.3 similar to contains Alu repetitive element.
3961	9093	14178	1.1	1.90E-02	AF141940.1	NT	Mycoplasma imitans VlnA1 precursor (vlnA1) and VlnA2 precursor (vlnA2) genes, partial cds
4099	9225	14309	1.5	1.90E-02	P09081	SWISSPROT	HOMEOTIC BICOID PROTEIN (PRD-4)
4099	9225	14310	1.5	1.90E-02	P09081	SWISSPROT	HOMEOTIC BICOID PROTEIN (PRD-4)
4441	9561	14657	2.5	1.90E-02	A45299.1	EST_HUMAN	ij46d04.x1 Soares, NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2144551
4944	7557	12762	1.9	1.90E-02	AL161550.2	NT	3 similar to contains Alu repetitive element;
85	5291		1.1	1.80E-02	O929H0	SWISSPROT	Arbiddopsis thaliana DNA chromosome 4, contig fragment No. 50 [PROTEIN-PII] URIDYL-TRANSFERASE (PII URIDYL-TRANSFERASE) (URIDYL-REMOVING ENZYME) (UTASE)
343	5524	10849	1.4	1.80E-02	AW771104.1	EST_HUMAN	hns2cd6.x1 NCI_CGAP_Co17 Homo sapiens cDNA clone IMAGE:3027274.3 similar to contains element MER29 repetitive element;
1144	6279	11432	1.3	1.80E-02	X17684.1	NT	H.franscd mRNA for myelin basic protein (MBP)
1417	6545	11719	1.2	1.80E-02	AF243362.1	NT	Drosophila melanogaster cytoplasmic protein encore (enc) mRNA, complete cds
3174	8323		0.9	1.80E-02	AI805829.1	EST_HUMAN	h652d09.x1 Soares, NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2090296.3
3489	8630	13742	1.1	1.80E-02	Z75059.1	NT	S.cerevisiae chromosome XV reading frame ORF YOR151c
3812	8849	14045	1.1	1.80E-02	AW879122.1	EST_HUMAN	MR1-OT001-280300-009-g04 OT0011 Homo sapiens cDNA
3812	8949	14046	1.1	1.80E-02	AW879122.1	EST_HUMAN	MR1-OT001-280300-009-g04 OT0011 Homo sapiens cDNA
3986	9128		1.2	1.80E-02	AA861446.1	EST_HUMAN	ak24hd04.s1 Soares, testis_NH1 Homo sapiens cDNA clone IMAGE:1406935.3
4332	9455	14543	1.4	1.80E-02	AW936363.1	EST_HUMAN	CV4-DT0021-301289-071-b11 DT0021 Homo sapiens cDNA
4873	9980	15064	1.1	1.80E-02	O60610	SWISSPROT	gm06b04.x1 NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1881007.3
4887	9994	15076	1.1	1.80E-02	AI288701.1	EST_HUMAN	h0310626F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3632190.5
888	6036	11194	1.3	1.70E-02	BE394869.1	EST_HUMAN	h0310626F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:2933740.3 similar to contains L1.11 L1 repetitive element;
1750	6872	12051	0.8	1.70E-02	AW573183.1	EST_HUMAN	h34a03.x1 Soares, NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2933740.3 similar to contains L1.11 L1 repetitive element;
1750	6872	12052	0.8	1.70E-02	AW573183.1	EST_HUMAN	h34a03.x1 Soares, NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2933740.3 similar to contains L1.11 L1 repetitive element;
1828	6947		1.1	1.70E-02	AL163204.2	NT	to contains L1.11 L1 repetitive element;
2066	7178		4.7	1.70E-02	AB004816.1	NT	Homo sapiens chromosome 21 segment HS21C004
2603	7693		1.4	1.70E-02	7657495	NT	Oryctolagus cuniculus mRNA for mitogenin29, complete cds
2968	8119	13227	0.9	1.70E-02	AI147615.1	EST_HUMAN	Homo sapiens putative Rab5 GDP/GTP exchange factor homologue (RABEX5), mRNA
3467	8608		4.2	1.70E-02	AW827368.1	EST_HUMAN	qb22a08.x1 Soares, pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:1696982.3
3573	8712		0.9	1.70E-02	P04929	SWISSPROT	hm45a04.x1 NCI_CGAP_RDF1 Homo sapiens cDNA clone IMAGE:3015534.3 similar to contains MER19.b1 MER19 repetitive element;
4078	9205		1.0	1.70E-02	AA669618.1	EST_HUMAN	HISTIDINE-RICH GLYCOPROTEIN PRECURSOR
							ac18f04.s1 Stratiagene ovary (#937217) Homo sapiens cDNA clone IMAGE:866927.3 similar to contains Alu repetitive element;contains element MER24 repetitive element;

Table 4

4105	9231	1.8	1.70E-02	R02506.1	EST_HUMAN	ye86108.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:124647 5'
4427	9548	1.2	1.70E-02	AW573183.1	EST_HUMAN	h134a03.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2933740 3' similar to contains L1/L1 repetitive element ;
4615	9729	1.8	1.70E-02	V00641.1	NT	Messenger RNA for angierfish (Lophius americanus) somatostatin II
4708	9820	5.3	1.70E-02	A015076.1	EST_HUMAN	ov51e02.s1 Soares testis NHT Homo sapiens cDNA clone IMAGE:1640858 3'
4967	10070	5.5	1.70E-02	AF105037.1	NT	Murid herpesvirus 4 complete genome
501	5665	0.5	1.60E-02	AL021929.1	NT	Mycobacterium tuberculosis H37Rv complete genome; segment 13/162
						Treponema mallophilum flaB2, flaB3 and flhD genes for flagellin subunit proteins and CAP protein homologue
1635	6761	1.1	1.60E-02	Y18889.1	NT	
2202	7311	1.1	1.60E-02	Q64176	SWISSPROT	LIVER CARBOXYLESTERASE 22 PRECURSOR (EGASYN) (ESTERASE-22)
2202	7311	1.1	1.60E-02	Q64176	SWISSPROT	LIVER CARBOXYLESTERASE 22 PRECURSOR (EGASYN) (ESTERASE-22)
2202	7311	1.1	1.60E-02	AJ006345.1	NT	Homo sapiens KLOT1 gene
2518	7614	1.0	1.60E-02	AA484872.1	EST_HUMAN	ne81d06.s1 NCI CGAP_Ew1 Homo sapiens cDNA clone IMAGE:910667
2606	7696	0.5	1.60E-02	AB014534.1	NT	Homo sapiens mRNA for KIAA0634 protein, partial cds
2662	7751	1.1	1.60E-02	AB014534.1	NT	Homo sapiens mRNA for KIAA0634 protein, partial cds
3481	8622	3.8	1.60E-02	AW850652.1	EST_HUMAN	IL3-CT0219-160200-063-C07 CT0219 Homo sapiens cDNA
						Mus musculus major histocompatibility complex region NG27, NG28, RPS28, NADH oxidoreductase, NG29, KIFC1, Fas-binding protein, BING1, Iapasin, RalGDS-like, KE2, BING4, beta 1,3-galactosyl transferase, and RPS18 genes, complete cds; Sacm21 gene, partial>
4084	9211	2.2	1.60E-02	AF110520.1	NT	QV2-PT0012-140100-030-107 PT0012 Homo sapiens cDNA
4203	9328	0.9	1.60E-02	AW875407.1	EST_HUMAN	Homo sapiens transcription factor (HSA130894), mRNA
734	5888	8.5	1.50E-02	8933734	NT	Homo sapiens cDNA clone IMAGE:243925 3'
2095	7206	1.4	1.50E-02	N39521.1	EST_HUMAN	iy27b07.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:243925 3'
2128	7238	0.9	1.50E-02	AL161594.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 90
3023	8175	1.4	1.50E-02	AJ006216.1	NT	Homo sapiens CACNA1F gene, exons 1 to 48
3023	8175	1.4	1.50E-02	AJ006216.1	NT	Homo sapiens CACNA1F gene, exons 1 to 48
3614	8753	1.2	1.50E-02	AA458787.1	EST_HUMAN	aa88c10.s1 Stratagene fetal retina 937202 Homo sapiens cDNA clone IMAGE:838386 3'
4049	9176	1.2	1.50E-02	AA160967.1	EST_HUMAN	zq40g10.r1 Stratagene hNT neuron (#937233) Homo sapiens cDNA clone IMAGE:632226 5'
411	5579	1.5	1.40E-02	AE002230.2	NT	Chlamydia pneumoniae AR39, section 58 of 94 of the complete genome
1102	6240	1.2	1.40E-02	7705980	NT	Homo sapiens NESH protein (LOC51225), mRNA
1236	6365	1.4	1.40E-02	U32800.1	NT	Haemophilus influenzae Rd section 115 of 163 of the complete genome
1276	6406	1.0	1.40E-02	U67779.1	NT	Xenopus laevis neurogenin related 1b (X-NGNR-1b) mRNA, complete cds
1374	6502	0.9	1.40E-02	AF216854.1	NT	Homo sapiens haadpin gene, complete cds
3352	8486	1.0	1.40E-02	AW074212.1	EST_HUMAN	xb08d09.x1 NCI CGAP GU1 Homo sapiens cDNA clone IMAGE:2575793 3'
3439	8581	5.2	1.40E-02	AL161586.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 82
3439	8581	5.2	1.40E-02	AL161586.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 82
3476	8617	1.0	1.40E-02	4503628	NT	Homo sapiens coagulation factor XII (Hageman factor) (F12), mRNA
3606	8745	6.2	1.40E-02	6996918	NT	Mus musculus histocompatibility 2, complement component factor B (H2-B), mRNA

Table 4

4387	9509	14594	7.3	1.40E-02	AW962688.1	EST_HUMAN	EST374761 MAGE (resequences, MAGG Homo sapiens cDNA
4387	9509	14595	7.3	1.40E-02	AW962688.1	EST_HUMAN	EST374761 MAGE (resequences, MAGG Homo sapiens cDNA
1912	7029	12216	0.9	1.30E-02	AL163201.2	NT	Homo sapiens chromosome 21 segment HS21C001
3888	9024		1.4	1.30E-02	AF169288.1	NT	Mus musculus beta-sarcoglycan gene, complete cds
5176	7029	12216	1.0	1.30E-02	AL163201.2	NT	Homo sapiens chromosome 21 segment HS21C001
206	5399		0.9	1.20E-02	X67344.1	NT	H. sapiens DNA, DMB, HLA-Z1, IIP2, LMP2, TAP1, LMP7, TAP2, DOB, DOB2 and RING8, 9, 13 and 14 genes
352	5532	10660	0.6	1.20E-02	AA059299.1	EST_HUMAN	z65g01.1 Soares retina NB24HR Homo sapiens cDNA clone IMAGE:381840 5' similar to contains element L1 repetitive element;
445	5611	10742	1.5	1.20E-02	P38898	SWISSPROT	HYPOTHETICAL 17.1 KD PROTEIN IN PUR5 3REGION
721	5875	11015	1.0	1.20E-02	AI183522.1	EST_HUMAN	q66a12.x1 Soares, testis, NHT Homo sapiens cDNA clone IMAGE:1734670 3' similar to contains L1, L1 repetitive element;
2130	7240	12448	0.7	1.20E-02	AL163213.2	NT	Homo sapiens chromosome 21 segment HS21C013
2393	7493	12699	1.2	1.20E-02	AW172350.1	EST_HUMAN	x37e09.x1 Soares, NFL, T, GBC, S1 Homo sapiens cDNA clone IMAGE:2659432 3'
2596	7493	12699	1.3	1.20E-02	AW172350.1	EST_HUMAN	x37e09.x1 Soares, NFL, T, GBC, S1 Homo sapiens cDNA clone IMAGE:2659432 3'
3063	8214		6.2	1.20E-02	AA075418.1	EST_HUMAN	zn86a03.1 Striatogene ovarian cancer (#937219) Homo sapiens cDNA clone IMAGE:545020 5'
3250	8397	13503	1.9	1.20E-02	R62805.1	EST_HUMAN	y11b08.s1 Soares placenta NB2HP Homo sapiens cDNA clone IMAGE:138903 3'
4830	9938	15027	2.0	1.20E-02	U91328.1	NT	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (H4-H) gene, RoRet gene, and sodium phosphate transporter (NPT3) gene, complete cds
4974	10077		1.7	1.20E-02	AB019786.1	NT	Cynops pyrrhogaster CpUbiq1 mRNA, partial cds
1246	6377	11536	1.3	1.10E-02	AA070364.1	EST_HUMAN	zn69a11.s1 Striatogene neuroepithelium (#937231) Homo sapiens cDNA clone IMAGE:530924 3'
1679	6803	11983	0.7	1.10E-02	X75491.1	NT	H. sapiens LIPA gene, exon 4
1679	6803	11984	0.7	1.10E-02	X75491.1	NT	H. sapiens LIPA gene, exon 4
2846	7999		3.5	1.10E-02	N99523.1	EST_HUMAN	z240a05.1 Soares fetal liver spleen 1NPLS Homo sapiens cDNA clone IMAGE:295040 5'
2933	8084	13192	10.4	1.10E-02	AF055086.1	NT	Homo sapiens MHC class 1 region
3478	8619	13732	2.5	1.10E-02	AI653508.1	EST_HUMAN	iq95b10.x1 NCI CGAP OX23 Homo sapiens cDNA clone IMAGE:2216539 3' similar to SW:XP_F_HUMAN Q82889 DNA-REPAIR PROTEIN COMPLEMENTING XP-F CELL;
3937	9071		0.9	1.10E-02	BE144637.1	EST_HUMAN	PM3-HT017-300899-001-h06 HT0175 Homo sapiens cDNA
4016	9146		1.0	1.10E-02	AW813796.1	EST_HUMAN	RC3-ST0197-120200-015-g11 ST0197 Homo sapiens cDNA
4723	9835	14927	1.8	1.10E-02	AL048383.2	EST_HUMAN	DKFZps86E0924_s1 586 (synonym: hule1) Homo sapiens cDNA clone DKFZps86E0924
4821	9930		0.9	1.10E-02	AW820281.1	EST_HUMAN	QV2-ST0296-150200-028-c11 ST0296 Homo sapiens cDNA
6	5214	10317	1.1	1.00E-02	AW846120.1	EST_HUMAN	MR3-CT0176-11099-003-e10 CT0176 Homo sapiens cDNA
1506	6633	11802	0.9	1.00E-02	AW368128.1	EST_HUMAN	CM2-HT0177-441089-017-h12 HT0177 Homo sapiens cDNA
2525	7621		1.2	1.00E-02	AA808388.1	EST_HUMAN	oc22n08.s1 NCI CGAP GCB1 Homo sapiens cDNA clone IMAGE:1350495 3'
3484	8605		1.0	1.00E-02	AW845621.1	EST_HUMAN	MR0-CT0060-081089-003-h10 CT0060 Homo sapiens cDNA
3805	8942	14037	0.8	1.00E-02	AI065086.1	EST_HUMAN	HA0821 Human fetal liver cDNA library Homo sapiens cDNA

Table 4

4667	9779	14877	4.3	1.00E-02	6753521	NT	Mus musculus corticotropin releasing hormone receptor 2 (Chr12), mRNA
4736	9847	14939	2.4	1.00E-02	R96567.1	EST_HUMAN	yq5sh01.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:199633 5'
4995	10098	15165	0.9	1.00E-02	AF218910.1	NT	Homo sapiens atractin precursor (ATRN) gene, exon 25 and complete cds, alternatively spliced
875	6023	11183	0.6	9.00E-03	A1796126.1	EST_HUMAN	hm4209.x1 NCL_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2383433 3' similar to contains element MER22 MER22 repetitive element;
2346	7448	12655	1.2	9.00E-03	AL161559.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 59
2593	7685	12887	1.1	9.00E-03	AJ243727.1	NT	Oncomyctus nerka proviral gypsy retrotransposon partial reverse transcriptase and protease genes (pol gene)
2593	7685	12887	1.1	9.00E-03	AJ243727.1	NT	Oncomyctus nerka proviral gypsy retrotransposon partial reverse transcriptase and protease genes (pol gene)
2593	7685	12888	1.1	9.00E-03	AJ243727.1	NT	protease genes (pol gene)
2876	8027	13128	0.8	9.00E-03	AJ251744.1	EST_HUMAN	q18009.x1 Soares NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1854281 3'
2876	8027	13130	0.8	9.00E-03	AJ251744.1	EST_HUMAN	q18009.x1 Soares NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1854281 3'
3617	8756	13849	0.9	9.00E-03	J05184.1	NT	S.acidocalcarus thermophil gene, complete cds
4914	10021	15100	1.2	9.00E-03	BE047949.1	EST_HUMAN	tz44e10.y1 NCL_CGAP_Bim52 Homo sapiens cDNA clone IMAGE:2291466 5'
5181	10273		2.6	9.00E-03	AF137240.1	NT	Sargocentron sp. mixed lineage leukemia-like protein (Mll) gene, partial cds
493	5668		1.1	8.00E-03	AA723007.1	EST_HUMAN	zh30603.s1 Soares pineal gland_N3HPG Homo sapiens cDNA clone IMAGE:413596 3'
973	6119	11276	15.0	8.00E-03	AF106656.1	NT	similar to contains Alu repetitive element;
2113	7224	12432	0.9	8.00E-03	AL163283.2	NT	Homo sapiens adenylosuccinate lyase gene, complete cds
							Homo sapiens chromosome 21 segment HS21C083
2930	8081		0.9	8.00E-03	U47048.1	NT	Escherichia coli microcin 24 region, DNA binding protein (mndA), immunity protein (mnl), microcin 24 (mncS), and microcin transport protein (mncA, mncB) genes, complete cds
3270	8415	13522	1.0	8.00E-03	BE171225.1	EST_HUMAN	RC1-HT0545-120200-011-B09 HT0545 Homo sapiens cDNA
3314	8459	13571	0.9	8.00E-03	AJ131016.1	NT	Homo sapiens SCL gene locus
3792	8929		1.1	8.00E-03	AF058764.1	NT	Xenopus laevis bone morphogenetic protein 4 (BMP-4) gene, complete cds
679	5834	10965	3.9	7.00E-03	AF097183.1	NT	Cryptosporidium parvum HC-10 gene, complete cds
679	5834	10966	3.9	7.00E-03	AF097183.1	NT	Cryptosporidium parvum HC-10 gene, complete cds
1341	6469		1.2	7.00E-03	Q61060	SWISSPROT	FORKHEAD BOX PROTEIN D3 (HNF3FH TRANSCRIPTION FACTOR GENESIS)
1373	6501	11667	5.0	7.00E-03	AA668298.1	EST_HUMAN	(HEPATOCYTE NUCLEAR FACTOR 3 FORKHEAD HOMOLOG 2) (HNF-2)
1486	6613	11783	1.7	7.00E-03	AW303559.1	EST_HUMAN	ab79b09.s1 Stratagene fetal retina 937202 Homo sapiens cDNA clone IMAGE:853145 3'
2210	7937	12533	0.8	7.00E-03	P04929	SWISSPROT	xy21b02.x1 Soares NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2813739 3'
3127	8276	13362	1.9	7.00E-03	AW503321.1	EST_HUMAN	HISTIDINE-RICH GLYCOPROTEIN PRECURSOR
3702	8641	13932	1.3	7.00E-03	AW444463.1	EST_HUMAN	UI-HF-BNO-alk-d-03-0-UI.r1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3078580 5'
3741	8878	13968	1.0	7.00E-03	AF196344.1	NT	UI-H-B13-alk-d-10-0-UI.s1 NCL_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:2733691 3'
							Rattus norvegicus neuronal nicotinic acetylcholine receptor subunit (Alpha10) mRNA, complete cds

Table 4

4434	9555	1.2	7.00E-03	AW117711.1	EST_HUMAN	xe3409.x1 NCI_CGAP_UT1 Homo sapiens cDNA clone IMAGE:2609033 3' similar to TR:Q12987 Q12987 ACIDIC 82 KDA PROTEIN.;
4495	9615	1.0	7.00E-03	AW530888.1	EST_HUMAN	hh89a05.y1 NCI_CGAP_GUT1 Homo sapiens cDNA clone IMAGE:2969936 5'
4916	10023	1.8	7.00E-03	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C078
5038	10138	1.1	7.00E-03	BE044191.1	EST_HUMAN	ho39h08.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:3039807 3' similar to TR:O93434 O93434 RETICULOCALBIN.;
5038	10138	1.1	7.00E-03	BE044191.1	EST_HUMAN	ho39h08.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:3039807 3' similar to TR:O93434 O93434 RETICULOCALBIN.;
5038	10138	1.1	7.00E-03	BE044191.1	EST_HUMAN	hd22a05.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2910224 3' similar to SW:PXR_HUMAN 075469 ORPHAN NUCLEAR RECEPTOR PXR.;
1220	6351	3.2	6.00E-03	AW511148.1	EST_HUMAN	hd22a05.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2910224 3' similar to SW:PXR_HUMAN 075469 ORPHAN NUCLEAR RECEPTOR PXR.;
1220	6351	3.2	6.00E-03	AW511148.1	EST_HUMAN	hd22a05.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2910224 3' similar to SW:PXR_HUMAN 075469 ORPHAN NUCLEAR RECEPTOR PXR.;
1220	6351	3.2	6.00E-03	AW511148.1	EST_HUMAN	hd22a05.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2910224 3' similar to SW:PXR_HUMAN 075469 ORPHAN NUCLEAR RECEPTOR PXR.;
2744	7828	1.1	6.00E-03	AF112374.1	NT	Danio rerio odorant receptor gene cluster
2862	8013	3.1	6.00E-03	AA759135.1	EST_HUMAN	ah79e11.s1 Soares_testis_NHT Homo sapiens cDNA clone 1321772 3'
2862	8013	3.1	6.00E-03	AA759135.1	EST_HUMAN	ah79e11.s1 Soares_testis_NHT Homo sapiens cDNA clone 1321772 3'
3208	8356	2.1	6.00E-03	H75690.1	EST_HUMAN	yr77h04.r1 Soares_fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:211351 5'
3336	8480	1.2	6.00E-03	U90880.1	NT	Fugu rubripes zinc finger protein, isotocin, fatty acid binding protein, septaplerin reductase and vasotocin genes, complete cds
3336	8480	1.2	6.00E-03	U90880.1	NT	Fugu rubripes zinc finger protein, isotocin, fatty acid binding protein, septaplerin reductase and vasotocin genes, complete cds
3489	8641	1.1	6.00E-03	W37985.1	EST_HUMAN	zc13a11.r1 Soares_parityroid_tumor_NbHPA Homo sapiens cDNA clone IMAGE:322172 5'
3711	8849	1.3	6.00E-03	6754029	NT	Mus musculus glucosamine-6-phosphate deaminase (Gnpl), mRNA
3848	8982	0.9	6.00E-03	AW847284.1	EST_HUMAN	RCO-CT0204-240899-021-b10 CT0204 Homo sapiens cDNA
3873	9009	1.2	6.00E-03	BE250108.1	EST_HUMAN	600942804.F NIH_MGC_15 Homo sapiens cDNA clone IMAGE:2969513 5'
4231	9355	0.9	6.00E-03	NS8946.1	EST_HUMAN	yy62h10.s1 Soares_multiple_sclerosis_2NbhMSP Homo sapiens cDNA clone IMAGE:278179 3'
4267	9392	1.4	6.00E-03	AI016833.1	EST_HUMAN	ov33c11.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1639124 3'
4597	9711	6.8	6.00E-03	AA324242.1	EST_HUMAN	EST27116 Cerebellum II Homo sapiens cDNA 5' end similar to EST containing Alu repeat
5115	10211	1.8	6.00E-03	AL163281.2	NT	Homo sapiens chromosome 21 segment HS21C081
5129	10224	0.9	6.00E-03	AA889972.1	EST_HUMAN	aj99g09.s1 Soares_parityroid_tumor_NbHPA Homo sapiens cDNA clone IMAGE:1404256 3'
653	5811	0.7	5.00E-03	L25105.1	NT	Chlamydia trachomatis partial ORFB: aminoacyl-tRNA synthase, complete cds; complete ORFA, and grpE-like protein, complete cds
653	5811	0.7	5.00E-03	L25105.1	NT	Chlamydia trachomatis partial ORFB: aminoacyl-tRNA synthase, complete cds; complete ORFA, and grpE-like protein, complete cds
654	5811	1.0	5.00E-03	L25105.1	NT	Chlamydia trachomatis partial ORFB: aminoacyl-tRNA synthase, complete cds; complete ORFA, and grpE-like protein, complete cds
654	5811	1.0	5.00E-03	L25105.1	NT	Chlamydia trachomatis partial ORFB: aminoacyl-tRNA synthase, complete cds; complete ORFA, and grpE-like protein, complete cds
654	5811	1.0	5.00E-03	L25105.1	NT	Chlamydia trachomatis partial ORFB: aminoacyl-tRNA synthase, complete cds; complete ORFA, and grpE-like protein, complete cds



Table 4

1096	6234	11386	1.4	5.00E-03	AJ010457.1	NT	Arabidopsis thaliana mRNA for DEAD box RNA helicase, RH3
1115	6252	11402	1.3	5.00E-03	AW293363.1	EST_HUMAN	U1-H-B12-ah1-d-06-0-U1.s1 NCI_CGAP_Sub4 Homo sapiens cDNA clone IMAGE:2727203 3'
1115	6252	11403	1.3	5.00E-03	AW293363.1	EST_HUMAN	U1-H-B12-ah1-d-06-0-U1.s1 NCI_CGAP_Sub4 Homo sapiens cDNA clone IMAGE:2727203 3'
1552	6679		0.9	5.00E-03	AI138977.1	EST_HUMAN	cd79c05.x1 Soares testis NHT Homo sapiens cDNA clone IMAGE:1735689 3'
2648	7737	12837	1.2	5.00E-03	AB033006.1	NT	Homo sapiens mRNA for KIAA1180 protein, partial cds
2905	8056	13161	1.0	5.00E-03	BE268657.1	EST_HUMAN	601184796F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3538799 5'
3097	8246	13352	4.1	5.00E-03	T87623.1	EST_HUMAN	y81109.s1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:22395 3'
3116	8265		1.8	5.00E-03	AL161491.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 3
3129	8278	13385	1.0	5.00E-03	R71794.1	EST_HUMAN	y186g02.s1 Soares breast 2N1HBst Homo sapiens cDNA clone IMAGE:155668 3'
3240	8387		1.1	5.00E-03	AJ297357.1	NT	Homo sapiens partial LIMD1 gene for LIM domains containing protein 1 and KIAA0851 gene
3641	8780	13873	4.2	5.00E-03	AF147449.2	NT	Pseudomonas aeruginosa strain PAO1 penicillin-binding protein 1B (ponB) gene, complete cds
3698	8837	13928	0.8	5.00E-03	U38914.1	NT	Citrus sinensis seed storage protein cDNA, complete cds
3890	9026		1.4	5.00E-03	AA299675.1	EST_HUMAN	EST12218 Uterus tumor 1 Homo sapiens cDNA 5' end
4207	9332	14418	0.9	5.00E-03	H78355.1	EST_HUMAN	yv79g10.r1 Soares fetal liver spleen 1N1FLS Homo sapiens cDNA clone IMAGE:240066 5'
4209	9837	13928	0.9	5.00E-03	U38914.1	NT	Citrus sinensis seed storage protein cDNA, complete cds
4503	9622	14713	0.9	5.00E-03	AJ131016.1	NT	Homo sapiens SCL gene locus
4619	9733	14828	2.5	5.00E-03	A1752367.1	EST_HUMAN	cn156c02.x1 Normal Human Trabecular Bone Cells Homo sapiens cDNA clone
232	5423	10547	1.0	4.00E-03	AW500196.1	EST_HUMAN	U1-HF-BN0-akc-h-04-0-U1.r1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3076831 5'
318	5502	10629	0.7	4.00E-03	R46482.1	EST_HUMAN	y951e04.s1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:35988 3'
436	5602	10735	0.9	4.00E-03	P64675	SWISSPROT	PHOSPHATIDYLINOSITOL 3-KINASE 3 (PI3-KINASE) (PI3K)
588	5748	10865	1.0	4.00E-03	AA938338.1	EST_HUMAN	ont79t12.s1 Soares NFL_T_G8C_S1 Homo sapiens cDNA clone IMAGE:1562566 3'
659	6007	11169	0.6	4.00E-03	R46482.1	EST_HUMAN	y951e04.s1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:35988 3'
893	6041		1.2	4.00E-03	AW749101.1	EST_HUMAN	RC3-BT0333-110100-012-01 BT0333 Homo sapiens cDNA
1133	6269	11421	11.0	4.00E-03	AA098777.1	EST_HUMAN	z81a08.r1 Stralagene colon (#937204) Homo sapiens cDNA clone IMAGE:510998 5'
1153	6288	11442	0.5	4.00E-03	AW794740.1	EST_HUMAN	RC6-UM0014-170400-023-G01 UM0014 Homo sapiens cDNA
1281	6411	11572	1.3	4.00E-03	AA284374.1	EST_HUMAN	z85a01.r1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:701736 5'
1709	6832	12012	0.8	4.00E-03	U33472.1	NT	Rattus norvegicus type 1 astrocyte and olfactory-limbic associated protein AT1-46 mRNA, complete cds
1971	7086	12289	7.6	4.00E-03	AA098777.1	EST_HUMAN	z181a08.r1 Stralagene colon (#937204) Homo sapiens cDNA clone IMAGE:510998 5'
2200	7309		0.8	4.00E-03	BE410556.1	EST_HUMAN	6011304161F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3638510 5'
2232	7339	12551	0.5	4.00E-03	AW794740.1	EST_HUMAN	RC6-UM0014-170400-023-G01 UM0014 Homo sapiens cDNA

Table 4

2526	7622	12822	0.7	4.00E-03	U52111.2	NT	Homo sapiens X28 region near ALD locus containing dual specificity phosphatase 9 (DUSP9), ribosomal protein L18a (RPL18a), Ca2+/Calmodulin-dependent protein kinase I (CAMKI1), creatine transporter (CRTTR), CDM protein (CDM), adrenoleukodystrophy protein >
2526	7622	12823	0.7	4.00E-03	U52111.2	NT	Homo sapiens X28 region near ALD locus containing dual specificity phosphatase 9 (DUSP9), ribosomal protein L18a (RPL18a), Ca2+/Calmodulin-dependent protein kinase I (CAMKI1), creatine transporter (CRTTR), CDM protein (CDM), adrenoleukodystrophy protein >
2664	7752	12950	1.0	4.00E-03	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
3487	8628	13739	0.9	4.00E-03	AW188426.1	EST_HUMAN	X98104.x1 NCI CGAP C018 Homo sapiens cDNA clone IMAGE:2665279.3
3487	8628	13740	0.9	4.00E-03	AW188426.1	EST_HUMAN	X98104.x1 NCI CGAP C018 Homo sapiens cDNA clone IMAGE:2665279.3
3572	8711	13810	0.8	4.00E-03	Q13606	SWISSPROT	OLFACTORY RECEPTOR 511 (OLFACTORY RECEPTOR-LIKE PROTEIN OLF1)
3836	8711	13810	0.8	4.00E-03	Q13606	SWISSPROT	OLFACTORY RECEPTOR 511 (OLFACTORY RECEPTOR-LIKE PROTEIN OLF1)
3852	8988	14088	0.9	4.00E-03	AF060868.1	NT	Mus musculus tumor susceptibility protein 101 (Tsg101) gene, complete cds
3914	9048		1.8	4.00E-03	AJ011712.1	NT	Homo sapiens TNNT1 gene, exons 1-11 (and joined CDS)
4509	9628	14722	1.1	4.00E-03	AJ732754.1	EST_HUMAN	ab18a08.x5 Stragene lung (#937210) Homo sapiens cDNA clone IMAGE:841142.3 similar to contains Alu repetitive element;
4842	9849	15038	0.8	4.00E-03	AL163301.2	NT	Homo sapiens chromosome 21 segment HS21C101
5164	10258	15328	13.2	4.00E-03	J02187.1	NT	Foot and mouth disease virus serotype A-12 119ab capsid protein VP3
367	5545	10678	0.8	3.00E-03	AF011920.1	NT	Homo sapiens protein kinase CK2 catalytic subunit alpha gene, exon 1
861	6009	11170	2.6	3.00E-03	AF011920.1	NT	Homo sapiens protein kinase CK2 catalytic subunit alpha gene, exon 1
1456	6585	11759	0.8	3.00E-03	A1133024.1	EST_HUMAN	HA1611 Human fetal liver cDNA library Homo sapiens cDNA
1638	6764	11933	0.7	3.00E-03	AA468110.1	EST_HUMAN	nc73c05.s1 NCI CGAP P12 Homo sapiens cDNA clone IMAGE:782984 similar to contains Alu repetitive element;
1707	6630		1.0	3.00E-03	X87344.1	NT	H. sapiens DMA, DMB, HLA-Z1, IAPP2, LMP2, TAP1, LMP7, TAP2, DOB, DOB2 and RING6, 9, 13 and 14 genes
2211	7319		0.9	3.00E-03	AF055066.1	NT	Homo sapiens MHC class 1 region
2248	7354		1.4	3.00E-03	Z32521.1	NT	S. cereale (cv. Halo) mRNA for triosephosphate isomerase
2249	7355	12561	1.1	3.00E-03	AJ271004.1	NT	Mus musculus TTF3/ITF gene for Trefoll Factor 3/Intestinal Trefoll Factor protein, exons 1-3
2249	7355	12562	1.1	3.00E-03	AJ271004.1	NT	Mus musculus TTF3/ITF gene for Trefoll Factor 3/Intestinal Trefoll Factor protein, exons 1-3
2683	7770	12970	4.0	3.00E-03	AF034863.1	NT	Rattus norvegicus synaptic scaffolding molecule (S-SCAM) mRNA, complete cds
2963	8114		0.8	3.00E-03	Y09006.1	NT	Arabidopsis thaliana pmmt gene
3044	8195	13297	4.5	3.00E-03	BE379266.1	EST_HUMAN	601237892F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:360933.5
3112	8281	13365	2.6	3.00E-03	AW802687.1	EST_HUMAN	IL2-UM0076-24030C-056-D03 UM0076 Homo sapiens cDNA
3371	8514	13621	2.0	3.00E-03	U34606.1	NT	Mus musculus alpha-1(XVII) collagen (COL18A1) gene, exon 1 and 2
3379	8522		6.8	3.00E-03	Y12500.1	NT	C. elegans sandc gene
3950	9083	14164	1.6	3.00E-03	AJ792278.1	EST_HUMAN	ah04109.y5 Gessler Wilms tumor Homo sapiens cDNA clone IMAGE:1155689.5
4058	9185		1.3	3.00E-03	Z32521.1	NT	S. cereale (cv. Halo) mRNA for triosephosphate isomerase
4296	9420	14510	11.9	3.00E-03	AJ011432.1	NT	Rattus norvegicus gdnf gene

Table 4

4417	9537	14628	4.4	3.00E-03	AI536141.1	EST_HUMAN	xu8.P10.H3 conom Homo sapiens cDNA 3'
4630	9744	14841	0.9	3.00E-03	AL119067.1	EST_HUMAN	DKFZp761B0712_r1 761 (synonym: hamy2) Homo sapiens cDNA clone DKFZp761B0712 5'
4727	9839	14931	1.5	3.00E-03	A1732754.1	EST_HUMAN	ab18a08.x3 Sciatagene lung (8937210) Homo sapiens cDNA clone IMAGE:841142 3' similar to cDNAs Alu repetitive element:
5089	10187	15265	1.1	3.00E-03	4508414	NT	Homo sapiens RAP1, GTPase activating protein 1 (RAP1GA1) mRNA
5089	10187	15266	1.1	3.00E-03	4508414	NT	Homo sapiens RAP1, GTPase activating protein 1 (RAP1GA1) mRNA
504	5668	10790	0.9	2.00E-03	Q04652	SWISSPROT	RING CANAL PROTEIN (KELCH PROTEIN)
504	5668	10791	0.9	2.00E-03	Q04652	SWISSPROT	RING CANAL PROTEIN (KELCH PROTEIN)
768	7899		2.4	2.00E-03	T70874.1	EST_HUMAN	yd15h03.r1 Soares fetal liver spleen 1NF.LS Homo sapiens cDNA clone IMAGE:108341 5'
1340	6468	11636	0.7	2.00E-03	M20783.1	NT	Human alpha-2-plasmin inhibitor gene, exons 6 and 7
1343	6471	11638	0.6	2.00E-03	AA661605.1	EST_HUMAN	nu8801.s1 NCI CGAP Alvi1 Homo sapiens cDNA clone IMAGE:1217593
1474	6601	11775	1.1	2.00E-03	P48509	SWISSPROT	PLATELET-ENDOTHELIAL TETRASPAN ANTIGEN 3 (PETA-3) (GP27) (MEMBRANE GLYCOPROTEIN SFA-1) (CD151 ANTIGEN)
1500	6626	11795	0.7	2.00E-03	4557836	NT	Homo sapiens procollagen-lysine, 2-oxoglutarate 5-dioxygenase (lysine hydroxylase, Ehlers-Danlos syndrome type VI) (PLOD) mRNA
1500	6626	11796	0.7	2.00E-03	4557836	NT	Homo sapiens procollagen-lysine, 2-oxoglutarate 5-dioxygenase (lysine hydroxylase, Ehlers-Danlos syndrome type VI) (PLOD) mRNA
1573	6699		1.8	2.00E-03	P29400	SWISSPROT	Danlos syndrome type VI) (PLOD) mRNA
1733	6856	12034	1.4	2.00E-03	AA450138.1	EST_HUMAN	COLLAGEN ALPHA 5(V) CHAIN PRECURSOR
2203	7312	12524	1.0	2.00E-03	AL163302.2	NT	zx42a10.r1 Soares fetal_livus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:769114 5'
2535	7631		1.7	2.00E-03	AW137782.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C102
3370	8513	13620	4.0	2.00E-03	AA450138.1	EST_HUMAN	U1-H-B1+ad-g-10-U.s1 NCI CGAP Sub3 Homo sapiens cDNA clone IMAGE:2717010 3'
3615	8754	13847	4.9	2.00E-03	X87344.1	NT	zx42a10.r1 Soares fetal_livus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:769114 5'
3689	9005	14104	0.9	2.00E-03	AB040802.1	NT	H.sapiens DNA, DMB, HLA-Z1, IPP2, LMP2, TAP1, LMP7, TAP2, DOB, DOB2 and RING8, 9, 13 and 14 genes
4024	9152	14235	2.2	2.00E-03	P03374	SWISSPROT	Rattus norvegicus mRNA for SREB1, complete cds
4127	9253		9.8	2.00E-03	U68491.1	NT	ENV POLYPEPTIDE (CONTAINS COAT PROTEIN GP82 COAT PROTEIN GP36)
4446	9566	14662	1.9	2.00E-03	L42512.1	NT	Rattus norvegicus 5-hydroxytryptamine7 receptor gene, partial cds
4446	9566	14663	1.9	2.00E-03	L42512.1	NT	Drosophila melanogaster short sighted class 2 (shs) mRNA, complete cds
4608	9722	14817	0.9	2.00E-03	AF223391.1	NT	Drosophila melanogaster short sighted class 2 (shs) mRNA, complete cds
4612	9726		1.7	2.00E-03	R87773.1	EST_HUMAN	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
5077	10175		0.8	2.00E-03	AJ245167.1	NT	yc45602.s1 Soares adult brain N264HB55Y Homo sapiens cDNA clone IMAGE:180890 3'
368	5555		1.1	1.00E-03	BE388904.1	EST_HUMAN	Camelus dromedarius cchp19 gene for immunoglobulin heavy chain variable region
432	5599	10730	1.4	1.00E-03	H96477.1	EST_HUMAN	601294694.F NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3606670 5'
							yg98c08.r1 Soares pineal_gland_N3HPG Homo sapiens cDNA clone IMAGE:232334 5'

Table 4

812	5962	11119	0.8	1.00E-03	AIJ20263.1	EST_HUMAN	as70b08.x1 Barstead colon HPLRB7 Homo sapiens cDNA clone IMAGE:2334039 3' similar to TR:Q13825 Q13825 AU-BINDING PROTEIN/ENVOYL-COA HYDRATASE. ;
812	5962	11120	0.8	1.00E-03	AIJ20263.1	EST_HUMAN	as70b08.x1 Barstead colon HPLRB7 Homo sapiens cDNA clone IMAGE:2334039 3' similar to TR:Q13825 Q13825 AU-BINDING PROTEIN/ENVOYL-COA HYDRATASE. ;
1079	6217	11368	0.7	1.00E-03	AI865788.1	EST_HUMAN	wk68a06.x1 NCI CGAP Pan1 Homo sapiens cDNA clone IMAGE:2422258 3'
1099	6237	11386	1.4	1.00E-03	AI954572.1	EST_HUMAN	wx93a10.x1 NCI CGAP Malt15 Homo sapiens cDNA clone IMAGE:2551242 3'
							wd86a01.x1 NCI CGAP Lu24 Homo sapiens cDNA clone IMAGE:2339440 3' similar to contains Alu repetitive element;
1150	6285	11438	1.5	1.00E-03	AI692616.1	EST_HUMAN	HIGH MOLECULAR WEIGHT FORM OF MYOSIN I (HMMI)
1882	7097	12300	1.3	1.00E-03	PA7808	SWISSPROT	Homo sapiens SCL gene locus
2108	7219	12428	2.9	1.00E-03	AI131016.1	NT	Homo sapiens mRNA for KIAA1291 protein, partial cds
2951	8102	13208	1.2	1.00E-03	AB033177.1	NT	CARBONIC ANHYDRASE VI PRECURSOR (CARBONATE DEHYDRATASE VI) (CA-VI)
3154	8303	13411	2.3	1.00E-03	P18915	SWISSPROT	(SECRETED CARBONIC ANHYDRASE) (SALIVARY CARBONIC ANHYDRASE)
3154	8303	13412	2.3	1.00E-03	P18915	SWISSPROT	(SECRETED CARBONIC ANHYDRASE) (SALIVARY CARBONIC ANHYDRASE)
3262	8408	13516	1.2	1.00E-03	P08547	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
3468	8638	13750	0.8	1.00E-03	U88061.1	NT	Human MUC2 gene, promoter region
3468	8638	13751	0.8	1.00E-03	U88061.1	NT	Human MUC2 gene, promoter region
3655	8991	14091	1.0	1.00E-03	Z49649.1	NT	S.cerevisiae chromosome X reading frame ORF YJR149w
4377	9499	14586	3.8	1.00E-03	BE246536.1	EST_HUMAN	TCBAP-ID4909 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project=TCBA Homo sapiens cDNA clone TCBAP4909
4564	9682	14776	0.9	1.00E-03	U29449.1	NT	Cenotriabullis elegans spliced leader RNA (SL3 alpha), (SL4), and (SL5) genes
4717	9828	14920	1.8	1.00E-03	AI073485.1	EST_HUMAN	ov45c04.x1 Soares testis NHT Homo sapiens cDNA clone IMAGE:1640262 3'
4717	9829	14921	1.8	1.00E-03	AI073485.1	EST_HUMAN	ov45c04.x1 Soares testis NHT Homo sapiens cDNA clone IMAGE:1640262 3'
4718	9830		6.2	1.00E-03	BE154067.1	EST_HUMAN	PMO-HT0339-200400-010-D02 HT0339 Homo sapiens cDNA
5009	10111	15181	17.0	1.00E-03	O46409	SWISSPROT	APOLIPROTEIN A-IV PRECURSOR (APO-AIV)
							UI-H-BV1-ama-e-03-0-UI.s1 NCI CGAP_Sub7 Homo sapiens cDNA clone IMAGE:3069388 3'
1453	6580	11754	1.0	9.00E-04	AW453046.1	EST_HUMAN	Human retinoblastoma susceptibility gene exons 1-27, complete cds
5131	10226	15301	0.8	9.00E-04	L11910.1	NT	Human retinoblastoma susceptibility gene exons 1-27, complete cds
1472	6599		1.4	8.00E-04	X66469.1	NT	Xlaeis mRNA for CASR protein
3843	8979	14080	1.3	8.00E-04	R07008.1	EST_HUMAN	yf12h10.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:126691 5'
4089	9215		4.2	8.00E-04	P08547	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
4656	9768	14864	2.4	8.00E-04	U29185.1	NT	Homo sapiens p10n protein (P1P) gene, complete cds
1766	6906	12094	0.6	7.00E-04	L41825.1	NT	Homo sapiens p10n protein (P1P) gene, complete cds
2350	7462	12659	1.1	7.00E-04	U28185.1	NT	Homo sapiens CYP17 gene, 5' end
2682	7769	12969	3.3	7.00E-04	AL163210.2	NT	Homo sapiens p10n protein (P1P) gene, complete cds
3243	8390	13497	1.0	7.00E-04	4885170	NT	Homo sapiens chromosome 21 segment HS21C010
967	6112	11268	1.6	6.00E-04	P07207	SWISSPROT	Homo sapiens chromosome X open reading frame 6 (CXORF6) mRNA
967	6112	11269	1.6	6.00E-04	P07207	SWISSPROT	NEUROGENIC LOCUS NOTCH PROTEIN PRECURSOR
967	6112	11270	1.6	6.00E-04	P07207	SWISSPROT	NEUROGENIC LOCUS NOTCH PROTEIN PRECURSOR

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Table 4

169	5363	10489	1.2	2.00E-04	AF217796.1	NT	Homo sapiens SCG10 like-protein, helicase-like protein NHL, M68, and ADP-ribosylation factor related protein 1 (ARFRP1) genes, complete cds
889	6037	11195	1.5	2.00E-04	M86524.1	NT	Human dystrophin gene
889	6037	11196	1.5	2.00E-04	M86524.1	NT	Human dystrophin gene
1162	6297		1.4	2.00E-04	A1286021.1	EST_HUMAN	qh98e11.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1855052 3' similar to contains MER3.b2 MER3 repetitive element;
1169	6303		0.7	2.00E-04	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
1791	6911		0.5	2.00E-04	AF224268.1	NT	Mus musculus 5' flanking region of Pib3 gene
2136	7246		1.3	2.00E-04	AA478980.1	EST_HUMAN	zu39b05.s1 Soares ovary tumor NbHOT Homo sapiens cDNA clone IMAGE:740337 3' similar to contains Alu repetitive element;
2528	7624	12825	1.5	2.00E-04	U66061.1	NT	Human germ-line T-cell receptor beta chain TCRBV17S1A1T, TCRBV2S1, TCRBV10S1P, TCRBV29S1P, TCRBV19S1P, TCRBV15S1, TCRBV11S1A1T, HVB relic, TCRBV28S1P, TCRBV34S1, TCRBV14S1, TCRBV3S1, TCRBV4S1A1T, TRY4, TRY5, TRY6, TRY7, TRY8, TCRBD1, TCRBJ1S1, TCRBJ1S2.>
2958	8109	13215	1.0	2.00E-04	A1124529.1	EST_HUMAN	am58c09.x1 Johnston frontal cortex Homo sapiens cDNA clone IMAGE:1539760 3'
3389	8532	13637	2.5	2.00E-04	BE082317.1	EST_HUMAN	QV2-BT0636-070500-194-b07 BT0636 Homo sapiens cDNA
3417	8559	13670	1.0	2.00E-04	U34374.1	NT	Human tyrosine kinase TXK (tk) gene, exons 9 and 10
3837	8973	14073	0.8	2.00E-04	AW97844.1	EST_HUMAN	EST190050 MAGE resequences, MAGEP Homo sapiens cDNA
4051	9178		4.6	2.00E-04	U01029.1	NT	Phaseolus vulgaris nitrate reductase (PVNR2) gene, complete cds
4569	9687	14781	1.3	2.00E-04	H96265.1	EST_HUMAN	yu01e11.t1 Soares_pineal_gland_N3HPG Homo sapiens cDNA clone IMAGE:232556 5'
4569	9687	14782	1.3	2.00E-04	H96265.1	EST_HUMAN	yu01e11.t1 Soares_pineal_gland_N3HPG Homo sapiens cDNA clone IMAGE:232556 5'
4689	9801		1.3	2.00E-04	U09226.1	NT	Gallus gallus proteasome 28 kDa subunit homolog mRNA, complete cds
4946	10051	15122	1.3	2.00E-04	O99297	SWISSPROT	PUTATIVE MITOCHONDRIAL CARRIER YOR222V
4991	10094	15162	1.7	2.00E-04	AB037997.1	NT	Danio rerio hagoromo gene, exons 1 to 6, partial cds
750	5902	11048	1.0	1.00E-04	H99646.1	EST_HUMAN	iy28c09.s1 Soares melanocyte 2NBHM Homo sapiens cDNA clone IMAGE:262864 3' similar to contains L1.11 L1 repetitive element;
1059	6198	11351	0.8	1.00E-04	P11369	SWISSPROT	RETROVIRUS-RELATED POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE; ENDONUCLEASE]
1098	6236	11387	1.3	1.00E-04	AW013847.1	EST_HUMAN	UI-H-B10-aab-e-09-0-UI.s1 NCI_CGAP_Sub1 Homo sapiens cDNA clone IMAGE:2708825 3'
1098	6236	11388	1.3	1.00E-04	AW013847.1	EST_HUMAN	UI-H-B10-aab-e-09-0-UI.s1 NCI_CGAP_Sub1 Homo sapiens cDNA clone IMAGE:2708825 3'
1310	6438		1.0	1.00E-04	U62918.1	NT	Anguilla anguilla dopamine D1A1 receptor (d1A1) gene, complete cds
1610	6737	11906	1.2	1.00E-04	AF148805.1	NT	Kaposi's sarcoma-associated herpesvirus ORF 68 gene, partial cds; and ORF 69, kaposin, v-FLIP, v-cyclin, latent nuclear antigen, ORF K14, v-GPCR, putative phosphothiosylformylglycinamide synthase, and LAMP (LAMP) genes, complete cds
1610	6737	11907	1.2	1.00E-04	AF148805.1	NT	Kaposi's sarcoma-associated herpesvirus ORF 68 gene, partial cds; and ORF 69, kaposin, v-FLIP, v-cyclin, latent nuclear antigen, ORF K14, v-GPCR, putative phosphothiosylformylglycinamide synthase, and LAMP (LAMP) genes, complete cds
2600	7691	12895	1.3	1.00E-04	AA714263.1	EST_HUMAN	nv95a02.s1 NCI_CGAP_Pt18 Homo sapiens cDNA clone IMAGE:1237514 similar to contains Alu repetitive element;

Table 4

2600	7691	12896	1.3	1.00E-04	AA714263.1	EST_HUMAN	inv5a02.s1 NCI_CGAP_P118 Homo sapiens cDNA clone IMAGE:1237514 similar to contains
2655	7744	12943	1.2	1.00E-04	BE218833.1	EST_HUMAN	Alu repetitive element;
2655	7744	12944	1.2	1.00E-04	BE218833.1	EST_HUMAN	inv5c08.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3176366 3'
3247	8394	13501	1.0	1.00E-04	Q62203	SWISSPROT	inv5c08.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3176366 3'
3675	8814	13908	1.1	1.00E-04	AA40282.1	EST_HUMAN	SPICEOSOME ASSOCIATED PROTEIN 62 (SAP 62) (SPLICING FACTOR 3A SUBUNIT 2) (SFC3A6B)
3971	9103	14186	1.8	1.00E-04	M14042.1	NT	ip0111.x1 NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2140269 3' similar to
4382	9484	14575	0.9	1.00E-04	P08547	SWISSPROT	contains Alu repetitive element;
4665	9777	14874	3.0	1.00E-04	O15117	SWISSPROT	Mouse alpha 1 type-IV collagen mRNA
5028	10129	15203	1.6	1.00E-04	7662015	NT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
5028	10129	15204	1.6	1.00E-04	7662015	NT	FYN-BINDING PROTEIN (SLP-76 ASSOCIATED PROTEIN) (SLAP-130)
5033	10133	15208	1.0	1.00E-04	A1357156.1	EST_HUMAN	Human sapiens KIAA0237 gene product (KIAA0237), mRNA
5148	10243		0.9	1.00E-04	272560.1	NT	Human sapiens KIAA0237 gene product (KIAA0237), mRNA
5338	10971		0.6	9.00E-05	AA718933.1	EST_HUMAN	Human sapiens KIAA0237 gene product (KIAA0237), mRNA
5689	6715	11885	1.1	9.00E-05	AL043810.1	EST_HUMAN	S. cerevisiae chromosome VII reading frame ORF YGL038c
3995	9127	14210	0.8	9.00E-05	A1762209.1	EST_HUMAN	ah45c11.s1 Soares_testis_NHT Homo sapiens cDNA clone 1292468 3'
804	5955	11108	1.5	8.00E-05	AJ251646.1	NT	DKFZp434A0128_r1 434 (synonym: hies3) Homo sapiens cDNA clone DKFZp434A0128 5'
846	5955		1.2	8.00E-05	AJ251646.1	NT	wf54c11.x1 NCI_CGAP_Co16 Homo sapiens cDNA clone IMAGE:2394086 3' similar to
2820	8071		0.8	8.00E-05	M83575.1	NT	contains MER6.11 MER6 repetitive element;
4852	8859		1.2	8.00E-05	F28172.1	EST_HUMAN	Pisum sativum mRNA for beta-1,3 glucanase (gms2 gene)
344	5525	10650	1.0	7.00E-05	AW847445.1	EST_HUMAN	Pisum sativum mRNA for beta-1,3 glucanase (gms2 gene)
344	5525	10651	1.0	7.00E-05	AW847445.1	EST_HUMAN	Human platelet-derived growth factor A chain (PDGFA) gene, exons only
555	5718	10834	1.1	7.00E-05	L49075.1	EST_HUMAN	HSPD16734.HM3 Homo sapiens cDNA clone s3000003H04
555	5718	10835	1.1	7.00E-05	L49075.1	EST_HUMAN	RC3-CT0208-220989-011-E04 CT0208 Homo sapiens cDNA
1039	6179	11332	0.8	7.00E-05	Q22949	SWISSPROT	RC3-CT0208-220989-011-E04 CT0208 Homo sapiens cDNA
1083	6221	11372	0.7	7.00E-05	T05902.1	EST_HUMAN	HU0072014F Human fovea cDNA Homo sapiens cDNA clone EST HF0072014
2686	7773	12972	1.9	7.00E-05	AL163278.2	NT	HU0072014F Human fovea cDNA Homo sapiens cDNA clone EST HF0072014
3121	8270	13375	5.8	7.00E-05	AB00980.1	NT	PROBABLE GLYCEROL-3-PHOSPHATE ACYLTRANSFERASE, MITOCHONDRIAL
3475	8616	13728	1.1	7.00E-05	AL163303.2	NT	PRECUSOR (GPAT)
4276	9401	14485	1.3	7.00E-05	U60980.1	NT	EST03791 Fetal brain, Striatum (cat#936206) Homo sapiens cDNA clone HFBD136
4344	9467	14555	0.8	7.00E-05	AA367612.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C078
5202	10293		1.1	7.00E-05	AA367612.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C078
1981	7096	12298	0.6	6.00E-05	4885170	NT	Dictyostelium discoideum gene for TRFA, complete cds
1981	7096	12299	0.6	6.00E-05	4885170	NT	Homo sapiens chromosome 21 segment HS21C103
2544	7640	12841	0.5	6.00E-05	A1655241.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C001
							Caenorhabditis elegans Skp1p homolog mRNA, complete cds
							EST178713 Placenta 1 Homo sapiens cDNA
							Homo sapiens chromosome X open reading frame 6 (CXORF6) mRNA
							Homo sapiens chromosome X open reading frame 6 (CXORF6) mRNA
							W654N08.x1 NCI_CGAP_GC8 Homo sapiens cDNA clone IMAGE:2309531 3' similar to
							gb:103250 DNA TOPOISOMERASE I (HUMAN);

Table 4

2652	7741	12941	0.9	6.00E-05	Z84506.1	NT	H.sapiens flow-sorted chromosome 6 HindIII fragment, SC6pA28B.10
2652	7741	12942	0.9	6.00E-05	Z84506.1	NT	H.sapiens flow-sorted chromosome 6 HindIII fragment, SC6pA28B.10
2783	5620	10947	0.8	6.00E-05	AF053630.1	NT	Homo sapiens monocleoneurophil elastase inhibitor gene, complete cds
1382	6509	11673	5.2	5.00E-05	AW392086.1	EST_HUMAN	QV4-ST0234-241199-040-h11 ST0234 Homo sapiens cDNA
1819	6638		0.6	5.00E-05	8923891	NT	Homo sapiens 22kDa peroxisomal membrane protein-like (LOC55895), mRNA
2831	7982	13082	0.9	5.00E-05	AJ251058.1	NT	Homo sapiens MEPIA gene, promoter region and exon 1
							Homo sapiens partial SLC22A3 gene for extraneuronal monoamine transporter (EMT), exon 1
3697	9032	14125	3.0	5.00E-05	AJ251884.1	NT	
2220	7327		1.4	4.00E-05	AJ289880.1	NT	Homo sapiens KIAA0851 gene (partial), X13 gene and LZTFL1 gene
2776	5415		1.6	4.00E-05	U12821.1	NT	Human renin (REN) gene, 5' flanking region
4624	9738	14834	7.1	4.00E-05	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080
							qth6c10.x1 Soares_fetal_liver_spleen_1NPLS_S1 Homo sapiens cDNA clone IMAGE:1849458 3' similar to contains Alu repetitive element;contains element KER repetitive element;
665	5821	10949	0.8	3.00E-05	AI248061.1	EST_HUMAN	element;
1043	6183	11336	1.4	3.00E-05	AW273851.1	EST_HUMAN	xy2g03.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2814100 3'
2688	7775	12974	0.9	3.00E-05	Q62234	SWISSPROT	SKLEMIN
4285	9410	14496	6.9	3.00E-05	BE169211.1	EST_HUMAN	PM1-HT0521-120200-001-e10 HT0521 Homo sapiens cDNA
4285	9410	14497	6.9	3.00E-05	BE169211.1	EST_HUMAN	PM1-HT0521-120200-001-e10 HT0521 Homo sapiens cDNA
4385	9467	14577	1.2	3.00E-05	AA368679.1	EST_HUMAN	EST79986 Placenta 1 Homo sapiens cDNA similar to p53-associated protein
4385	9467	14578	1.2	3.00E-05	AA368679.1	EST_HUMAN	EST79986 Placenta 1 Homo sapiens cDNA similar to p53-associated protein
4519	9638	14729	0.9	3.00E-05	AF149773.1	NT	Homo sapiens NOD1 protein (NOD1) gene, exons 1, 2, and 3
							qth6c10.x1 Soares_fetal_liver_spleen_1NPLS_S1 Homo sapiens cDNA clone IMAGE:1849458 3' similar to contains Alu repetitive element;contains element KER repetitive element;
4731	5821	10949	0.8	3.00E-05	AI248061.1	EST_HUMAN	qth98e11.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1855052 3' similar to contains MER3.b2 MER3 repetitive element;
2276	7382	12590	0.6	2.00E-05	AI286021.1	EST_HUMAN	Human adenosine deaminase (ADA) gene, complete cds
2538	7634	12834	1.1	2.00E-05	M13782.1	NT	zq46a12.1 Stratagene hNT neuron (#937233) Homo sapiens cDNA clone IMAGE:632734 5' similar to contains Alu repetitive element;contains element L.1 repetitive element;
2681	7768		2.6	2.00E-05	AA160562.1	EST_HUMAN	RC3-BT0319-120200-014-408 BT0319 Homo sapiens cDNA
3098	8249	13353	1.5	2.00E-05	BE066036.1	EST_HUMAN	
3304	8449	13559	0.9	2.00E-05	AF184614.1	NT	Homo sapiens p47-phox (NCF1) gene, complete cds
3323	8467	13582	1.1	2.00E-05	X89211.1	NT	H.sapiens DNA for endogenous retroviral like element
3356	8501	13610	5.3	2.00E-05	AL163207.2	NT	Homo sapiens chromosome 21 segment HS21C007
3449	8591		1.0	2.00E-05	X95465.1	NT	S.cerevisiae 12.8 kbp fragment of the left arm of chromosome XV
3737	8874		0.9	2.00E-05	AL039107.1	EST_HUMAN	DKFZp5661064.t1 566 (synonym: htkd2) Homo sapiens cDNA clone DKFZp5661064 5'
4510	9629	14723	1.0	2.00E-05	AI263349.1	EST_HUMAN	qg13a08.x1 Soares_NihHMFu_S1 Homo sapiens cDNA clone IMAGE:3608653 5'
4592	9706		1.1	2.00E-05	BE378471.1	EST_HUMAN	contains MER18.b3 MER18 repetitive element;
4782	9892	14985	0.8	2.00E-05	AJ131016.1	NT	contains MER18.b3 MER18 repetitive element;
2663	7951	12949	0.6	1.00E-05	AL163282.2	NT	Homo sapiens SCL gene locus
							Homo sapiens chromosome 21 segment HS21C082



Table 4

3238	8385	13493	0.9	1.00E-05	AA631101.1	EST_HUMAN	ng77g06.s1 NCI_CGAP_P122 Homo sapiens cDNA clone IMAGE:1158394.3'
3599	8738	13833	1.7	1.00E-05	AF088273.1	NT	Drosophila melanogaster strain Lando 120 Suppressor of Hairless (Su(H)) gene, partial cds
3866	9022	14115	9.2	1.00E-05	P81274	SWISSPROT	MOSAIC PROTEIN LGN
4082	9209	14283	1.1	1.00E-05	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
4180	9306	14385	2.0	1.00E-05	AA431119.1	EST_HUMAN	z66904.t1 Soares testis NHT Homo sapiens cDNA clone IMAGE:781494.5'
4742	9853	14945	2.2	1.00E-05	AW419134.1	EST_HUMAN	xy49g11.x1 NCI_CGAP_Lu34.1 Homo sapiens cDNA clone IMAGE:2856548.3'
4882	9990	15071	4.5	1.00E-05	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
2637	7726	12830	2.4	9.00E-06	AF583811.1	EST_HUMAN	tr3a06.x1 NCI_CGAP_HSC3 Homo sapiens cDNA clone IMAGE:2246386.3'
3057	8208	13307	3.7	9.00E-06	AI218983.1	EST_HUMAN	qp11b08.x1 Soares placenta_80dweeks_2NHP808W Homo sapiens cDNA clone IMAGE:1759191.3'
3559	8698		2.9	9.00E-06	M61755.1	NT	Human alanine:glyoxylate aminotransferase (AGXT) gene, exons 1 and 2
2463	7944	12783	0.6	8.00E-06	AW362539.1	EST_HUMAN	RC3-CT0283-201199-011-h11 CT0283 Homo sapiens cDNA
963	6108		0.6	7.00E-06	AA669729.1	EST_HUMAN	ab90f10.s1 Striatogene lung (#937210) Homo sapiens cDNA clone IMAGE:854251.3' similar to contains MER20.t1 MER20 repetitive element;
1420	6548	11723	1.2	7.00E-06	7662177	NT	Homo sapiens KIAA0555 gene product (KIAA0555). mRNA
2844	7895		6.7	7.00E-06	AI368252.1	EST_HUMAN	qp116g09.x1 NCI_CGAP_U13 Homo sapiens cDNA clone IMAGE:1991296.3' similar to contains Alu repetitive element;
3516	8657		0.9	7.00E-06	AA385542.1	EST_HUMAN	EST199205 Thyroid Homo sapiens cDNA 5' end similar to EST containing L1 repeat
2887	8038	13139	1.1	6.00E-06	BE069189.1	EST_HUMAN	QV3-BT0379-010300-105-d11 BT0379 Homo sapiens cDNA
3635	8774	13868	1.0	6.00E-06	BE069189.1	EST_HUMAN	QV3-BT0379-010300-105-d11 BT0379 Homo sapiens cDNA
4647	8062	13169	1.8	6.00E-06	Q01456	SWISSPROT	OVARIAN ABUNDANT MESSAGE PROTEIN (OAM PROTEIN)
4653	9765	14860	2.0	6.00E-06	AI040099.1	EST_HUMAN	ox08a02.x1 Soares fetal_liver_spleen_1NPLS_S1 Homo sapiens cDNA clone IMAGE:1665738.3' similar to contains MER8.t2 MER8 repetitive element;
631	5790	10912	1.5	4.00E-06	R16267.1	EST_HUMAN	ya48c03.t1 Soares infant brain_1NIB Homo sapiens cDNA clone IMAGE:53254.5' similar to contains Alu repetitive element;contains L1 repetitive element;
828	5977	11137	3.2	4.00E-06	AW103354.1	EST_HUMAN	xc68g12.x1 NCI_CGAP_Eso2 Homo sapiens cDNA clone IMAGE:2589574.3' similar to contains Alu repetitive element;contains L1 repetitive element;
1312	6440	11606	1.8	4.00E-06	AI334928.1	EST_HUMAN	tb33e08.x1 NCI_CGAP_HSC2 Homo sapiens cDNA clone IMAGE:2056168.3'
1312	6440	11607	1.8	4.00E-06	AI334928.1	EST_HUMAN	tb33e08.x1 NCI_CGAP_HSC2 Homo sapiens cDNA clone IMAGE:2056168.3'
1328	6456		2.4	4.00E-06	X87344.1	NT	H.sapiens DNA, DMB, HLA-Z1, IPP2, LMP2, TAP1, LMP7, TAP2, DOB, DOB2 and RING8, 9, 13 and 14 genes
2218	7326	12540	1.2	4.00E-06	AW015401.1	EST_HUMAN	U1-H-BI0-aat4-05-0-U1.s1 NCI_CGAP_Sub1 Homo sapiens cDNA clone IMAGE:2710425.3'
3025	8177	13278	1.4	4.00E-06	AF198349.1	NT	Gallus gallus Dact2 protein (Dact2) mRNA, complete cds
3500	8642		0.9	4.00E-06	H92947.1	EST_HUMAN	y9a4c11.s1 Soares pineal_gland_N3HPG Homo sapiens cDNA clone IMAGE:231956.3' similar to contains LOR1 repetitive element;
3819	8956	14052	1.8	4.00E-06	AW848296.1	EST_HUMAN	IL3-CT0214-150200-074-B03 CT0214 Homo sapiens cDNA
4702	9814	14910	1.6	4.00E-06	AI886939.1	EST_HUMAN	wf94c10.x1 NCI_CGAP_Bmr2 Homo sapiens cDNA clone IMAGE:2432562.3' similar to contains element MER22 repetitive element;
4840	9947	15036	1.0	4.00E-06	AL163279.2	NT	Homo sapiens chromosome 21 segment HS21C078

Table 4

2117	7228	12436	1.3	3.00E-06	AA700562.1	EST_HUMAN	z134b08.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:432663 3' similar to contains L1.1 L1 repetitive element ;
2117	7228	12437	1.3	3.00E-06	AA700562.1	EST_HUMAN	z134b08.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:432663 3' similar to contains L1.1 L1 repetitive element ;
2891	8042	13142	1.0	3.00E-06	AA868218.1	EST_HUMAN	ak48g11.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1409252 3' similar to contains LTR1.13 LTR1 repetitive element ;
3228	8376		2.1	3.00E-06	AI857779.1	EST_HUMAN	w122a05.x1 NCI CGAP_U1 Homo sapiens cDNA clone IMAGE:2425616 3' similar to TR:060734 060734 LINE-1 LIKE PROTEIN ;contains L1.12 L1 repetitive element ;
3716	8853	13944	1.3	3.00E-06	BE047094.1	EST_HUMAN	hg64d12.x1 NCI CGAP_HN13 Homo sapiens cDNA clone IMAGE:3124151 3'
3716	8853	13945	1.3	3.00E-06	BE047094.1	EST_HUMAN	hg64d12.x1 NCI CGAP_HN13 Homo sapiens cDNA clone IMAGE:3124151 3'
4376	9498	14585	0.9	3.00E-06	TS0286.1	EST_HUMAN	yb7b10.l1 Stralagene ovary (#937217) Homo sapiens cDNA clone IMAGE:77275 5' similar to contains L1 repetitive element
4461	9581	14678	4.3	3.00E-06	X54816.1	NT	Homo sapiens gene for alpha-1-microglobulin-bikunin, exons 1-5 (encoding alpha-1- microglobulin, N-terminus.)
195	5389		1.1	2.00E-06	PS4366	SWISSPROT	HOMEBOX PROTEIN GOOSECOID POL POLYPEPTIDE [CONTAINS: PROTEASE : REVERSE TRANSCRIPTASE ; ENDONUCLEASE]
1550	6877		2.3	2.00E-06	P21414	SWISSPROT	w04a03.x1 NCI CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2297068 3' similar to contains MER30.b1 MER30 repetitive element ;
2326	7429	12638	1.1	2.00E-06	AI672138.1	EST_HUMAN	HISTIDINE-RICH GLYCOPROTEIN PRECURSOR
2418	7517	12724	0.8	2.00E-06	P04929	SWISSPROT	KNOB-ASSOCIATED HISTIDINE-RICH PROTEIN PRECURSOR (KAHRP)
2519	7615	12817	2.7	2.00E-06	P06719	SWISSPROT	zp20e05.r1 Stralagene ovarian cancer (#937219) Homo sapiens cDNA clone IMAGE:555232 5'
3700	8839	13930	1.5	2.00E-06	AA173518.1	EST_HUMAN	Mus musculus gene for odorant receptor A16, complete cds
3710	8848	13938	1.5	2.00E-06	AB030896.1	NT	ORGANIC CATION/CARNITINE TRANSPORTER 2 (SOLUTE CARRIER FAMILY 22, MEMBER 5) (HIGH-AFFINITY SODIUM-DEPENDENT CARNITINE COTRANSPORTER)
31	5240	10345	0.7	1.00E-06	O76082	SWISSPROT	Mus musculus DbpA5E protein (DbpA5E) mRNA, complete cds
641	5800	10926	0.6	1.00E-06	AF084384.1	NT	qg2b09.x1 NCI CGAP_Kid3 Homo sapiens cDNA clone IMAGE:1762361 3' similar to TR:Q13538 Q13538 ORF2, FUNCTION UNKNOWN. ;
1041	6181		1.0	1.00E-06	AI206097.1	EST_HUMAN	MEMOZOITE SURFACE PROTEIN CMZ-8
1435	6562	11736	0.8	1.00E-06	P09125	SWISSPROT	z106a12.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:429982 3' similar to contains Alu repetitive element ;
1507	6634	11803	1.1	1.00E-06	AL163278.2	NT	z106a12.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:429982 3' similar to contains Alu repetitive element ;
1554	6681	11849	0.9	1.00E-06	AA034141.1	EST_HUMAN	z106a12.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:429982 3' similar to contains Alu repetitive element ;
1554	6681	11850	0.9	1.00E-06	AA034141.1	EST_HUMAN	z106a12.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:429982 3' similar to contains Alu repetitive element ;
1565	6692		1.2	1.00E-06	P27625	SWISSPROT	DNA-DIRECTED RNA POLYMERASE III LARGEST SUBUNIT
1949	7066	12261	1.7	1.00E-06	AF184614.1	NT	Homo sapiens p47-phox (NCF1) gene, complete cds
1949	7066	12262	1.7	1.00E-06	AF184614.1	NT	Homo sapiens p47-phox (NCF1) gene, complete cds
4273	9398	14481	11.1	1.00E-06	U07561.1	NT	Human ABL gene, exon 1b and intron 1b, and putative M8604 Met protein (M8604 Met) gene, complete cds
5043	10143	15220	1.4	1.00E-06	AL163285.2	NT	Homo sapiens chromosome 21 segment HS21C085

Table 4

5043	10143	15221	1.4	1.0E-08	AL163285.2	NT	Homo sapiens chromosome 21 segment HS21C085
357	5536	10666	0.5	9.0E-07	AF003529.1	NT	Homo sapiens glycican 3 (GPC3) gene, partial cds and flanking repeat regions
357	5536	10667	0.5	9.0E-07	AF003529.1	NT	Homo sapiens glycican 3 (GPC3) gene, partial cds and flanking repeat regions
1034	6174		0.9	8.0E-07	BE047871.1	EST_HUMAN	z43306.y1 NCJ CGAP Bms2 Homo sapiens cDNA clone IMAGE:2291339 5'
3498	8640		1.4	8.0E-07	BE047871.1	EST_HUMAN	z43306.y1 NCJ CGAP Bms2 Homo sapiens cDNA clone IMAGE:2291339 5'
4661	9773	14868	4.5	8.0E-07	AZ288596.1	EST_HUMAN	qB2d07.x1 Soares NhlHNPu S1 Homo sapiens cDNA clone IMAGE:1878876 3'
4661	9773	14869	4.5	8.0E-07	AZ288596.1	EST_HUMAN	qB2d07.x1 Soares NhlHNPu S1 Homo sapiens cDNA clone IMAGE:1878876 3'
1822	6941	12131	0.9	7.0E-07	AF167341.1	NT	Homo sapiens membrane interleukin 1 receptor accessory protein (IL-1RAP) gene, exons 10 and 11
1870	6988	12173	0.9	6.0E-07	AW855558.1	EST_HUMAN	CN3-CT0277-221089-024-e11 CT0277 Homo sapiens cDNA
2442	7541	12749	0.9	6.0E-07	AF019413.1	NT	Homo sapiens HLA class III region containing tenascin X (tenascin-X) gene, partial cds; cytochrome P450 21-hydroxylase (CYP21B), complement component C4 (C4B) G11, heilicase (SKIZW), RD, complement factor B (Bf), and complement component C2 (C2) genes>
3891	9027		1.7	6.0E-07	P41479	SWISSPROT	HYPOTHETICAL 24.1 KD PROTEIN IN LEEF-P33 INTERGENIC REGION
323	5506		1.2	5.0E-07	AIG31893.1	EST_HUMAN	wB64TO.x1 NCJ CGAP Kid11 Homo sapiens cDNA clone IMAGE:2385547 3'
2995	8147		0.9	5.0E-07	AIG31893.1	EST_HUMAN	wB64TO.x1 NCJ CGAP Kid11 Homo sapiens cDNA clone IMAGE:2385547 3'
4547	9868	14755	1.4	5.0E-07	AF149774.1	NT	Homo sapiens NOD1 protein (NOD1) gene, exons 4 through 14 and complete cds
3818	9052	14140	2.0	4.0E-07	AWO09602.1	EST_HUMAN	wB84H05.x1 NCJ CGAP Co3 Homo sapiens cDNA clone IMAGE:2504897 3'
434	5601	10732	1.7	3.0E-07	U19719.1	NT	Human microtubule-associated glycoprotein (MfAP2) gene, putative promoter region and alternatively spliced untranslated exons
568	5729	10846	0.8	3.0E-07	AJ271735.1	NT	Homo sapiens Xq pseudautosomal region, segment 1/2
1352	6480	11646	0.8	3.0E-07	M99149.1	NT	Human polymorphic microsatellite DNA
1608	6735		0.8	3.0E-07	M64857.1	NT	Human Igk subgroup I germline gene, exons 1 and 2, V-region 018 allele nlsb08.s1 NCJ CGAP_Ov2 Homo sapiens cDNA clone IMAGE:980825 similar to contains Alu repetitive element;contains L1.13 L1 repetitive element ;
2000	7115		1.0	3.0E-07	AA526763.1	EST_HUMAN	Human polymorphic microsatellite DNA
2242	7348	12558	1.2	3.0E-07	M99149.1	NT	MR0-BN0115-020300-001-f11 BN0115 Homo sapiens cDNA
2420	7519	12726	6.2	3.0E-07	BE05077.1	EST_HUMAN	MR0-BN0115-020300-001-f11 BN0115 Homo sapiens cDNA
2420	7519	12727	6.2	3.0E-07	BE05077.1	EST_HUMAN	MR0-BN0115-020300-001-f11 BN0115 Homo sapiens cDNA
2998	8150	13250	0.9	3.0E-07	T84704.1	EST_HUMAN	yds012.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:111695 5'
3122	8271	13376	1.8	3.0E-07	P38739	SWISSPROT	HYPOTHETICAL 63.8 KD PROTEIN IN GLUT-1-RIM1 INTERGENIC REGION PRECURSOR
4195	9321	14406	2.4	3.0E-07	AF044206.1	NT	Homo sapiens cyclooxygenase (COX-2) gene, promoter and exon 1
4195	9321	14407	2.4	3.0E-07	AF044206.1	NT	Homo sapiens cyclooxygenase (COX-2) gene, promoter and exon 1
4364	9486	14576	0.9	3.0E-07	Q10384	SWISSPROT	PUTATIVE SERINE/THREONINE-PROTEIN KINASE C22E12.14C
4654	9766	14861	0.9	3.0E-07	A1797236.1	EST_HUMAN	wB8db12.x1 Soares NFL T GBC S1 Homo sapiens cDNA clone IMAGE:2247967 3'
4996	10099	15166	1.5	3.0E-07	T57850.1	EST_HUMAN	yc14h09.a1 Stratagene lung (#337210) Homo sapiens cDNA clone IMAGE:80705 3' similar to yc14h09.a1 Stratagene lung (#337210) Homo sapiens cDNA clone IMAGE:80705 3' similar to similar to gb-M62982 ARACHIDONATE 12-LIPOXYGENASE (HUMAN)
4996	10099	15167	1.5	3.0E-07	T57850.1	EST_HUMAN	yc14h09.a1 Stratagene lung (#337210) Homo sapiens cDNA clone IMAGE:80705 3' similar to similar to gb-M62982 ARACHIDONATE 12-LIPOXYGENASE (HUMAN)
26	5235	10339	0.9	2.0E-07	AF262988.1	NT	Homo sapiens TRF2-interacting telomeric RAP1 protein (RAP1) mRNA, complete cds

Table 4

148	5344	10472	1.6	2.00E-07	L77569.1	NT	Homo sapiens DLGeorge syndrome critical region, telomeric end
148	5344	10473	1.6	2.00E-07	L77569.1	NT	Homo sapiens DLGeorge syndrome critical region, telomeric end
175	5368	10494	40.0	2.00E-07	U38949.1	NT	Fugu ruhmpes beta-cytoplasmic(vascular) actin gene, complete cds
731	5885	11027	0.6	2.00E-07	AF003530.1	NT	Homo sapiens homeobox protein CDX4 (CDX4) gene, complete cds and flanking repeat regions
731	5885	11028	0.6	2.00E-07	AF003530.1	NT	Homo sapiens homeobox protein CDX4 (CDX4) gene, complete cds and flanking repeat regions
928	6075	11233	1.1	2.00E-07	AA223260.1	EST_HUMAN	zr08b07.s1 Stratagene NT2 neuronal precursor 937230 Homo sapiens cDNA clone IMAGE:560869 3' similar to gb:L31860 GLYCOPHORIN A PRECURSOR (HUMAN);contains Alu repetitive element;
929	6076	11234	1.2	2.00E-07	T63042.1	EST_HUMAN	yc15g04.s1 Stratagene lung (#337210) Homo sapiens cDNA clone IMAGE:80790 3' similar to contains L1 repetitive element :
1147	6282	11435	1.3	2.00E-07	Q26768	SWISSPROT	I/6 AUTOANTIGEN
1582	6708	11879	0.7	2.00E-07	Q09701	SWISSPROT	HYPOTHETICAL 72.5 KD PROTEIN C2F7.10 IN CHROMOSOME 1
3633	8772	13866	14.7	2.00E-07	AF125348.1	NT	Homo sapiens caveolin 1 (CAV1) gene, exon 3 and partial cds
5078	10176	15255	1.0	2.00E-07	AW070995.1	EST_HUMAN	xa05h07.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2567485 3' similar to WP-C38H2.1 CE00923 PROBABLE RABGAP DOMAINS :
5078	10176	15256	1.0	2.00E-07	AW070995.1	EST_HUMAN	xa05h07.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2567485 3' similar to WP-C38H2.1 CE00923 PROBABLE RABGAP DOMAINS :
5198	10289	15358	1.0	2.00E-07	AL163301.2	NT	Homo sapiens chromosome 21 segment HS21C101
1086	6224	12642	1.2	1.00E-07	AL163282.2	NT	Homo sapiens chromosome 21 segment HS21C082
2331	7434	12642	0.9	1.00E-07	P10263	SWISSPROT	RETROVIRUS-RELATED GAG POLYPROTEIN (VERSION 1)
2403	7502	12709	0.9	1.00E-07	7549818	NT	Homo sapiens RAB, member of RAS oncogene family-like 2A (RABL2A), transcript variant 2, mRNA
2797	6632	11801	0.6	1.00E-07	P09256	SWISSPROT	GLYCOPROTEIN GPV
3684	6224		1.3	1.00E-07	AL163282.2	NT	Homo sapiens chromosome 21 segment HS21C082
591	7893		0.9	8.00E-08	AI911352.1	EST_HUMAN	wd16b05.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2328273 3'
73	5278	10406	1.1	7.00E-08	Q02357	SWISSPROT	ANKYRIN 1 (ERYTHROCYTE ANKYRIN)
1338	6466	11634	4.6	7.00E-08	X04809.1	NT	Rat mRNA for ribosomal protein L31
3528	8669	13772	1.1	7.00E-08	P15305	SWISSPROT	DYNEIN HEAVY CHAIN (DYHC)
3528	8669	13773	1.1	7.00E-08	P15305	SWISSPROT	DYNEIN HEAVY CHAIN (DYHC)
800	5951	11101	1.0	6.00E-08	AL163248.2	NT	Homo sapiens chromosome 21 segment HS21C048
800	5951	11102	1.0	6.00E-08	AL163248.2	NT	Homo sapiens chromosome 21 segment HS21C048
2312	7415	12624	0.6	6.00E-08	BE144398.1	EST_HUMAN	MR0-HT0166-191199-004-g09 HT0166 Homo sapiens cDNA
4155	9281	14361	1.0	6.00E-08	AL163248.2	NT	Homo sapiens chromosome 21 segment HS21C048
79	5285	10412	1.0	5.00E-08	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103
2189	7298	12513	0.7	5.00E-08	AA493851.1	EST_HUMAN	m03b09.s1 NCI_CGAP_Thy1 Homo sapiens cDNA clone IMAGE:943193 similar to contains Alu repetitive element;
5178	10270	15341	1.1	5.00E-08	Q06278	SWISSPROT	ALDEHYDE OXIDASE
1724	8847	12025	1.1	4.00E-08	P25723	SWISSPROT	DORSAL-VENTRAL PATTERNING TOLL-PROTEIN PRECURSOR
1724	8847	12026	1.1	4.00E-08	P25723	SWISSPROT	DORSAL-VENTRAL PATTERNING TOLL-PROTEIN PRECURSOR

Table 4

5184	10276	15344	7.2	3.00E-08	AA191195.1	EST_HUMAN	zq45d05.r1 Strata gene hNT neuron (#937233) Homo sapiens cDNA clone IMAGE:632649 5'
5184	10276	15345	7.2	3.00E-08	AA191195.1	EST_HUMAN	zq45d05.r1 Strata gene hNT neuron (#937233) Homo sapiens cDNA clone IMAGE:632649 5'
199	5393		5.4	2.00E-08	AW302996.1	EST_HUMAN	xr87f06.x1 NCI CGAP L126 Homo sapiens cDNA clone IMAGE:2767139 3'
							zw48f07.r1 Scores total fetus Nb2Hf8 9w Homo sapiens cDNA clone IMAGE:773317 5'
							similar to contains Alu repetitive element; contains element MER15 repetitive element ;
223	5416		2.7	2.00E-08	AA425598.1	EST_HUMAN	Gallus gallus Dact2 protein (Dact2) mRNA, complete cds
488	5653	10777	0.5	2.00E-08	AF198349.1	NT	MR6-OT0080-240200-001-g08 OT0080 Homo sapiens cDNA
644	5603	10928	3.7	2.00E-08	AW886438.1	EST_HUMAN	MR6-OT0080-240200-001-g08 OT0080 Homo sapiens cDNA
644	5603	10929	3.7	2.00E-08	AW886438.1	EST_HUMAN	MR6-OT0080-240200-001-g08 OT0080 Homo sapiens cDNA
974	6120		13.0	2.00E-08	BE280477.1	EST_HUMAN	601155321F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3138893 5'
1319	6448	11614	0.7	2.00E-08	AL163247.2	NT	Homo sapiens chromosome 21 segment HS21C047
1363	6491	11656	0.9	2.00E-08	4505538	NT	Homo sapiens oxytocin receptor (OXTR) mRNA
1811	6930		1.4	2.00E-08	AW270271.1	EST_HUMAN	XP4311.X1 NCI CGAP HN11 Homo sapiens cDNA clone IMAGE:2743149 3'
							ww03c08.x1 NCI CGAP Kd3 Homo sapiens cDNA clone IMAGE:2528462 3' similar to
							contains L1 L2 L1 repetitive element ;
2368	7470	12672	0.5	2.00E-08	AW024364.1	EST_HUMAN	Sheep His-IRNA-GUG
2496	7563		0.8	2.00E-08	K00216.1	NT	WNT-14 PROTEIN PRECURSOR
3171	8320	13433	6.0	2.00E-08	CA2280	SWISSPROT	WNT-14 PROTEIN PRECURSOR
3171	8320	13434	6.0	2.00E-08	CA2280	SWISSPROT	WNT-14 PROTEIN PRECURSOR
3783	8920		1.7	2.00E-08	AW813620.1	EST_HUMAN	RC3-ST0197-161099-012-503 ST0197 Homo sapiens cDNA
3858	8994	14093	3.7	2.00E-08	P48960	SWISSPROT	LEUCOCYTE ANTIGEN CD97 PRECURSOR
3868	9118	14201	0.8	2.00E-08	U82668.1	NT	Homo sapiens shox gene, alternatively spliced products, complete cds
							aa26d07.r1 NCI CGAP GC81 Homo sapiens cDNA clone IMAGE:814380 5' similar to
							contains L1 L2 L1 repetitive element ;
4305	9429		3.4	2.00E-08	AA459040.1	EST_HUMAN	he17h08.x2 NCI CGAP CML1 Homo sapiens cDNA clone IMAGE:2919327 3' similar to
							contains Alu repetitive element;
4876	9983		2.9	2.00E-08	AW572981.1	EST_HUMAN	POL POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE ; ENDONUCLEASE]
1493	7918	11789	1.1	1.00E-08	P31792	SWISSPROT	POL POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE ; ENDONUCLEASE]
2005	7119		1.1	1.00E-08	BE141959.1	EST_HUMAN	PM2-HT0130-150899-001-412 HT0130 Homo sapiens cDNA
2504	7601	12789	1.3	1.00E-08	P33999	SWISSPROT	HYPOTHETICAL 25.3 KD PROTEIN IN RIM-PRFC INTERGENIC REGION
							TCBAP1D5232 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC
							project=CBA Homo sapiens cDNA clone TCBAP5232
3155	8304	13413	1.2	1.00E-08	BE246844.1	EST_HUMAN	TCBAP1D5232 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC
							project=CBA Homo sapiens cDNA clone TCBAP5232
3155	8304	13414	1.2	1.00E-08	BE246844.1	EST_HUMAN	TCBAP1D5232 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC
5191	10282	15350	1.4	1.00E-08	AL163280.2	NT	project=CBA Homo sapiens cDNA clone TCBAP5232
4149	9275	14355	3.0	9.00E-09	AL163279.2	NT	Homo sapiens chromosome 21 segment HS21C079
4149	9275	14356	3.0	9.00E-09	AL163279.2	NT	Homo sapiens chromosome 21 segment HS21C079
3444	8586		1.1	8.00E-09	BE012076.1	EST_HUMAN	RC3-BN1058-270400-031-C06 BN1058 Homo sapiens cDNA
							Homo sapiens DNA for 3-ketolacyl-CoA thiolase beta-subunit of mitochondrial trifunctional
3555	8694		1.7	7.00E-09	D86842.1	NT	protein, exon 2, 3
4175	9301	14382	2.6	7.00E-09	U8918.1	NT	Macaca mulatta homeobox protein putative pseudogene

Table 4

4556	9676	14768	1.0	7.00E-09	D00849.1	NT	Homo sapiens gene for enteric smooth muscle gamma-actin, exon 2, 3
2107	7218		1.1	6.00E-09	AL040439.1	EST_HUMAN	DKFZp434C0514_r1 434 (synonym: hess3) Homo sapiens cDNA clone DKFZp434C0514 5'
3941	9074	14157	1.1	6.00E-09	AA557940.1	EST_HUMAN	nt17a11.s1 NCL_CGAP_HSC1 Homo sapiens cDNA clone IMAGE:1040924 similar to contains L1.12 L1 repetitive element ;
4906	10013	15094	4.4	6.00E-09	BE169421.1	EST_HUMAN	PIM-1 HT0527-160200-001-h05 HT0527 Homo sapiens cDNA
1394	6521	11689	1.1	5.00E-09	BE149264.1	EST_HUMAN	RC2-HT0252-120200-014-h10 HT0252 Homo sapiens cDNA
510	5674		0.6	4.00E-09	AL163282.2	NT	Homo sapiens chromosome 21 segment HS21C082
949	6095		0.8	4.00E-09	AL163285.2	NT	Homo sapiens chromosome 21 segment HS21C085
2379	7481	12683	2.3	4.00E-09	AA350878.1	EST_HUMAN	EST58385 Infant brain Homo sapiens cDNA 5' end similar to similar to heat shock protein, 90 kDa
2303	7406	12614	1.4	3.00E-09	BE222239.1	EST_HUMAN	hu06e09.x1 NCL_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3166120 3' similar to contains MER18.13 MER18 repetitive element ;
2506	7602	12802	1.3	3.00E-09	BE222239.1	EST_HUMAN	hu06e09.x1 NCL_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3166120 3' similar to contains MER18.13 MER18 repetitive element ;
2614	7704	12903	1.1	3.00E-09	P23249	SWISSPROT	PROTEIN MCV-10
3287	8432	13540	1.1	3.00E-09	BE222239.1	EST_HUMAN	hu06e09.x1 NCL_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3166120 3' similar to contains MER18.13 MER18 repetitive element ;
4329	9452	14540	3.2	3.00E-09	AF173325.1	NT	Homo sapiens eukaryotic initiation factor 4A1 (EIF4A1) gene, partial cds
4411	9531	14620	1.5	3.00E-09	Q9Y3R5	SWISSPROT	258.1 KDA PROTEIN C21ORF5 (KIAA0933)
795	5946		0.9	2.00E-09	X16674.1	NT	H. sapiens PADPRP-1 gene for NAD(+) ADP-ribosyltransferase
1237	6366	11527	1.8	2.00E-09	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
1637	6763		3.8	2.00E-09	AL118573.1	EST_HUMAN	DKFZp761B1710_r1 761 (synonym: hamy2) Homo sapiens cDNA clone DKFZp761B1710 5'
2278	7384	12591	0.8	2.00E-09	Q9Y3R5	SWISSPROT	258.1 KDA PROTEIN C21ORF5 (KIAA0933)
1093	6231	11382	0.9	1.00E-09	5031624	NT	Homo sapiens CCAAT-box-binding transcription factor (CBF2) mRNA
1093	6231	11383	0.9	1.00E-09	5031624	NT	Homo sapiens CCAAT-box-binding transcription factor (CBF2) mRNA
1616	6742		1.0	1.00E-09	AJ229041.1	NT	Homo sapiens 959 kb contig between AML1 and CBR1 on chromosome 21q22; segment 1/3
2453	7552		0.9	1.00E-09	AI356086.1	EST_HUMAN	qy64e11.x1 NCL_CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2016812 3' similar to contains MER12.12 MER12 repetitive element ;
2860	8011	13112	1.5	1.00E-09	U80017.1	NT	Homo sapiens basic transcription factor 2 p44 (btf2p44) gene, partial cds, neuronal apoptosis inhibitory protein (naip) and survival motor neuron protein (smn) genes, complete cds
2895	8046	13146	3.3	1.00E-09	M28699.1	NT	Homo sapiens nuclear phosphoprotein B23 (NPM1) mRNA, complete cds
2895	8046	13147	3.3	1.00E-09	M28699.1	NT	Homo sapiens nuclear phosphoprotein B23 (NPM1) mRNA, complete cds
2949	8100	13206	1.2	1.00E-09	P11799	SWISSPROT	MYOSIN LIGHT CHAIN KINASE, SMOOTH MUSCLE AND NON-MUSCLE ISOZYMES (MLCK) (CONTAINS: TELOKIN)
4692	9804		4.3	1.00E-09	AA719297.1	EST_HUMAN	zh35b03.s1 Soares, pituitary gland, N3H-PG Homo sapiens cDNA clone IMAGE:414029 3' similar to contains Alu repetitive element; contains element MER22 repetitive element ;
1287	6417	11580	0.6	9.00E-10	AW867740.1	EST_HUMAN	MRO-SN0040-050500-002-c07 SN0040 Homo sapiens cDNA

Table 4

2803	7955	13064	6.0	9.00E-10	AL870071.1	EST_HUMAN	w678n03.x1 Soares_Dieckgrafe_colon_NHCD Homo sapiens cDNA clone IMAGE:2347253 3' similar to SW/R129_HUMAN P47914 60S RIBOSOMAL PROTEIN L29 ;contains element PTR5 repetitive element ;
141	5337	10467	3.2	8.00E-10	U83630.2	NT	Homo sapiens MCMA (MCM4) and DNA-PKcs (PRKDC) genes, partial cds
3300	8446	13554	0.9	8.00E-10	BE080748.1	EST_HUMAN	QV1-BT0631-150200-071-01 BT0631 Homo sapiens cDNA
4106	9232	14314	2.8	8.00E-10	AA376832.1	EST_HUMAN	EST89564 Small Intestine I Homo sapiens cDNA 5' end
666	5841	10976	4.2	7.00E-10	7706225	NT	Homo sapiens TPA inducible protein (LOC51586), mRNA
666	5841	10977	4.2	7.00E-10	7706225	NT	Homo sapiens TPA inducible protein (LOC51586), mRNA
1605	6732	11903	0.7	7.00E-10	Q13342	SWISSPROT	LYSP100 PROTEIN (LYMPHOID-RESTRICTED HOMOLOG OF SP100)
1974	7089		1.0	7.00E-10	P08548	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
2512	7608		6.1	7.00E-10	P08547	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
3049	8200	13300	2.7	7.00E-10	X00856.1	NT	H.sapiens DHFR gene, exon 3
895	6043	11198	1.0	6.00E-10	AL400877.1	NT	Homo sapiens ASC13 gene, CEGP1 gene, C11orf14 gene, C11orf15 gene, C11orf16 gene and C11orf17 gene
2644	7733	12934	0.5	6.00E-10	AL424405.1	EST_HUMAN	h02d07.x1 NC1_CGAP_P128 Homo sapiens cDNA clone IMAGE:2095021 3'
4634	9748		2.5	6.00E-10	AW853719.1	EST_HUMAN	RC3-CT0254-031099-012-g12 CT0254 Homo sapiens cDNA
744	5897		1.5	5.00E-10	AL046804.1	EST_HUMAN	DKFZp434N219_r1 434 (synonym: hies3) Homo sapiens cDNA clone DKFZp434N219 5'
3430	8572	13664	1.5	5.00E-10	Q01033	SWISSPROT	HYPOTHETICAL GENE 48 PROTEIN
106	5309		3.0	4.00E-10	AI221083.1	EST_HUMAN	q9b9109.x1 Soares_placenta_8103weeks_2NbhP8109W Homo sapiens cDNA clone IMAGE:1759049 3' similar to contains LTR8.b2 LTR8 repetitive element ;
1951	7068	12264	1.4	4.00E-10	AW594709.1	EST_HUMAN	hgs5g03.x1 NC1_CGAP_G06 Homo sapiens cDNA clone IMAGE:2949844 3' similar to contains Alu repetitive element ;
2527	7623	12824	2.2	4.00E-10	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103
3244	8391	13498	1.1	4.00E-10	H01109.1	EST_HUMAN	y12b12.s1 Soares_placenta_Nb2HP Homo sapiens cDNA clone IMAGE:149927 3' similar to contains THR repetitive element ;
897	6044	11200	0.6	3.00E-10	N36113.1	EST_HUMAN	y23f06.s1 Soares_melanocyte_2NbhW Homo sapiens cDNA clone IMAGE:272963 3' similar to contains L1.1f1 L1 repetitive element ;
4435	9556	14649	1.1	3.00E-10	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
4435	9556	14650	1.1	3.00E-10	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
32	5241	10346	1.4	2.00E-10	P48988	SWISSPROT	MAJOR CENTROMERE AUTOANTIGEN B (CENTROMERE PROTEIN B) (CENP-B)
32	5241	10347	1.4	2.00E-10	P48988	SWISSPROT	MAJOR CENTROMERE AUTOANTIGEN B (CENTROMERE PROTEIN B) (CENP-B)
1955	6973		2.1	2.00E-10	U80017.1	NT	Homo sapiens basic transcription factor 2 p44 (btf2p44) gene, partial cds, neuronal apoptosis inhibitory protein (naip) and survival motor neuron protein (smn) genes, complete cds
1492	6619		1.3	1.00E-10	AW867767.1	EST_HUMAN	MRO-SN0038-290300-001-01 SN0038 Homo sapiens cDNA
2537	7633		0.9	1.00E-10	AW852001.1	EST_HUMAN	QVO-CT0225-191199-058-e08 CT0225 Homo sapiens cDNA
3456	8597	13710	0.9	1.00E-10	AW832912.1	EST_HUMAN	QV2-TT0003-161199-013-g10 TT0003 Homo sapiens cDNA
3770	8636		0.9	1.00E-10	AL041685.1	EST_HUMAN	DKFZp434N1317_r1 434 (synonym: hies3) Homo sapiens cDNA clone DKFZp434N1317 5'

Table 4

3933	9067		5.4	1.00E-10	AF213884.1	NT	Homo sapiens nuclear factor of kappa light polypeptide gene enhancer in B-cells 1 (NFKB1) gene, complete cds
4036	9164	14248	4.5	1.00E-10	U52111.2	NT	Homo sapiens X28 region near ALD locus containing dual specificity phosphatase 9 (DUSP9), ribosomal protein L18a (RPL18a), Ca2+/Calmodulin-dependent protein kinase I (CAMKI), creatine transporter (CRTTR), CDM protein (CDM), adrenoleukodystrophy protein >
4036	9164	14249	4.5	1.00E-10	U52111.2	NT	Homo sapiens X28 region near ALD locus containing dual specificity phosphatase 9 (DUSP9), ribosomal protein L18a (RPL18a), Ca2+/Calmodulin-dependent protein kinase I (CAMKI), creatine transporter (CRTTR), CDM protein (CDM), adrenoleukodystrophy protein >
4042	9170	14256	2.3	1.00E-10	AB031069.1	NT	Homo sapiens PCCX1 mRNA for protein containing CXXC domain 1, complete cds
4079	9206		2.1	1.00E-10	M30829.1	NT	Human pregnancy-specific glycoprotein beta-1 (SP1) mRNA, last exon
5145	10240		0.9	1.00E-10	X87344.1	NT	H.sapiens DMA, DMB, HLA-Z1, IPP2, LMP2, TAP1, LMP7, TAP2, DOB, DOB2 and RING8, 9, 13 and 14 genes
261	5448	10574	1.2	9.00E-11	BE145600.1	EST_HUMAN	IL2-HT0203-291099-016-c08 HT0203 Homo sapiens cDNA
2057	7169	12375	2.0	9.00E-11	AL134395.1	EST_HUMAN	DKFZp547D225_r1 547 (synonym: hbr1) Homo sapiens cDNA clone DKFZp547D225 5'
2057	7169	12376	2.0	9.00E-11	AL134395.1	EST_HUMAN	DKFZp547D225_r1 547 (synonym: hbr1) Homo sapiens cDNA clone DKFZp547D225 5'
3337	8481	13596	2.3	9.00E-11	AL134395.1	EST_HUMAN	DKFZp547D225_r1 547 (synonym: hbr1) Homo sapiens cDNA clone DKFZp547D225 5'
3337	8481	13597	2.3	9.00E-11	AL134395.1	EST_HUMAN	DKFZp547D225_r1 547 (synonym: hbr1) Homo sapiens cDNA clone DKFZp547D225 5'
4400	9521	14611	1.1	9.00E-11	AA775985.1	EST_HUMAN	ae78f01.s1 Striatogene schizo brain S11 Homo sapiens cDNA clone IMAGE:970297 3'
3078	8229		10.0	8.00E-11	H19971.1	EST_HUMAN	ym55f11.s1 Soares adult brain N25H85Y Homo sapiens cDNA clone IMAGE:172173 3'
3881	9017	14112	0.8	8.00E-11	AA78617.1	EST_HUMAN	im54c09.x1 NC1 CGAP Kid11 Homo sapiens cDNA clone IMAGE:2161936 3'
3957	9090	14173	4.0	8.00E-11	N23712.1	EST_HUMAN	ym46e06.s1 Weizmann Olfactory Epithelium Homo sapiens cDNA clone IMAGE:255298 3'
1431	6658	11734	0.8	7.00E-11	AA330842.1	EST_HUMAN	EST134392 Embryo, 8 week I Homo sapiens cDNA 5' end
406	5574	10712	1.8	6.00E-11	M55270.1	NT	Human matrix Gla protein (MGp) gene, complete cds
406	5574	10713	1.8	6.00E-11	M55270.1	NT	Human matrix Gla protein (MGp) gene, complete cds
11	5219	10320	0.9	5.00E-11	AL163283.2	NT	Homo sapiens chromosome 21 segment HS21C083
3320	5219	10320	1.5	5.00E-11	AL163283.2	NT	Homo sapiens chromosome 21 segment HS21C083
4135	6261	14343	1.5	5.00E-11	P48034	SWISSPROT	ALDEHYDE OXIDASE
1380	6507		1.4	4.00E-11	AA436042.1	EST_HUMAN	ZU01B12.1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:730559 5'
4518	9637	14728	1.4	4.00E-11	DA4666.1	EST_HUMAN	HUMSLJPY069 Human brain cDNA Homo sapiens cDNA clone 069
1476	6603	11777	0.8	3.00E-11	6679077	NT	Mus musculus expressed in non-metastatic cells 2, protein (NM23B) (Nme2), mRNA
4179	9305		1.5	3.00E-11	AA309248.1	EST_HUMAN	EST180120 Liver, hepatocellular carcinoma Homo sapiens cDNA 5' end
944	6091	11248	0.5	2.00E-11	AI150502.1	EST_HUMAN	q136c04.x1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:1752102 3' similar to contains MER10.13 MER10 repetitive element ;



Table 4

1166	6302	11458	1.2	2.00E-11	R24607.1	EST_HUMAN	yg43e12.1 Soares infant brain 11NB Homo sapiens cDNA clone IMAGE:35144.5'
1168	6302	11459	1.2	2.00E-11	R24607.1	EST_HUMAN	yg43e12.1 Soares infant brain 11NB Homo sapiens cDNA clone IMAGE:35144.5'
1596	6722	11891	1.4	2.00E-11	L17432.1	NT	Gallus gallus rho-globin, beta-H globin, beta-A globin, epsilon-globin, and olfactory receptor-like protein COR3beta (COR3beta) genes, complete cds
1596	6722	11892	1.4	2.00E-11	L17432.1	NT	Gallus gallus rho-globin, beta-H globin, beta-A globin, epsilon-globin, and olfactory receptor-like protein COR3beta (COR3beta) genes, complete cds
1600	6727	11897	1.0	2.00E-11	A112637.1	EST_HUMAN	gc51c10.x1 Soares_pregnant_uterus_NBHPU Homo sapiens cDNA clone IMAGE:1713138.3' similar to gb-l:02832 PEROXISOME PROLIFERATOR ACTIVATED RECEPTOR ALPHA (HUMAN); contains L1.11 L1 repetitive element;
2737	7621	13025	1.1	2.00E-11	AF087913.1	NT	Human endogenous retrovirus HERV-P-T47D
3160	8309	13421	4.2	2.00E-11	P10263	SWISSPROT	RETROVIRUS-RELATED GAG POLYPROTEIN (VERSION 1)
3284	8428	13537	0.9	2.00E-11	A478617.1	EST_HUMAN	tm54d09.x1 NCJ CGAP Kid11 Homo sapiens cDNA clone IMAGE:2161936.3'
3452	8593		1.0	2.00E-11	AF020503.1	NT	Homo sapiens FRA3B common fragile region, diadenosine triphosphate hydrolase (FHT)
4501	9821		1.0	2.00E-11	AL163227.2	NT	gene, exon 5
4851	9958		5.5	2.00E-11	BE062558.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C027
4861	10064	15136	1.3	2.00E-11	AA307331.1	EST_HUMAN	QV2-BT0258-261099-014-a01 BT0258 Homo sapiens cDNA
660	5816	10944	1.2	1.00E-11	AJ131016.1	NT	EST178228 Colon carcinoma (HCC) cell line Homo sapiens cDNA 5' end similar to alpha-2-macroglobulin
1199	6331	11486	0.9	1.00E-11	AL163279.2	NT	Homo sapiens SCL gene locus
1249	6378	11537	1.6	1.00E-11	AA489871.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C079
1483	6610		0.7	1.00E-11	AF115914.1	NT	Homo sapiens chromosome 21 segment HS21C079
1638	6957		1.2	1.00E-11	AB030947.1	NT	ab01b12.1 Stratigene fetal retina 937202 Homo sapiens cDNA clone IMAGE:839519.5' similar to contains OFR12 MER10 repetitive element;
2079	7191	12394	1.1	1.00E-11	AF000573.1	NT	Homo sapiens PRO3078 mRNA, complete cds
3454	8565	13706	1.3	1.00E-11	BE004315.1	EST_HUMAN	Rattus norvegicus mRNA for high-affinity choline transporter CHT1, complete cds
3788	8935	14028	27.7	1.00E-11	AB001523.1	NT	Homo sapiens homogenisate 1,2-dioxygenase gene, complete cds
3798	8935	14029	27.7	1.00E-11	AB001523.1	NT	CMO-BND105-170300-262-d12 BND105 Homo sapiens cDNA
2922	8073	13181	0.8	9.00E-12	P20742	SWISSPROT	Homo sapiens gene for TNEM1 and PWP2, complete and partial cds
4562	9680	14773	2.8	7.00E-12	Q05904	SWISSPROT	Homo sapiens gene for TNEM1 and PWP2, complete and partial cds
4252	9377	14457	7.9	6.00E-12	AA732516.1	EST_HUMAN	PREGNANCY ZONE PROTEIN PRECURSOR
1027	6167	11322	1.0	5.00E-12	T06573.1	EST_HUMAN	34 KD SPICULE MATRIX PROTEIN PRECURSOR (LSM34)
3344	8488	13602	1.2	5.00E-12	BE047779.1	EST_HUMAN	n28811.s1 NCJ CGAP GCB1 Homo sapiens cDNA clone IMAGE:1302573.3' similar to contains Alu repetitive element;
3666	8805	13899	5.9	5.00E-12	AJ271736.1	NT	EST104462 Fetal brain, Stragene (cat#936206) Homo sapiens cDNA clone HFBDV33
5171	10265		0.8	5.00E-12	AA720661.1	EST_HUMAN	IZ4D05.Y1 NCJ CGAP Bms52 Homo sapiens cDNA clone IMAGE:2291217.5'
244	5433	10559	1.2	4.00E-12	AA700326.1	EST_HUMAN	Homo sapiens Xq pseudocautosomal region, segment 2/2
245	5433	10559	1.2	4.00E-12	AA700326.1	EST_HUMAN	nm24b11.s1 NCJ CGAP GCB0 Homo sapiens cDNA clone IMAGE:1241373.3'
3126	8275	13380	2.2	4.00E-12	Q04791	SWISSPROT	zj74g11.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:460676
							zj74g11.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:460676
							zj74g11.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:460676
							FATTY ACYL-COA HYDROLASE PRECURSOR, MEDIUM CHAIN (THIOESTERASE B)

Table 4

3126	8275	13381	2.2	4.00E-12	Q04791	SWISSPROT	FATTY ACYL-CoA HYDROLASE PRECURSOR, MEDIUM CHAIN (THIOESTERASE B)
4520	9639	14730	0.9	4.00E-12	A669984.1	EST_HUMAN	h26n05.x1 NC1_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2270745 3' similar to TR:Q13539 Q13539 MARINER TRANSPOSASE. ;
420	5209	10310	1.3	3.00E-12	O42163	SWISSPROT	COCHLIN PRECURSOR (COCH-5B2)
600	5758	10877	1.3	3.00E-12	AW341683.1	EST_HUMAN	hd13d01.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:290377 3' similar to TR:O14517 O14517 SMRP. ;
600	5758	10877	1.3	3.00E-12	AW341683.1	EST_HUMAN	hd13d01.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:290377 3' similar to TR:O14517 O14517 SMRP. ;
600	5758	10878	1.3	3.00E-12	AW341683.1	EST_HUMAN	hd13d01.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:290377 3' similar to TR:O14517 O14517 SMRP. ;
2864	8015	13117	1.4	2.00E-12	AW341809.1	EST_HUMAN	ha02d05.x1 NC1_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2872521 3'
2864	8015	13118	1.4	2.00E-12	AW341809.1	EST_HUMAN	ha02d05.x1 NC1_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2872521 3'
3421	8563	13675	1.0	2.00E-12	6754495	NT	Mus musculus keratin-associated protein 6.2 (Ktap6-2), mRNA
4025	9153	14236	1.0	2.00E-12	J01884.1	NT	Rat U3A small nuclear RNA
4025	9153	14237	1.0	2.00E-12	J01884.1	NT	Rat U3A small nuclear RNA
4288	8015	13117	3.3	2.00E-12	AW341809.1	EST_HUMAN	ha02d05.x1 NC1_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2872521 3'
4288	8015	13118	3.3	2.00E-12	AW341809.1	EST_HUMAN	ha02d05.x1 NC1_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2872521 3'
4324	9447		1.8	2.00E-12	BE063509.1	EST_HUMAN	CMD-BT0281-031199-087-a03 BT0281 Homo sapiens cDNA
4804	9914	15005	0.8	2.00E-12	O70306	SWISSPROT	TBX15 PROTEIN (T-BOX PROTEIN 15)
4804	9914	15006	0.8	2.00E-12	O70306	SWISSPROT	TBX15 PROTEIN (T-BOX PROTEIN 15)
117	5317	10446	0.6	1.00E-12	AW627674.1	EST_HUMAN	hb9ba09.x1 NC1_CGAP_GU1 Homo sapiens cDNA clone IMAGE:2970040 3' similar to contains MER18.11 MER18 repetitive element ;
1944	7081		0.7	1.00E-12	AB71726.1	EST_HUMAN	wm51f07.x1 NC1_CGAP_U12 Homo sapiens cDNA clone IMAGE:2439493 3' similar to contains L1.b3 L1 repetitive element ;
3032	8184	13284	1.2	1.00E-12	AF000991.1	NT	Homo sapiens testis-specific Testis Transcript Y 2 (TTY2) mRNA, partial cds
3032	8184	13285	1.2	1.00E-12	AF000991.1	NT	Homo sapiens testis-specific Testis Transcript Y 2 (TTY2) mRNA, partial cds
3575	8714		1.1	9.00E-13	AJ271735.1	NT	Homo sapiens Xq pseudautosomal region, segment 1/2
3865	9001	14102	1.2	9.00E-13	AB029900.1	NT	Homo sapiens CST gene for carbocyste sulfoltransferase, exon 1, 2, 3, 4, 5
700	5855	10990	1.7	8.00E-13	U29185.1	NT	Homo sapiens prion protein (PrP) gene, complete cds
700	5855	10991	1.7	8.00E-13	U29185.1	NT	Homo sapiens prion protein (PrP) gene, complete cds
							Homo sapiens basic transcription factor 2, p44 (btf2p44) gene, partial cds, neuronal apoptosis inhibitory protein (naip) and survival motor neuron protein (smn) genes, complete cds
1796	6916	12102	1.4	8.00E-13	UB0017.1	NT	Homo sapiens chromosome 21 segment HS21C007
2054	7166	12372	6.7	6.00E-13	AL163207.2	NT	Homo sapiens chromosome 21 segment HS21C007
1815	6934	12123	1.8	5.00E-13	Q04899	SWISSPROT	SERINE/THREONINE-PROTEIN KINASE PCTAIRE-3
1815	6934	12124	1.8	5.00E-13	Q04899	SWISSPROT	SERINE/THREONINE-PROTEIN KINASE PCTAIRE-3
3280	8425		1.1	5.00E-13	R78338.1	EST_HUMAN	y02b04.11 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:145759 5'
3351	8495		1.5	5.00E-13	AA435773.1	EST_HUMAN	z77a12.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:728350 3' similar to contains Alu repetitive element;contains element MER22 repetitive element ;
1824	6943		1.1	4.00E-13	AW378614.1	EST_HUMAN	PM2-HT0224-221099-001-e11 HT0224 Homo sapiens cDNA
2411	7510		0.6	4.00E-13	AF003529.1	NT	Homo sapiens glypican 3 (GPC3) gene, partial cds and flanking repeat regions
173	5366		1.3	3.00E-13	AF003528.1	NT	Homo sapiens X-linked anhidrotic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions

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Table 4

602	5760	10860	1.3	5.00E-14	Q63120	SWISSPROT	CANALICULAR MULTISPECIFIC ORGANIC ANION TRANSPORTER 1 (MULTIDRUG RESISTANCE-ASSOCIATED PROTEIN 2) (CANALICULAR MULTIDRUG RESISTANCE PROTEIN)
4985	10088	15160	1.1	5.00E-14	AW073791.1	EST_HUMAN	xb03305.x1 NCI_CGAP_GU1 Homo sapiens cDNA clone IMAGE:2575185 3' similar to contains L1.2 L1 repetitive element ;
1107	7907		0.6	4.00E-14	P04928	SWISSPROT	S-ANTIGEN PROTEIN PRECURSOR
1835	6654	12140	2.4	4.00E-14	AL007973.1	NT	Homo sapiens LGMD2B gene
3693	8632		0.9	4.00E-14	AA046502.1	EST_HUMAN	zk67a06.t1 Soares_pregnant_uterus_NbhPU Homo sapiens cDNA clone IMAGE:487858 5'
4194	9320	14405	1.0	4.00E-14	N46328.1	EST_HUMAN	yy73c12.s1 Soares_multiple_sclerosis_2NBHMSF Homo sapiens cDNA clone IMAGE:279190 3' similar to contains L1.3 L1 repetitive element ;
934	6081	11237	0.7	3.00E-14	X95466.1	NT	R.norvegicus mRNA for CP62 protein
4841	9948	15037	0.8	3.00E-14	AW265354.1	EST_HUMAN	xp45t12.x1 NCI_CGAP_HN11 Homo sapiens cDNA clone IMAGE:2743343 3' similar to contains Alu repetitive element;contains element MER9 repetitive element ;
4844	9951	15039	1.1	3.00E-14	7656864	NT	Homo sapiens a disintegrin and metalloproteinase domain 29 (ADAM29).mRNA
5104	10200		1.2	3.00E-14	BE466372.1	EST_HUMAN	hx94t11.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3195501 3' similar to contains MER4.b2 MER4 repetitive element ;
5157	10252	15323	1.5	3.00E-14	P02894	SWISSPROT	CIRCUMSPOROZOITE PROTEIN PRECURSOR (CS)
384	5553	10686	1.4	2.00E-14	AJ271736.1	NT	Homo sapiens Xq pseudautosomal region: segment 2/2
384	5553	10687	1.4	2.00E-14	AJ271736.1	NT	Homo sapiens Xq pseudautosomal region: segment 2/2
675	7895	10960	2.2	2.00E-14	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103
2339	7441		1.4	2.00E-14	AW372888.1	EST_HUMAN	RCS-BT0377-091299-031-D12 BT0377 Homo sapiens cDNA
2416	7515		1.1	2.00E-14	7657529	NT	Homo sapiens thalidoid tumor deletion region protein 1 (RTDR1). mRNA
2479	7577	12778	1.2	2.00E-14	AL163209.2	NT	Homo sapiens chromosome 21 segment HS21C009
2640	7729		1.0	2.00E-14	P08548	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
1051	6190	11342	1.3	1.00E-14	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
1384	6511	11675	2.8	1.00E-14	AL163268.2	NT	Homo sapiens chromosome 21 segment HS21C068
1384	6511	11676	2.8	1.00E-14	AL163268.2	NT	Homo sapiens chromosome 21 segment HS21C068
1956	7073	12270	7.8	1.00E-14	LA4140.1	NT	Homo sapiens chromosome X region from filamin (FLN) gene to glucose-6-phosphate dehydrogenase (G6PD) gene, complete cds's
2137	7247	12453	2.2	1.00E-14	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103
2358	7460	12866	2.3	1.00E-14	AF001669.1	NT	Homo sapiens ribosomal protein L23A (RPL23A) gene, complete cds
2914	8065	13173	1.4	1.00E-14	P05227	SWISSPROT	HISTIDINE-RICH PROTEIN PRECURSOR (CLONE PFHRP-II)
3811	8648	14044	2.0	1.00E-14	AA662994.1	EST_HUMAN	ae99c12.s1 Stralagene schizo brain S11 Homo sapiens cDNA clone IMAGE:971350 3'
4374	9496	14563	1.7	1.00E-14	AW275852.1	EST_HUMAN	xc39h10.x1 NCI_CGAP_LU28 Homo sapiens cDNA clone IMAGE:2753059 3'
1558	6685	11852	1.0	9.00E-15	7427522	NT	Homo sapiens protein tyrosine phosphatase, receptor type, T (PTPRT). mRNA
1703	6626	12007	1.2	9.00E-15	AL163283.2	NT	Homo sapiens chromosome 21 segment HS21C083
1703	6626	12008	1.2	9.00E-15	AL163283.2	NT	Homo sapiens chromosome 21 segment HS21C083

Table 4

2126	7236	0.6	8.00E-15	AF196779.1	NT	Homo sapiens transcription factor (GHM enhancer 3, JM11 protein, JM4 protein, JM5 protein, T54 protein, JM10 protein, A4 differentiation-dependent protein, triple LIM domain protein 6, and synaptophysin genes, complete cds; and L-type calcium channel a-2)
2780	5637	1.0	8.00E-15	BE261482.1	EST_HUMAN	601148632F NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3164023 5'
978	6123	2.1	6.00E-15	AJ271736.1	NT	Homo sapiens Xq pseudautosomal region, segment 22
404	5572	2.0	5.00E-15	AL163208.2	NT	Homo sapiens chromosome 21 segment HS21C008
						Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, RoRet gene, and sodium phosphate transporter (NPT3) gene, complete cds
2733	7817	1.4	5.00E-15	U91328.1	NT	
						UI-H-BW0-4b-g-10-0-UI.s1 NCL_CGAP_Sub6 Homo sapiens cDNA clone IMAGE:2731219 3'
3423	8565	1.0	5.00E-15	AW296817.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C103
421	5210	0.9	4.00E-15	AL163303.2	NT	CHR220550 Chromosome 22 exon Homo sapiens cDNA clone C22_749 5'
2812	7702	3.0	4.00E-15	H55611.1	EST_HUMAN	DKFZp761C0810_1 761 (synonym: hamy2) Homo sapiens cDNA clone DKFZp761C0810 5'
4039	9167	0.8	4.00E-15	AL118596.1	EST_HUMAN	LY1142F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA clone LY1142 5'
4123	9249	5.9	3.00E-15	N89452.1	EST_HUMAN	similar to ANF(CARDIOLATIN)
4843	9950	1.4	3.00E-15	P82485	SWISSPROT	NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 5
4955	10060	0.9	3.00E-15	AA078097.1	EST_HUMAN	7P01F03 Chromosome 7 Placental cDNA Library Homo sapiens cDNA clone 7P01F03
4955	10060	0.9	3.00E-15	AA078097.1	EST_HUMAN	7P01F03 Chromosome 7 Placental cDNA Library Homo sapiens cDNA clone 7P01F03
						Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
250	5438	1.1	2.00E-15	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
364	5542	1.1	2.00E-15	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
364	5542	1.1	2.00E-15	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
384	5542	1.1	2.00E-15	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
1512	6639	1.1	2.00E-15	8923201	NT	Homo sapiens hypothetical protein FLJ20212 (FLJ20212), mRNA
3465	8606	1.0	2.00E-15	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
3465	8606	1.0	2.00E-15	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
4522	9841	2.1	2.00E-15	AI806335.1	EST_HUMAN	W0706.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2349923 3' similar to TR-061043 Q61043 NINEIN.1
5097	10194	1.3	2.00E-15	P13993	SWISSPROT	REPEATITIVE PROLINE-RICH CELL WALL PROTEIN 2 PRECURSOR
5097	10194	1.3	2.00E-15	P13993	SWISSPROT	REPEATITIVE PROLINE-RICH CELL WALL PROTEIN 2 PRECURSOR
						REPETITIVE PROLINE-RICH CELL WALL PROTEIN 2 PRECURSOR
						REPETITIVE PROLINE-RICH CELL WALL PROTEIN 2 PRECURSOR
						REPETITIVE PROLINE-RICH CELL WALL PROTEIN 2 PRECURSOR
2747	7831	0.7	1.00E-15	AI689984.1	EST_HUMAN	TRQ13539 Q13539 MARINER TRANSPOSASE.1
2979	8130	0.8	1.00E-15	BE043584.1	EST_HUMAN	hK0602.y1 NCL_CGAP_Ov34 Homo sapiens cDNA clone IMAGE:2999162 5'
3103	8253	1.0	1.00E-15	P08647	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
4262	9387	0.8	1.00E-15	BE182696.1	EST_HUMAN	RC3-HT0849-100500-022-505 HT0849 Homo sapiens cDNA

Table 4

5086	10184	15263	1.2	1.00E-15	AI984928.1	EST_HUMAN	hw86a04.x1 NCI CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2494580 3'
4404	9524	14614	1.0	9.00E-16	4603168	NT	Homo sapiens cut (Drosophila)-like 1 (CCAAT displacement protein) (CUTL1) mRNA
2094	7205		3.0	6.00E-16	AW972611.1	EST_HUMAN	EST1384702 MAGE resequences, MAGI. Homo sapiens cDNA
1477	6604	11778	1.1	5.00E-16	AJ251154.1	NT	Mus musculus olfactory receptor cluster, OR37A, OR37B, OR37C, OR37E genes and OR37D pseudogene
2647	7736	12936	0.7	5.00E-16	AA992176.1	EST_HUMAN	ol80c04.s1 Soares, total, fetus, Nb2HF8, 9w Homo sapiens cDNA clone IMAGE:1623078 3' similar to contains element L1 repetitive element:
2192	7301		1.3	4.00E-16	AB001523.1	NT	Homo sapiens gene for TMEI1 and PWP2, complete and partial cds
2328	7431	12639	1.3	4.00E-16	AW797168.1	EST_HUMAN	QV1-UM0036-200300-115-g02 UM0036 Homo sapiens cDNA
2328	7431	12640	1.3	4.00E-16	AW797168.1	EST_HUMAN	QV1-UM0036-200300-115-g02 UM0036 Homo sapiens cDNA
3411	8553	13661	3.9	4.00E-16	Q16653	SWISSPROT	MYELIN-OLIGODENDROCYTE GLYCOPROTEIN PRECURSOR
4050	9177	14260	3.6	4.00E-16	BE083875.1	EST_HUMAN	PMA-BT0650-010400-002-g09 BT0650 Homo sapiens cDNA
4050	9177	14261	3.6	4.00E-16	BE083875.1	EST_HUMAN	PMA-BT0650-010400-002-g09 BT0650 Homo sapiens cDNA
5092	10190	15269	1.0	4.00E-16	P08548	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
128	5324	10456	0.5	3.00E-16	AW022862.1	EST_HUMAN	dl45cd1.y1 Morton Fetal Cochlea Homo sapiens cDNA clone IMAGE:2486376 5'
128	5324	10457	0.5	3.00E-16	AW022862.1	EST_HUMAN	dl45cd1.y1 Morton Fetal Cochlea Homo sapiens cDNA clone IMAGE:2486376 5'
458	5624		1.5	3.00E-16	AL046445.1	EST_HUMAN	DKFZp434P037.t1 434 (synonym: hies3) Homo sapiens cDNA clone DKFZp434P037 5'
467	5632		0.6	3.00E-16	AF135446.1	NT	Homo sapiens TSX (TSX) pseudogene, exon 5
1436	6563	11739	0.7	3.00E-16	Q28983	SWISSPROT	ZONADHESIN PRECURSOR
2946	8097	13202	4.1	3.00E-16	P03200	SWISSPROT	ENVELOPE GLYCOPROTEIN GP340 (MEMBRANE ANTIGEN) (MA) (CONTAINS: GLYCOPROTEIN GP220)
3756	8894	13985	1.1	3.00E-16	BE52133.1	EST_HUMAN	601113712F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3354291 5'
3874	9010		8.2	3.00E-16	AF020503.1	NT	Homo sapiens FRA3B common fragile region, diadenosine triphosphate hydrolase (FHT) gene, exon 5
3875	9011		1.0	3.00E-16	U03887.1	NT	Human BXP20 gene
956	6102		1.2	2.00E-16	AL163279.2	NT	Homo sapiens chromosome 21 segment HS21C079
2337	7439		1.0	2.00E-16	AA621761.1	EST_HUMAN	atf6d04.s1 Soares, testis, NIH Homo sapiens cDNA clone IMAGE:1030855 3'
2657	7746		0.6	2.00E-16	U03081.1	NT	Human SSAV-related endogenous retroviral LTR-like element
4087	8213	14296	1.3	2.00E-16	X89211.1	NT	H.sapiens DNA for endogenous retroviral like element
178	5371	10495	0.9	1.00E-16	AF200719.1	NT	Homo sapiens pituitary tumor transforming gene protein (PTTG) gene, complete cds
377	5593		7.6	1.00E-16	AA628592.1	EST_HUMAN	atf39g11.s1 Soares, total, fetus, Nb2HF8, 9w Homo sapiens cDNA clone IMAGE:1034084 3' similar to contains ORF12 ORF repetitive element:
4345	9468	14556	1.2	1.00E-16	P10272	SWISSPROT	POL POLYPROTEIN (CONTAINS: PROTEASE ; REVERSE TRANSCRIPTASE ; ENDONUCLEASE)
3679	8818	13911	2.5	8.00E-17	AW900048.1	EST_HUMAN	CM1-NN1003-200300-153-g01 NN1003 Homo sapiens cDNA
1001	6141		0.6	8.00E-17	AW860701.1	EST_HUMAN	QV0-OT0032-080300-155-d01 OT0032 Homo sapiens cDNA
3817	8954		0.9	8.00E-17	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080
959	6104	11282	0.9	7.00E-17	Q91081	SWISSPROT	ALPHA-2 ADRENERGIC RECEPTOR (ALPHA-2 ADRENOCEPTOR)
1442	6569		1.2	7.00E-17	6753097	NT	Mus musculus apolipoprotein B editing complex 2 (ApoBec2), mRNA
196	5390	10518	1.6	8.00E-17	AW983860.1	EST_HUMAN	RC1-HN0003-220300-021-b04 HN0003 Homo sapiens cDNA

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Table 4

2118	7229	12438	0.5	1.00E-19	H30795.1	EST_HUMAN	y079g07.r1 Soares adult brain N2b4HB55Y Homo sapiens cDNA clone IMAGE:184188 5'
2685	7772		1.0	1.00E-19	D3804.1	NT	similar to contains MER10 repetitive element ;
2617	7968		5.0	1.00E-19	4758977	NT	Human gene for Ah-receptor, exon 7-9
3355	8498	13607	1.3	1.00E-19	AA834967.1	EST_HUMAN	Homo sapiens protein tyrosine phosphatase, non-receptor type substrate 1 (PTPNS1) mRNA
4826	9740	14837	1.3	8.00E-20	H68656.1	EST_HUMAN	a49b12.s1 Soares testis NHT Homo sapiens cDNA clone IMAGE:1393631 3' similar to
3508	8649	13759	3.9	6.00E-20	P39188	SWISSPROT	contains MER37.12 MER37 repetitive element ;
2092	7203	12408	1.0	3.00E-20	U03888.1	NT	
4115	9241	14327	1.7	3.00E-20	P23273	SWISSPROT	OLFACTORY RECEPTOR-LIKE PROTEIN114
4524	9643	14733	0.9	3.00E-20	AA037616.1	EST_HUMAN	Human BXP21 gene
813	5963		1.5	2.00E-20	AW303868.1	EST_HUMAN	OLFACTORY RECEPTOR-LIKE PROTEIN114
1095	6233	11384	0.7	2.00E-20	AA516335.1	EST_HUMAN	similar to contains L1.13 L1 repetitive element ;
1095	6233	11385	0.7	2.00E-20	AA516335.1	EST_HUMAN	similar to contains L1.13 L1 repetitive element ;
2173	7282	12495	0.6	2.00E-20	H68656.1	EST_HUMAN	similar to contains L1.13 L1 repetitive element ;
2786	5963		0.9	2.00E-20	AW303868.1	EST_HUMAN	similar to contains L1.13 L1 repetitive element ;
4866	8973	15057	4.3	2.00E-20	Q28983	SWISSPROT	similar to contains L1.13 L1 repetitive element ;
4866	8973	15058	4.3	2.00E-20	Q28983	SWISSPROT	similar to contains L1.13 L1 repetitive element ;
5090	10188		11.4	2.00E-20	5174538	NT	similar to contains L1.13 L1 repetitive element ;
1967	7870	12283	1.9	1.00E-20	AA281961.1	EST_HUMAN	similar to contains L1.13 L1 repetitive element ;
4764	9875	14970	1.0	1.00E-20	7681767	NT	similar to contains L1.13 L1 repetitive element ;
308	5492	10621	1.0	9.00E-21	BE16564.1	EST_HUMAN	similar to contains L1.13 L1 repetitive element ;
2883	8034		1.1	9.00E-21	AJ003514.1	EST_HUMAN	similar to contains L1.13 L1 repetitive element ;
172	5365	10490	1.0	8.00E-21	AT95842.1	EST_HUMAN	similar to contains L1.13 L1 repetitive element ;
172	5365	10491	1.0	8.00E-21	AT95842.1	EST_HUMAN	similar to contains L1.13 L1 repetitive element ;
2023	7136	12335	0.8	7.00E-21	P15800	SWISSPROT	similar to contains L1.13 L1 repetitive element ;
2023	7136	12336	0.8	7.00E-21	P15800	SWISSPROT	similar to contains L1.13 L1 repetitive element ;
4161	9287		5.0	7.00E-21	AA046502.1	EST_HUMAN	similar to contains L1.13 L1 repetitive element ;
4014	9145	14228	0.9	6.00E-21	BE408611.1	EST_HUMAN	similar to contains L1.13 L1 repetitive element ;
907	6053	11210	0.6	5.00E-21	5902031	NT	similar to contains L1.13 L1 repetitive element ;

Table 4

2234	7341	12553	1.1	5.00E-21	AA928194.1	EST_HUMAN	om23g03.s1 Soares_NF_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1541908 3' similar to TR:Q02711 PRO-POL-DUTPASE POLYPEPTIDE
4696	9808	14907	6.0	5.00E-21	4885474.1	NT	Homo sapiens melanoma antigen, family C, 1 (MAGEC1), mRNA
5109	10205		1.0	5.00E-21	D87675.1	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
							co08608.s1 NCI_CGAP_Kids Homo sapiens cDNA clone IMAGE:1573094 3' similar to TR:Q16330 Q16530 PHAS3 MRNA; contains OFR.11 OFR repetitive element
1701	6824	12005	1.2	4.00E-21	AA970713.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C001
2228	7335	12547	1.1	3.00E-21	AL163201.2	NT	Homo sapiens LGMD2B gene
3041	8192	13294	4.0	3.00E-21	AJ007973.1	NT	GV3-HT0458-170200-090-012 HT0458 Homo sapiens cDNA
140	5336		5.0	2.00E-21	BE163247.1	EST_HUMAN	Homo sapiens mRNA for KIAA0397 protein, partial cds
919	6065	11220	0.9	2.00E-21	AB007857.2	NT	Homo sapiens mRNA for KIAA0397 protein, partial cds
919	6065	11221	0.9	2.00E-21	AB007857.2	NT	Homo sapiens mRNA for KIAA0397 protein, partial cds
							zq78b11.1 Stratigene hNT neuron (#937233) Homo sapiens cDNA clone IMAGE:647805 5' similar to SW:YGAL1_YEAST P48234 HYPOTHETICAL 81.7 KD PROTEIN IN MOL-1-NAT2 INTERGENIC REGION. [1]:
1164	6299	11454	2.6	2.00E-21	AA206749.1	EST_HUMAN	RCA-BT0311-141199-011-h06 BT0311 Homo sapiens cDNA
1196	6328		0.7	2.00E-21	BE064410.1	EST_HUMAN	Human DNA, SINE repetitive element
2260	7366	12575	2.6	2.00E-21	D14547.1	NT	seq1487 b4HB3MA-Cont-HAP-F1 Homo sapiens cDNA clone b4HB3MA-COT8-HAP-F1259 5'
2516	7612	12814	0.8	2.00E-21	T10311.1	EST_HUMAN	ZONADHESIN PRECURSOR
2599	7690	12893	1.0	2.00E-21	Q28983	SWISSPROT	ZONADHESIN PRECURSOR
2599	7690	12894	1.0	2.00E-21	Q28983	SWISSPROT	n146204.s1 NCI_CGAP_P4 Homo sapiens cDNA clone IMAGE:1043718 similar to contains MER28.b2 MER29 repetitive element
1235	6364	11526	0.6	1.00E-21	AA557657.1	EST_HUMAN	MER28.b2 MER29 repetitive element
1381	6508		0.9	1.00E-21	AI601264.1	EST_HUMAN	ar88b12.x1 Bartsied colton HPLRB7 Homo sapiens cDNA clone IMAGE:2152343 3'
							tz94a03.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2296204 3' similar to TR:Q15408 Q15408 NEUTRAL PROTEASE LARGE SUBUNIT
4312	9435	14525	2.6	9.00E-22	AI702438.1	EST_HUMAN	CMO-HT0179-281099-076-h05 HT0179 Homo sapiens cDNA
933	6080		1.6	8.00E-22	BE144748.1	EST_HUMAN	ALPHA-2-MACROGLOBULIN PRECURSOR (ALPHA2M)
649	5807	10933	1.4	7.00E-22	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
4186	8312	14393	2.3	7.00E-22	Q61838	SWISSPROT	ALPHA-2-MACROGLOBULIN PRECURSOR (ALPHA2M)
4969	10072	15145	1.2	7.00E-22	AB008681.1	NT	Homo sapiens gene for actin receptor type IIB, complete cds
3584	8723		0.9	4.00E-22	AJ271735.1	NT	Homo sapiens Xq pseudautosomal region; segment 1/2
							bm14h10.x1 NCI_CGAP_Co14 Homo sapiens cDNA clone IMAGE:2156611 3' similar to gbL19593 HIGH AFFINITY INTERLEUKIN-8 RECEPTOR B (HUMAN); contains L1.1 L1 repetitive element
943	6090		1.2	3.00E-22	AI469679.1	EST_HUMAN	wf66b04.x1 NCI_CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2429839 3' similar to SW:RL21_HUMAN P46778 60S RIBOSOMAL PROTEIN L21
2523	7619	12820	0.7	3.00E-22	AI859038.1	EST_HUMAN	Human chromosomal protein HMGI related gene
3620	8759		1.5	3.00E-22	D14718.1	NT	HSB10E082 STRATAGENE Human skeletal muscle cDNA library, cat. #936215. Homo sapiens cDNA clone 10E08
4212	9336	14419	0.8	3.00E-22	F00548.1	EST_HUMAN	HSB10E082 STRATAGENE Human skeletal muscle cDNA library, cat. #936215. Homo sapiens cDNA clone 10E08
4212	9336	14420	0.8	3.00E-22	F00548.1	EST_HUMAN	HSB10E082 STRATAGENE Human skeletal muscle cDNA library, cat. #936215. Homo sapiens cDNA clone 10E08

Table 4

4695	9807	14906	2.7	3.00E-22	AI090125.1	EST_HUMAN	qb28cd7.x1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:1697580 3'
1910	7027		1.0	2.00E-22	N24942.1	EST_HUMAN	similar to contains MER12.12 MER12 repetitive element;
2476	7514	12776	1.3	2.00E-22	P24916	SWISSPROT	YX73d05.s1 Soares melanocyte 2NBHM Homo sapiens cDNA clone IMAGE:267369 3'
							IMMEDIATE EARLY GENE 13 PROTEIN PRECURSOR
							Homo sapiens protein kinase, AMP-activated, gamma 3 non-catalytic subunit (PRKAG3), mRNA
3373	8516	13623	4.1	2.00E-22	8394043	NT	
3567	8726	13822	0.9	2.00E-22	R58726.1	EST_HUMAN	G4789 Fetal heart Homo sapiens cDNA clone G4789 5' end
4133	9239	14340	1.3	2.00E-22	AW617794.1	EST_HUMAN	PM1-ST0262-261199-001-012 ST0262 Homo sapiens cDNA
63	5271	10393	0.8	1.00E-22	AW686543.1	EST_HUMAN	RC1-OT0083-220300-021-c07 OT0083 Homo sapiens cDNA
63	5271	10394	0.8	1.00E-22	AW686543.1	EST_HUMAN	RC1-OT0083-220300-021-c07 OT0083 Homo sapiens cDNA
1836	6955	12141	0.6	1.00E-22	AW685517.1	EST_HUMAN	PM4-SN0020-010400-009-002 SN0020 Homo sapiens cDNA
							zq76f1.1 Striatogene hNT neuron (#937233) Homo sapiens cDNA clone IMAGE:647565 5' similar to SW:VPR1_HUMAN P10265 RETROVIRUS-RELATED PROTEASE :
2400	7943		0.5	1.00E-22	AA199812.1	EST_HUMAN	
2539	7635	12835	1.0	1.00E-22	U50871.1	NT	Human familial Alzheimer's disease (STM2) gene, complete cds
3365	8508	13616	1.7	1.00E-22	D14547.1	NT	Human DNA, SINE repetitive element
3523	8664	13768	0.8	8.00E-23	AF198349.1	NT	Gallus gallus Dact2 protein (Dact2) mRNA, complete cds
							zq45b06.s1 Striatogene hNT neuron (#937233) Homo sapiens cDNA clone IMAGE:632627 3' similar to contains Alu repetitive element;
2800	6795	11971	1.8	7.00E-23	AA189080.1	EST_HUMAN	
3367	8530		1.6	6.00E-23	AF199333.1	NT	Rattus norvegicus RIM1B (Rim1B) mRNA, complete cds
4171	9297	14378	3.1	6.00E-23	AL163249.2	NT	Homo sapiens chromosome 21 segment HS21C049
650	5808	10934	1.5	2.00E-23	AI289880.1	NT	Homo sapiens KIAA0851 gene (partial), X13 gene and LZTFL1 gene
1126	7866		0.9	2.00E-23	M55270.1	NT	Human matrix Gla protein (MGF) gene, complete cds
2765	7849	13051	1.1	2.00E-23	P22105	SWISSPROT	TENASCIN-X PRECURSOR (TN-X) (HEXABRACHION-LIKE)
2765	7849	13052	1.1	2.00E-23	P22105	SWISSPROT	TENASCIN-X PRECURSOR (TN-X) (HEXABRACHION-LIKE)
							g973t1.x1 NCL CGAP_P28 Homo sapiens cDNA clone IMAGE:1943757 3' similar to TR:Q13537 Q13537 MER37 TRANSPOSABLE ELEMENT, COMPLETE CONSENSUS SEQUENCE :
3325	8469		1.5	2.00E-23	AI201458.1	EST_HUMAN	
3655	8794		3.0	2.00E-23	BE165980.1	EST_HUMAN	MR3-HT0487-150200-113-g01 HT0487 Homo sapiens cDNA
							Y16a02.1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:205418 5'
3894	9029	14121	3.0	2.00E-23	H59931.1	EST_HUMAN	
							Y16a02.1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:205418 5'
3894	9029	14122	3.0	2.00E-23	H59931.1	EST_HUMAN	
4428	9549	14642	1.6	1.00E-23	AL163352.2	NT	Homo sapiens chromosome 21 segment HS21C052
4657	9769		4.5	1.00E-23	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
							ab75a08.s1 Striatogene fetal retina 837202 Homo sapiens cDNA clone IMAGE:852758 3' similar to TR:E19822 E19822 CA PROTEIN.;
540	5703		0.6	9.00E-24	AA663213.1	EST_HUMAN	
4549	9688	14757	1.1	8.00E-24	P23269	SWISSPROT	OLFACTORY RECEPTOR-LIKE PROTEIN 13
4549	9688	14758	1.1	8.00E-24	P23269	SWISSPROT	OLFACTORY RECEPTOR-LIKE PROTEIN 13
3796	8833		1.3	7.00E-24	AW937854.1	EST_HUMAN	QV0-DT0047-170200-122-a06 DT0047 Homo sapiens cDNA
690	5645		0.8	6.00E-24	AB001421.1	NT	Mus musculus mRNA for Testis-Specific Protein Y (TSPY), complete cds

Table 4

820	5970	11127	3.5	6.0E-24	AL163249.2	NT	Homo sapiens chromosome 21 segment HS21C049
4088	9195	14278	2.1	6.0E-24	AF199333.1	NT	Rattus norvegicus RIM1B (Rim1B) mRNA, complete cds
4088	9195	14278	2.1	6.0E-24	AF199333.1	NT	Rattus norvegicus RIM1B (Rim1B) mRNA, complete cds
3889	9025	14117	7.2	5.0E-24	AJ229043.1	NT	Homo sapiens 959 kb contig between AML1 and CBR1 on chromosome 21q22, segment 3/3
2298	7402	12610	0.8	2.0E-24	AA167539.1	EST_HUMAN	zp11109.t1 Stratiagene fetal retina 937202 Homo sapiens cDNA clone IMAGE:609161.5'
3216	8364	13475	1.0	2.0E-24	AA393327.1	EST_HUMAN	z66b06.t1 Soares testis NHT Homo sapiens cDNA clone IMAGE:727187.5'
3729	8866		1.0	2.0E-24	AW898189.1	EST_HUMAN	RC3-NN0088-090500-021-b03 NN0088 Homo sapiens cDNA
1670	6794	11970	0.8	1.0E-24	7706340	NT	Homo sapiens CGI-127 protein (LOC51646), mRNA
2636	7727		0.7	1.0E-24	AW820194.1	EST_HUMAN	QVO-5T0294-100400-185-c10 ST0294 Homo sapiens cDNA
2987	8139	13242	0.9	1.0E-24	D86423.1	NT	Mus musculus mRNA for HGT keratin, partial cds
4173	9299		1.6	1.0E-24	AF143313.1	NT	Homo sapiens PTEN (PTEN) gene, exon 2
4926	10033	15107	2.3	7.0E-25	AA483944.1	EST_HUMAN	ne82a10.s1 NCI CGAP Kid1 Homo sapiens cDNA clone IMAGE:911754 similar to contains MER1.b2 MER1 repetitive element:
4710	9822		5.5	6.0E-25	Q39575	SWISSPROT	DYNEIN GAMMA CHAIN, FLAGELLAR OUTER ARM
5168	10260	15331	1.0	5.0E-25	AW838171.1	EST_HUMAN	QV2-LT0051-260300-111-403 LT0051 Homo sapiens cDNA
1430	6557	11733	0.8	4.0E-25	T98107.1	EST_HUMAN	y656h04.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:121783.5'
3356	8499		2.8	4.0E-25	AW887671.1	EST_HUMAN	PM3-OT0093-280200-001-q07 OT0093 Homo sapiens cDNA
3979	9111	14193	0.8	4.0E-25	7106446	NT	Mus musculus wingless-related MMTV integration site 3A (Wn13a), mRNA
3979	9111	14194	0.8	4.0E-25	7106446	NT	Mus musculus wingless-related MMTV integration site 3A (Wn13a), mRNA
4221	9345		3.0	4.0E-25	BE170957.1	EST_HUMAN	QV3-HT0543-140400-149-e11 HT0543 Homo sapiens cDNA
3278	8423	13531	2.7	3.0E-25	8923321	NT	Homo sapiens hypothetical protein FLJ20344 (FLJ20344), mRNA
3278	8423	13532	2.7	3.0E-25	8923321	NT	Homo sapiens hypothetical protein FLJ20344 (FLJ20344), mRNA
4796	8909	15002	0.9	3.0E-25	P29622	SWISSPROT	KALLISTATIN PRECURSOR (KALLIKREIN INHIBITOR) (PROTEASE INHIBITOR 4)
1325	6454	11620	1.2	2.0E-25	5032158	NT	Homo sapiens transducin (beta)-like 1 (TBL1) mRNA
2363	7465	12670	1.3	2.0E-25	AW854060.1	EST_HUMAN	EST366130 IMAGE resequences, MAGC Homo sapiens cDNA
2801	7592	12795	1.6	2.0E-25	P17008	SWISSPROT	40S RIBOSOMAL PROTEIN S16
4096	9222	14305	1.9	2.0E-25	P17008	SWISSPROT	40S RIBOSOMAL PROTEIN S16
4096	9222	14306	1.9	2.0E-25	P17008	SWISSPROT	40S RIBOSOMAL PROTEIN S16
361	5539	10670	0.6	1.0E-25	AL040229.1	EST_HUMAN	DKFZp434H0313_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434H0313.5'
2384	7486	12668	2.8	1.0E-25	Q06055	SWISSPROT	ATP SYNTHASE LIPID-BINDING PROTEIN P2 PRECURSOR (ATPASE PROTEIN 9) (SUBUNIT C)
4753	9864	14957	2.7	1.0E-25	BE162737.1	EST_HUMAN	PM1-HT0454-080100-002-h09 HT0454 Homo sapiens cDNA
2433	7532	12738	0.7	9.0E-26	AL163218.2	NT	Homo sapiens chromosome 21 segment HS21C018
1559	6686	11853	0.5	7.0E-26	AF003528.1	NT	Homo sapiens X-linked anhidrotic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions
3898	8033	14128	1.4	7.0E-26	X89211.1	NT	H. sapiens DNA for endogenous retroviral like element
4067	9194	14277	2.0	7.0E-26	AW340153.1	EST_HUMAN	h002e12.x1 Soares NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2908366.3'

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Table 4

2178	7287	12499	0.9	6.00E-26	AF029308.1	NT	Homo sapiens chromosome 9 duplication of the T cell receptor beta locus and tyrosinogen gene families
3302	8447	13557	1.4	6.00E-26	AA206131.1	EST_HUMAN	zq52n04.r1 Stragene neuroepithelium (#937231) Homo sapiens cDNA clone IMAGE:645271 5'
1160	6295	11450	1.1	5.00E-26	A1708235.1	EST_HUMAN	as38n08.x1 Bartsiad aorta HPLRB6 Homo sapiens cDNA clone IMAGE:2319519 3' similar to WP:F49C12.11 CE03371 ;
1160	6295	11451	1.1	5.00E-26	A1708235.1	EST_HUMAN	as38n08.x1 Bartsiad aorta HPLRB6 Homo sapiens cDNA clone IMAGE:2319519 3' similar to WP:F49C12.11 CE03371 ;
2692	7778	12876	1.8	5.00E-26	U37012.1	NT	Human cleavage and polyadenylation specificity factor mRNA, complete cds
1525	6652		1.5	4.00E-26	AA329546.1	EST_HUMAN	EST33448 Embryo, 12 week II Homo sapiens cDNA 5' end
1958	7075	12272	0.5	3.00E-26	AL045855.2	EST_HUMAN	DKFZp4341066.r1 434 (synonym: hies3) Homo sapiens cDNA clone DKFZp4341066 5'
							z330d08.r1 Stragene neuroepithelium NT2RAMI 937234 Homo sapiens cDNA clone IMAGE:548943 5' similar to gb:M14338 VITAMIN K-DEPENDENT PROTEIN S
1987	7102		0.9	3.00E-26	AA115895.1	EST_HUMAN	PRECUSOR (HUMAN);
3712	8850	13940	1.2	3.00E-26	AA152464.1	EST_HUMAN	zo30f10.r1 Stragene colon (#937204) Homo sapiens cDNA clone IMAGE:588427 5' similar to TR:G695374 G695374 THYROID RECEPTOR INTERACTOR ;
3712	8850	13941	1.2	3.00E-26	AA152464.1	EST_HUMAN	zo30f10.r1 Stragene colon (#937204) Homo sapiens cDNA clone IMAGE:588427 5' similar to TR:G695374 G695374 THYROID RECEPTOR INTERACTOR ;
666	5822	10950	1.9	2.00E-26	AL163282.2	NT	Homo sapiens chromosome 21 segment HS21C082
1825	6944		1.2	2.00E-26	AL038099.2	EST_HUMAN	DKFZp566L171.g1 566 (synonym: htkd2) Homo sapiens cDNA clone DKFZp566L171 3'
3183	8342	13456	4.3	2.00E-26	X86894.1	NT	IMusculus mRNA for astrocytic phosphoprotein, PEA-15
132	5328	10459	0.8	1.00E-26	BE170371.1	EST_HUMAN	QV4-HT0538-020300-123-a02 HT0538 Homo sapiens cDNA
							DKFZp434H1910.r1 434 (synonym: hies3) Homo sapiens cDNA clone DKFZp434H1910 5'
2001	7116	12318	1.4	1.00E-26	AL038363.2	EST_HUMAN	Homo sapiens glyceraldehyde-3-phosphate dehydrogenase (GAPD), mRNA
2694	7743		6.1	1.00E-26	7669491	NT	Homo sapiens NCI_CGAP_Lu19 Homo sapiens cDNA clone IMAGE:2406150 3' similar to w149c04.x1 NCI_CGAP_Lu19 Homo sapiens cDNA clone IMAGE:2406150 3' similar to contains THR.b2 THR repetitive element ;
10	5218	10319	1.1	8.00E-27	AI831462.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C027
545	5708		1.4	8.00E-27	AL163227.2	NT	similar to gb:K00558 TUBULIN ALPHA-1 CHAIN (HUMAN);
1395	6522	11690	6.8	8.00E-27	AW162737.1	EST_HUMAN	au87n08.x1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2783295 3' similar to gb:K00558 TUBULIN ALPHA-1 CHAIN (HUMAN);
1395	6522	11691	6.8	8.00E-27	AW162737.1	EST_HUMAN	au87n08.x1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2783295 3' similar to gb:K00558 TUBULIN ALPHA-1 CHAIN (HUMAN);
2121	7231	12441	1.0	8.00E-27	AW864776.1	EST_HUMAN	similar to gb:K00558 TUBULIN ALPHA-1 CHAIN (HUMAN);
3148	8297	13406	3.3	8.00E-27	P12236	SWISSPROT	ADP-ATP CARRIER PROTEIN, LIVER ISOFORM T2 (ADP/ATP TRANSLOCASE 3)
3309	8454	13567	0.9	8.00E-27	AF181897.1	NT	(ADENINE NUCLEOTIDE TRANSLOCATOR 3) (ANT 3)
688	5824		1.2	7.00E-27	Z70684.1	NT	Homo sapiens WRN (WRN) gene, complete cds
5023	10124		2.1	7.00E-27	AW629172.1	EST_HUMAN	Human endogenous retroviral element HC2
1995	7111	12314	2.0	3.00E-27	X60658.1	NT	h15h12.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2875879 3' similar to TR:O76040 O76040 ORF2: FUNCTION UNKNOWN ;
							R, radius RYA3 mRNA for a potential ligand-binding protein

Table 4

4174	9300	14381	1.3	3.00E-27	BE071924.1	EST_HUMAN	PM0-BT0527-090100-001-d11 BT0527 Homo sapiens cDNA
36	5245	10352	8.0	2.00E-27	AF054187.1	NT	Homo sapiens alpha VAC mRNA, complete cds
1853	6971		6.7	2.00E-27	AA565345.1	EST_HUMAN	nk01b10.s1 NCI_CGAP_Pt11 Homo sapiens cDNA clone IMAGE:1000699 similar to gb:M17886.605 ACIDIC RIBOSOMAL PROTEIN P1 (HUMAN);
3071	8222		10.3	2.00E-27	AW629172.1	EST_HUMAN	h51h12.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2975879 3' similar to TR:076040 076040 ORF2: FUNCTION UNKNOWN.;
3187	8336	13448	1.4	2.00E-27	AF111167.2	NT	Homo sapiens jun dimerization protein gene, partial cds; cfos gene, complete cds; and unknown gene
3187	8336	13449	1.4	2.00E-27	AF111167.2	NT	Homo sapiens jun dimerization protein gene, partial cds; cfos gene, complete cds; and unknown gene
3844	9077	14159	1.1	2.00E-27	AF000368.1	NT	Rattus norvegicus voltage-gated sodium channel mRNA, complete cds
429	5596		0.5	1.00E-27	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
980	6125	11281	1.4	1.00E-27	AB026898.1	NT	Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)
1438	6565	11742	2.8	1.00E-27	AF029308.1	NT	Homo sapiens chromosome 9 duplication of the T cell receptor beta locus and tyrosinogen gene families
136	5331		0.8	9.00E-28	BE348399.1	EST_HUMAN	hwt7c11.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3183188 3' similar to TR:Q07314 Q07314 SECRETED NEUREXIN III-ALPHA-C PRECURSOR. [3] TR:Q07280 TR:Q07313.;
1140	6276	11428	1.1	9.00E-28	W23234.1	EST_HUMAN	81B2 Human retina cDNA Tsp509I-cleaved sublibrary Homo sapiens cDNA not directional
5118	10214	15292	1.2	9.00E-28	AI590115.1	EST_HUMAN	to12b09.x1 NCI_CGAP_U12 Homo sapiens cDNA clone IMAGE:2178809 3' similar to contains OFR.t1 OFR repetitive element.;
5118	10214	15293	1.2	9.00E-28	AI590115.1	EST_HUMAN	to12b09.x1 NCI_CGAP_U12 Homo sapiens cDNA clone IMAGE:2178809 3' similar to contains OFR.t1 OFR repetitive element.;
3987	9119	14202	1.3	6.00E-28	AB020673.1	NT	Homo sapiens mRNA for KIAA0866 protein, complete cds
3987	9119	14203	1.3	6.00E-28	AB020673.1	NT	Homo sapiens mRNA for KIAA0866 protein, complete cds
315	5499		1.1	5.00E-28	AI921003.1	EST_HUMAN	wo18c07.x1 NCI_CGAP_Par1 Homo sapiens cDNA clone IMAGE:2455692 3' similar to contains THR.b1 THR repetitive element.;
3927	5061	14148	1.9	5.00E-28	R79782.1	EST_HUMAN	y89f10.r1 Scores placenta NbZHP Homo sapiens cDNA clone IMAGE:146443 5'
2584	7677	12879	0.5	4.00E-28	AW195066.1	EST_HUMAN	xa33c09.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2695504 3' similar to SW:GG95 HUMAN Q08379 GOLGIN-95.;
3070	8221	13320	3.4	4.00E-28	BE409100.1	EST_HUMAN	601300703F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3635305 5'
1262	6391		0.6	3.00E-28	AF155382.1	NT	Homo sapiens metalloproteinase-like, disintegrin-like, cysteine-rich protein 2 epsilon (ADAM22) mRNA, complete cds
83	5289	10416	2.2	2.00E-28	BE082167.1	EST_HUMAN	RC1-8T0254-220300-019-c05 BT0254 Homo sapiens cDNA
1149	6284	11437	3.4	2.00E-28	Y11107.3	NT	Homo sapiens ITGB4 gene for Integrin beta 4 subunit, exons 3-41
2427	7526	12732	0.8	2.00E-28	AI348634.1	EST_HUMAN	qc55b06.x1 NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1910483 3' similar to contains L1.b2 L1 repetitive element.;
1463	6590	11765	0.9	1.00E-28	D38044.1	NT	Human gene for Ah-receptor, exon 7-9

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Table 4

2650	7739	12939	1.0	1.00E-28	AF000995.1	NT	Homo sapiens ubiquitous TPR motif, Y isoform (UTY) mRNA, alternative transcript 2, complete cds
1554	6710	11881	0.9	7.00E-29	AW968447.1	EST_HUMAN	EST378521 MAGE resequences, MAGI Homo sapiens cDNA
							wp68b01.x1 NC1_CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2465985 3' similar to TR:O15475 O15475 UNNAMED HERV-H PROTEIN ;contains LTR7.b1 LTR7 repetitive element ;
560	5740	10857	2.2	6.00E-29	AI936748.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C003
4928	10035		1.0	5.00E-29	AL163203.2	NT	cn15c02.x1 Normal Human Trabecular Bone Cells Homo sapiens cDNA clone
3194	8343		1.7	4.00E-29	AI752367.1	EST_HUMAN	NH-TBC, cn15c02 random
4317	9440	14529	1.5	3.00E-29	AB042297.1	NT	Homo sapiens PTS gene for 6-pyruvyltetrahydropterin synthase, complete cds
484	5649	10772	1.4	2.00E-29	AF084869.1	NT	Homo sapiens envelope protein RIC-8 (env) gene, complete cds
484	5849	10773	1.4	2.00E-29	AF084869.1	NT	Homo sapiens envelope protein RIC-8 (env) gene, complete cds
							wp6d10.x1 NC1_CGAP_Ut1 Homo sapiens cDNA clone IMAGE:2492563 3' similar to TR:O15548 O15548 HERV-E ENVELOPE GLYCOPROTEIN ;
1516	6643	11810	2.2	2.00E-29	AI963604.1	EST_HUMAN	TR:O15546 O15546 HERV-E ENVELOPE GLYCOPROTEIN ;
							wp65d10.x1 NC1_CGAP_Ut1 Homo sapiens cDNA clone IMAGE:2492563 3' similar to TR:O15546 O15546 HERV-E ENVELOPE GLYCOPROTEIN ;
1516	6643	11811	2.2	2.00E-29	AI963604.1	EST_HUMAN	TR:O15546 O15546 HERV-E ENVELOPE GLYCOPROTEIN ;
1602	6729	11900	0.5	2.00E-29	AW962209.1	EST_HUMAN	EST374282 MAGE resequences, MAGG Homo sapiens cDNA
1602	6729	11901	0.5	2.00E-29	AW962209.1	EST_HUMAN	EST374282 MAGE resequences, MAGG Homo sapiens cDNA
4182	8308	14387	2.0	2.00E-29	AL163268.2	NT	Homo sapiens chromosome 21 segment HS21C068
1499	6625		1.2	7.00E-30	BE091333.1	EST_HUMAN	PM4-BT0724-150400-004-d11 BT0724 Homo sapiens cDNA
1549	6676		1.0	6.00E-30	X51755.1	NT	Human lambda-immunoglobulin constant region complex (germline)
1736	6659	12037	1.3	6.00E-30	D25303.1	NT	Human mRNA for integrin alpha subunit, complete cds
3153	8302	13410	2.4	6.00E-30	BE008026.1	EST_HUMAN	QV0-BN0147-290400-214-f12 BN0147 Homo sapiens cDNA
							tg92g03.x1 NC1_CGAP_CLI1 Homo sapiens cDNA clone IMAGE:2116276 3' similar to
3931	9065	14152	31.2	5.00E-30	AI399992.1	EST_HUMAN	contains Alu repetitive element;
2096	7207	12412	0.6	4.00E-30	AW937471.1	EST_HUMAN	QV3-DT0043-090200-080-c06 DT0043 Homo sapiens cDNA
2096	7207	12413	0.6	4.00E-30	AW937471.1	EST_HUMAN	QV3-DT0043-090200-080-c06 DT0043 Homo sapiens cDNA
							qg93cd5.x1 Soares, total, fetus, Nb2HF8, 9w Homo sapiens cDNA clone IMAGE:1938920 3' similar to contains MER29.h2 MER29 repetitive element ;
1134	6270		0.6	3.00E-30	AI338551.1	EST_HUMAN	similar to contains MER29.h2 MER29 repetitive element ;
3697	8836	13927	0.9	3.00E-30	AF128893.1	NT	Homo sapiens telomerase reverse transcriptase (TERF) gene, exons 1-6
659	5815	10943	1.2	2.00E-30	AW857315.1	EST_HUMAN	CNO-C10307-310100-158-H03 CT0307 Homo sapiens cDNA
1068	6206		0.8	2.00E-30	F08688.1	EST_HUMAN	HSC2J3051 normalized infant brain cDNA Homo sapiens cDNA clone c-23105
1464	6591	11766	2.1	2.00E-30	BE175877.1	EST_HUMAN	RC5-HT0582-110400-013-H08 HT0582 Homo sapiens cDNA
2889	8040	13141	6.4	2.00E-30	AF114156.1	NT	Homo sapiens Y-linked zinc finger protein (ZFY) gene, complete cds
3721	8858	13951	2.1	2.00E-30	AW206581.1	EST_HUMAN	UL-H-B11-a1b-c-12-0-UL1 s1 NC1_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2172558 3'
4688	9780	14878	1.7	2.00E-30	BE298945.1	EST_HUMAN	601119860F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3029438 5'
4688	9780	14879	1.7	2.00E-30	BE298945.1	EST_HUMAN	601119860F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3029438 5'
284	5471	10601	3.5	1.00E-30	C18939.1	EST_HUMAN	C18939 Human placenta cDNA (TFIIJwara) Homo sapiens cDNA clone GEN-570C01 5'
							hc30b04.x1 Soares_NEL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2910991 3' similar to contains MER1.3 MER1 repetitive element ;
527	5691	10813	0.6	1.00E-30	AW468897.1	EST_HUMAN	

Table 4

699	5854	10989	1.0	1.00E-30	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
2165	7274	12485	1.2	1.00E-30	AA664377.1	EST_HUMAN	ac77b08.s1 Striatagene lung (#337210) Homo sapiens cDNA clone IMAGE:866599 3'
2973	8124	13231	1.0	1.00E-30	5803091	NT	Homo sapiens methionine aminopeptidase: eif-2-associated p67 (MNPEP). mRNA
3015	8187	13268	0.9	1.00E-30	AA315045.1	EST_HUMAN	EST186668 HCC cell line (matasistasis to liver in mouse) II Homo sapiens cDNA 5' end
1060	8199	11352	0.6	8.00E-31	8923369	NT	Homo sapiens hypothetical protein FLJ20420 (FLJ20420). mRNA
2362	7464		1.9	8.00E-31	AL163208.2	NT	Homo sapiens chromosome 21 segment HS21C008
694	5849		0.6	7.00E-31	AA372637.1	EST_HUMAN	EST184555 Colon adenocarcinoma IV Homo sapiens cDNA 5' end
2633	7722	12824	0.6	7.00E-31	BE326517.1	EST_HUMAN	hmo5a11.x1 NCI CGAP Lu24 Homo sapiens cDNA clone IMAGE:3182012 3'
2633	7722	12825	0.6	7.00E-31	BE326517.1	EST_HUMAN	hmo5a11.x1 NCI CGAP Lu24 Homo sapiens cDNA clone IMAGE:3182012 3'
3198	8347	13460	4.5	6.00E-31	AW881551.1	EST_HUMAN	RC4-OT0037-150200-011-g08 OT0037 Homo sapiens cDNA
3198	8347	13461	4.5	6.00E-31	AW881551.1	EST_HUMAN	RC4-OT0037-150200-011-g08 OT0037 Homo sapiens cDNA
3625	8764		2.8	6.00E-31	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
3827	8964	14063	1.1	6.00E-31	AW087805.1	EST_HUMAN	cn19d07.x1 Normal Human Trabecular Bone Cells Homo sapiens cDNA clone
185	5378	10505	1.0	5.00E-31	M60694.1	NT	NHTBC_cnt19d07 random
185	5378	10506	1.0	5.00E-31	M60694.1	NT	Homo sapiens type I DNA topoisomerase gene, exon 8
5026	10127	15200	1.7	5.00E-31	8924243	NT	Homo sapiens type I DNA topoisomerase gene, exon 8
5026	10127	15201	1.7	5.00E-31	8924243	NT	Homo sapiens hypothetical protein SIRP-b2 (SIRP-b2). mRNA
581	5741		1.3	4.00E-31	LA271735.1	NT	Homo sapiens hypothetical protein SIRP-b2 (SIRP-b2). mRNA
							Homo sapiens Xq pseudautosomal region: segment 1/2
1594	8720	11889	1.0	4.00E-31	Q10473	SWISSPROT	POLYPEPTIDE N-ACETYL GALACTOSAMINYLTRANSFERASE (PROTEIN-UDP
1775	6996		0.9	4.00E-31	AL163280.2	NT	ACETYL GALACTOSAMINYLTRANSFERASE) (UDP-GALNAc:POLYPEPTIDE, N-
2759	7843		1.4	4.00E-31	5730038	NT	ACETYL GALACTOSAMINYLTRANSFERASE) (GALNAc-T1)
2550	7845	12846	0.5	3.00E-31	6005871	NT	Homo sapiens chromosome 21 segment HS21C080
3055	8206		1.1	3.00E-31	4505752	NT	Homo sapiens SET domain and mariner transposase fusion gene (SETMAR) mRNA
4303	9427	14517	1.4	3.00E-31	AI938829.1	EST_HUMAN	Homo sapiens SEC63, endoplasmic reticulum translocon component (S. cerevisiae) like (SEC63L). mRNA
1875	6993	12178	0.7	2.00E-31	AW838171.1	EST_HUMAN	Homo sapiens phosphoglycerate mutase 1 (brain) (PGAM1) mRNA
2167	7276	12467	1.3	2.00E-31	AI393388.1	EST_HUMAN	wp70a02.x1 NCI CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2467082 3' similar to TR:O60794 O60794 DJ393P12.2;
2292	7396	12606	0.8	2.00E-31	AL119245.1	EST_HUMAN	GV2-LT0051-260300-111-f03 LT0051 Homo sapiens cDNA
2391	7491	12686	1.6	2.00E-31	AA458824.1	EST_HUMAN	ig44g05.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:211672 3'
16	5224	10326	2.8	1.00E-31	U93163.1	NT	DKFZp761G1513_r1761 (synonym: hamy2) Homo sapiens cDNA clone DKFZp761G1513 5'
1640	6766	11935	0.7	1.00E-31	O95371	SWISSPROT	aa88f11.s1 Striatagene fetal retina 837202 Homo sapiens cDNA clone IMAGE:838413 3'
1640	6766	11936	0.7	1.00E-31	O95371	SWISSPROT	similar to contains THR12 THR repetitive element;
1640	6766	11937	0.7	1.00E-31	O95371	SWISSPROT	Homo sapiens IMAGE-B2 (IMAGE-B2), IMAGE-B3 (IMAGE-B3), IMAGE-B4 (IMAGE-B4), and IMAGE-B1 (IMAGE-B1) genes, complete cds
							OLFACTORY RECEPTOR 2C1
							OLFACTORY RECEPTOR 2C1
							OLFACTORY RECEPTOR 2C1



Table 4

4535	9854	14741	1.0	1,00E-31	AL134376.1	EST_HUMAN	DKFZp547B235_1 547 (synonym: hbr1) Homo sapiens cDNA clone DKFZp547B235 5'
4535	9854	14742	1.0	1,00E-31	AL134376.1	EST_HUMAN	DKFZp547B235_1 547 (synonym: hbr1) Homo sapiens cDNA clone DKFZp547B235 5'
2835	7886		1.0	8,00E-32	U50871.1	NT	Human familial Alzheimer's disease (STM2) gene, complete cds
2032	7145	12347	1.2	8,00E-32	AI056770.1	EST_HUMAN	oz15a09.x1 Soares, fetal_liver, spleen, 1NFLS, S1 Homo sapiens cDNA clone IMAGE:1875394.3'
4754	9865	14958	1.2	7,00E-32	P52591	SWISSPROT	NUCLEAR ENVELOPE PORE MEMBRANE PROTEIN POM 121 (PORE MEMBRANE PROTEIN OF 121 KD) (P145)
2702	7788	12988	0.9	6,00E-32	AK478104.1	EST_HUMAN	tm34a10.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2159994.3' similar to
1018	6158	11311	10.0	5,00E-32	AF116627.1	NT	contains MER29.13 MER29 repetitive element :
915	6061		0.6	4,00E-32	AL163246.2	NT	Homo sapiens PRO1181 mRNA, complete cds
448	5614	10745	1.2	3,00E-32	Y17293.1	NT	Homo sapiens chromosome 21 segment HS21C046
4783	9893	14986	0.9	2,00E-32	BE296613.1	EST_HUMAN	Homo sapiens FLI-1 gene, partial
3435	8577		5.0	9,00E-33	BE327112.1	EST_HUMAN	hw07c05.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3529159.5'
54	5263	10382	0.7	7,00E-33	5031736	NT	TR:O88539 O88539 WW DOMAIN BINDING PROTEIN 11.:
54	5263	10383	0.7	7,00E-33	5031736	NT	Homo sapiens short-chain alcohol dehydrogenase family member (HEP27) mRNA
2115	7226	12434	1.0	7,00E-33	AI590115.1	EST_HUMAN	Homo sapiens short-chain alcohol dehydrogenase family member (HEP27) mRNA
3204	8362		12.9	7,00E-33	AW871307.1	EST_HUMAN	to12b09.x1 NCI_CGAP_U22 Homo sapiens cDNA clone IMAGE:2178809.3' similar to
3676	8815		0.9	6,00E-33	AL163285.2	NT	contains OFR11 OFR repetitive element :
1856	6974	12158	1.4	5,00E-33	4507208	NT	EST3833398 MAGE resequences, MAGL Homo sapiens cDNA
1856	6974	12159	1.4	5,00E-33	4507208	NT	Homo sapiens chromosome 21 segment HS21C085
2226	7333		1.3	5,00E-33	AL163285.2	NT	Homo sapiens spermidine synthase (SRM) mRNA
1112	6249		3.3	4,00E-33	AL163207.2	NT	Homo sapiens chromosome 21 segment HS21C085
2078	7180	12393	0.6	4,00E-33	4758987	NT	Homo sapiens chromosome 21 segment HS21C007
2370	7472		2.7	4,00E-33	AA626621.1	EST_HUMAN	Homo sapiens RAB1, member RAS oncogene family (RAB1) mRNA
2498	7595	12797	1.4	4,00E-33	AL163210.2	NT	ab51b11.r1 Striatogene lung carcinoma 937218 Homo sapiens cDNA clone IMAGE:844317.5'
4382	9504	14589	1.6	4,00E-33	AW293349.1	EST_HUMAN	similar to contains Alu repetitive element; contains MER28.b2 MER28 repetitive element :
1073	6211		1.5	3,00E-33	BE350127.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C010
1074	6211		1.2	3,00E-33	BE350127.1	EST_HUMAN	UI-H-Biz-ant-c-03-0-UJ.s1 NCI_CGAP_Su04 Homo sapiens cDNA clone IMAGE:2727149.3'
4761	9872	14967	3.1	3,00E-33	AB035346.1	NT	h09g01.x1 NCI_CGAP_Kid13 Homo sapiens cDNA clone IMAGE:3146256.3' similar to
99	5225		0.8	2,00E-33	AI160189.1	EST_HUMAN	h09g01.x1 NCI_CGAP_Kid13 Homo sapiens cDNA clone IMAGE:3146256.3' similar to
							contains MER29.b3 MER29 repetitive element :
							h09g01.x1 NCI_CGAP_Kid13 Homo sapiens cDNA clone IMAGE:3146256.3' similar to
							contains MER29.b3 MER29 repetitive element :
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							contains MER29.b3 MER29 repetitive element :
							h09g01.x1 NCI_CGAP_Kid13 Homo sapiens cDNA clone IMAGE:3146256.3' similar to

Table 4

4322	9445		4.3	2.00E-33	BE159039.1	EST_HUMAN	MR0-HT0405-160300-202-d08 HT0405 Homo sapiens cDNA
4911	10018	15097	5.1	2.00E-33	AA626683.1	EST_HUMAN	ab516t1.1 Stratagene lung carcinoma 837218 Homo sapiens cDNA clone IMAGE:844388 5' similar to gb:XM00734_cds1 TUBULIN BETA-5 CHAIN (HUMAN);
8	5216		1.4	1.00E-33	AF003528.1	NT	Homo sapiens X-linked anhidrotic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions
1427	6554	11730	0.7	7.00E-34	TT0845.1	EST_HUMAN	yd15605.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:108320 5'
463	5628	10757	1.5	6.00E-34	U10991.1	NT	Human G2 protein mRNA, partial cds
463	5628	10758	1.5	6.00E-34	U10991.1	NT	Human G2 protein mRNA, partial cds
1837	6956		0.8	5.00E-34	7706500	NT	Homo sapiens Npw38-binding protein NpwBP (LOC51729), mRNA
4363	9485		1.1	5.00E-34	AA316404.1	EST_HUMAN	EST188123 HCC cell line (metastasis to liver in mouse) 11 Homo sapiens cDNA 5' end similar to similar to SKD3
4993	10096	15163	4.0	5.00E-34	U30883.1	NT	Human splicing factor SRSF5-1 (SRP55) mRNA, complete cds
1853	7070	12267	0.8	4.00E-34	A1804687.1	EST_HUMAN	h84cd6.x1 NCI CGAP P728 Homo sapiens cDNA clone IMAGE:2249194 3'
2687	7774	12973	1.0	4.00E-34	8922807	NT	Homo sapiens hypothetical protein FLJ10989 (FLJ10989), mRNA
1488	8615	11786	3.1	1.00E-34	P12236	SWISSPROT	ADP ATP CARRIER PROTEIN, LIVER ISOFORM T2 (ADP/ATP TRANSLOCASE 3) (ADENINE NUCLEOTIDE TRANSLOCATOR 3) (ANT 3)
3621	8760	13852	1.5	1.00E-34	AF003628.1	NT	Homo sapiens X-linked anhidrotic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions
4361	9503		4.0	1.00E-34	BE071414.1	EST_HUMAN	RC2-BT0506-240400-016-h08 BT0506 Homo sapiens cDNA
4920	10027		0.9	1.00E-34	AW845706.1	EST_HUMAN	MR0-CT0068-280999-002-d11 CT0068 Homo sapiens cDNA
3594	8733	13828	1.3	8.00E-35	AW663302.1	EST_HUMAN	h177808.y1 NCI CGAP GU1 Homo sapiens cDNA clone IMAGE:2968787 5'
219	5411		8.3	8.00E-35	6031190	NT	Homo sapiens profilin (PHB) mRNA
1391	6518	11686	1.3	6.00E-35	AA757115.1	EST_HUMAN	ah53h03.at Soares testis NHT Homo sapiens cDNA clone 1309397 3'
1925	7042	12231	0.6	6.00E-35	6006975	NT	Homo sapiens zinc finger protein 208 (ZNF208), mRNA
1681	6805	11986	0.8	5.00E-35	X63392.1	NT	H sapiens immunoglobulin kappa light chain variable region L14
4311	9434	14524	2.2	5.00E-35	AF023268.1	NT	Homo sapiens cdc2 kinase (CLK2), profilin, cdc1, glucocerebrosidase (GBA), and melaxin genes, complete cds; melaxin pseudogene and glucocerebrosidase pseudogene; and thrombospondin3 (THBS3) gene, partial cds
1415	6543	11718	5.4	4.00E-35	BE257907.1	EST_HUMAN	601109719F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3350405 5'
1776	6897	12084	1.9	4.00E-35	H91193.1	EST_HUMAN	y998a07.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:241236 5' similar to contains PTR5 repetitive element;
5042	10142		1.3	4.00E-35	BE409102.1	EST_HUMAN	601300705F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3635401 5'
1561	6868	11856	3.5	3.00E-35	BE268182.1	EST_HUMAN	601125260F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3345063 5'
2283	7389		0.9	3.00E-35	AF224492.1	NT	Homo sapiens phospholipid scramblase 1 gene, complete cds
103	7881	10434	0.6	2.00E-35	N88965.1	EST_HUMAN	K6932F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA clone K6932 5' similar to REPEATITIVE ELEMENT
1171	6305	11460	1.3	2.00E-35	T11909.1	EST_HUMAN	AG71F Heart Homo sapiens cDNA clone AG71
1203	6335	11491	0.7	2.00E-35	6912459	NT	Homo sapiens Gtb2-associated binder 2 (KIAA0571), mRNA
2171	7280	12493	1.9	2.00E-35	6912459	NT	Homo sapiens Gtb2-associated binder 2 (KIAA0571), mRNA
3272	8417	13523	1.0	2.00E-35	6912459	NT	Homo sapiens Gtb2-associated binder 2 (KIAA0571), mRNA

Table 4

3272	8417	13524	1.0	2.00E-35	6912459	NT	Homo sapiens Gm2-associated binder 2 (KIAA0571), mRNA
3511	8652		0.9	2.00E-35	AB020702.1	NT	Homo sapiens mRNA for KIAA0895 protein, partial cds
3835	8972	14071	1.1	2.00E-35	BE247575.1	EST_HUMAN	TCBAP2E4328 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project=TCBA Homo sapiens cDNA clone TCBAP4328
3835	8972	14072	1.1	2.00E-35	BE247575.1	EST_HUMAN	TCBAP2E4328 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project=TCBA Homo sapiens cDNA clone TCBAP4328
4570	9688		2.6	2.00E-35	H49239.1	EST_HUMAN	yq19a12.r1 Soares fetal liver spleen 1N.FLS Homo sapiens cDNA clone IMAGE:274079.5'
40	5250	10360	1.5	1.00E-35	AA631949.1	EST_HUMAN	fm1c16 Regional genomic DNA specific cDNA library Homo sapiens cDNA clone CR12-1
40	5250	10361	1.5	1.00E-35	AA631949.1	EST_HUMAN	fm1c16 Regional genomic DNA specific cDNA library Homo sapiens cDNA clone CR12-1
735	5889	11032	15.0	1.00E-35	AW389473.1	EST_HUMAN	IL2-ST0162-131099-008-d12 ST0162 Homo sapiens cDNA
735	5889	11033	15.0	1.00E-35	AW389473.1	EST_HUMAN	IL2-ST0162-131099-008-d12 ST0162 Homo sapiens cDNA
891	6039		1.2	1.00E-35	T87947.1	EST_HUMAN	yds3a01.r1 Soares fetal liver spleen 1N.FLS Homo sapiens cDNA clone IMAGE:115752.5' similar to SF:A44282 A44282 RETROVIRUS-RELATED POL POLYPROTEIN - HUMAN ;
2495	7591	12794	0.8	1.00E-35	7705994	NT	Homo sapiens hypothetical protein (LOC51233), mRNA
2740	7824	13028	1.1	1.00E-35	BE350127.1	EST_HUMAN	h09g01.x1 NCI CGAP Kd13 Homo sapiens cDNA clone IMAGE:3146256.3' similar to contains MER29.D3 MER29 repetitive element ;
2740	7824	13029	1.1	1.00E-35	BE350127.1	EST_HUMAN	h09g01.x1 NCI CGAP Kd13 Homo sapiens cDNA clone IMAGE:3146256.3' similar to contains MER29.D3 MER29 repetitive element ;
3084	8245	13347	5.6	1.00E-35	R67324.1	EST_HUMAN	y32c04.s1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:140934.3'
3094	8245	13348	5.6	1.00E-35	R67324.1	EST_HUMAN	y32c04.s1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:140934.3'
3104	8254	13358	1.1	1.00E-35	6006030	NT	Homo sapiens transcription elongation factor B (SIII), polypeptide 1-like (TCEB1L), mRNA
4325	9448	14535	4.7	1.00E-35	7656905	NT	Mus musculus actin receptor interacting protein 1 (Arp1-pending), mRNA
4325	9448	14536	4.7	1.00E-35	7656905	NT	Mus musculus actin receptor interacting protein 1 (Arp1-pending), mRNA
2800	8051	13154	0.9	7.00E-36	AW857579.1	EST_HUMAN	CM1-CT0315-091299-063-007 CT0315 Homo sapiens cDNA
3080	8231		4.0	7.00E-36	4557498	NT	Homo sapiens C-terminal binding protein 2 (CTBP2), mRNA
1959	7076	12273	0.7	6.00E-36	7706622	NT	Homo sapiens nhl1ufln 2 (NHLJ2), mRNA
2367	7469		2.2	6.00E-36	AB035346.1	NT	Homo sapiens TCL6 gene, exon 12
133	5329	10460	2.3	5.00E-36	AJ271735.1	NT	Homo sapiens Xq pseudautosomal region, segment 1/2
2722	7806	13010	2.8	5.00E-36	BE388438.1	EST_HUMAN	60128567F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3607289.5'
3561	8700	13798	2.0	5.00E-36	AL163209.2	NT	Homo sapiens chromosome 21 segment HS21C009
4676	9790	14890	1.4	5.00E-36	5728729	NT	Homo sapiens API5-like 1 (API5L.1), mRNA
4676	9790	14891	1.4	5.00E-36	5728729	NT	Homo sapiens API5-like 1 (API5L.1), mRNA
1205	6337	11493	1.4	4.00E-36	BE010038.1	EST_HUMAN	PM3-BN0176-100400-001-g04 BN0176 Homo sapiens cDNA
1424	6551	11728	0.6	4.00E-36	P10266	SWISSPROT	RETROVIRUS-RELATED POL POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE : ENDONUCLEASE]
1826	6752	11921	0.6	4.00E-36	BE382574.1	EST_HUMAN	601298674F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3628386.5'
2175	7284		0.6	4.00E-36	AW247772.1	EST_HUMAN	2820020.5prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2820020.5'

Table 4

2707	7782	12892	0.9	4.00E-36	AI392661.1	EST_HUMAN	ig47b01.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2111881 3'
2707	7782	12993	0.9	4.00E-36	AI392661.1	EST_HUMAN	ig47b01.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2111881 3'
3310	8455	13568	3.2	4.00E-36	BE389299.1	EST_HUMAN	601282266F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3604168 5'
3310	8455	13569	3.2	4.00E-36	BE389299.1	EST_HUMAN	601282266F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3604168 5'
681	5836	10969	0.9	3.00E-36	AF099810.1	NT	Homo sapiens neurxin III-alpha gene, partial cds
2252	7358	12565	0.9	3.00E-36	7662401	NT	Homo sapiens KIAA0952 protein (KIAA0952), mRNA
3005	8157	13258	1.8	2.00E-36	BE267054.1	EST_HUMAN	601193483F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3537590 5'
3132	8281	13389	2.7	2.00E-36	BE256287.1	EST_HUMAN	601108343F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3342708 5'
4877	9984	15066	4.6	2.00E-36	AW880376.1	EST_HUMAN	QV0-OT0030-240300-174-h04 OT0030 Homo sapiens cDNA
867	6015	11175	0.7	1.00E-36	BE409310.1	EST_HUMAN	601300938F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3635460 5'
2098	7209	12416	0.9	1.00E-36	BE146523.1	EST_HUMAN	RC1-HT0217-131199-021-h07 HT0217 Homo sapiens cDNA
2098	7209	12417	0.9	1.00E-36	BE146523.1	EST_HUMAN	RC1-HT0217-131199-021-h07 HT0217 Homo sapiens cDNA
2155	7285	12474	1.3	1.00E-36	AW205546.1	EST_HUMAN	UI-H-B1-adf-e-09-0-UI.s1 NCL_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2718041 3'
5143	10238	15313	1.4	8.00E-37	AB020684.1	NT	Homo sapiens mRNA for KIAA0877 protein, partial cds
1263	6392		0.9	7.00E-37	AL042800.1	EST_HUMAN	DKFZp434E0422_r1 434 (synonym: hhes3) Homo sapiens cDNA clone DKFZp434E0422 5'
2374	7476	12677	0.8	4.00E-37	AA702794.1	EST_HUMAN	Z9B004.s1 Soares_fetal_liver_spleen_TNFRS_S1 Homo sapiens cDNA clone IMAGE:448015 3'
5160	10255		1.1	4.00E-37	NG2051.1	EST_HUMAN	EST52g10.WATM1 Homo sapiens cDNA clone 52g10 similar to human STS G04101
1970	7085	12287	1.0	3.00E-37	AL048956.1	EST_HUMAN	DKFZp434L2418_r1 434 (synonym: hhes3) Homo sapiens cDNA clone DKFZp434L2418
1970	7085	12288	1.0	3.00E-37	AL048956.1	EST_HUMAN	DKFZp434L2418_r1 434 (synonym: hhes3) Homo sapiens cDNA clone DKFZp434L2418
2465	7563		0.6	3.00E-37	AW961150.1	EST_HUMAN	EST1373222 MAGE resequences, MAGEF Homo sapiens cDNA
2936	8087		3.0	3.00E-37	AW961150.1	EST_HUMAN	EST1373222 MAGE resequences, MAGEF Homo sapiens cDNA
4072	9199	14285	1.0	3.00E-37	8923313	NT	Homo sapiens hypothetical protein FLJ20337 (FLJ20337), mRNA
1921	7038	12227	0.5	2.00E-37	AL163247.2	NT	Homo sapiens chromosome 21 segment HS21C047
3818	8955	14051	5.1	2.00E-37	4503210	NT	Homo sapiens cytochrome P450, subfamily XXVIIA (steroid 27-hydroxylase, cerebrotendinous xanthomatosis), polypeptide 1 (CYP27A1b) mRNA
1141	8277	11429	0.8	1.00E-37	AA018283.1	EST_HUMAN	ze4DB05.r1 Soares retina N2b4HR Homo sapiens cDNA clone IMAGE:361425 5'
2041	7154	12360	1.3	1.00E-37	AL163281.2	NT	Homo sapiens chromosome 21 segment HS21C081
3878	9014	14109	22.5	1.00E-37	AF189011.1	NT	Homo sapiens ribonuclease III (RN3) mRNA, complete cds
2135	7245	12452	1.4	7.00E-38	AW972825.1	EST_HUMAN	EST1384920 MAGE resequences, MAGL Homo sapiens cDNA
710	5864	11000	1.2	5.00E-38	AW971819.1	EST_HUMAN	EST1383908 MAGE resequences, MAGL Homo sapiens cDNA
2404	7503	12710	0.7	5.00E-38	AJ237740.1	NT	Homo sapiens RIBL1F gene (partial), exon 8
113	5314	10441	2.6	4.00E-38	Z25466.1	NT	B.taurus mitochondrial aspartate aminotransferase mRNA, complete CDS
113	5314	10442	2.6	4.00E-38	Z25466.1	NT	B.taurus mitochondrial aspartate aminotransferase mRNA, complete CDS
1783	6803		1.4	4.00E-38	AA562476.1	EST_HUMAN	m54112.s1 NCL_CGAP_Kid6 Homo sapiens cDNA clone IMAGE:1087727 3'
2053	7165		1.6	3.00E-38	AF003530.1	NT	Homo sapiens homeobox protein CDX4 (CDX4) gene, complete cds and flanking repeat regions

Table 4

3638	8777	14012	1.1	3.00E-38	7549807	NT	Homo sapiens HIRA interacting protein 4 (dnal-like) (HIRP4), mRNA
3781	8918	14013	1.7	3.00E-38	P53538	SWISSPROT	SSU72 PROTEIN
3781	8918	14013	1.7	3.00E-38	P53538	SWISSPROT	SSU72 PROTEIN
4513	8632		0.9	3.00E-38	BE279301.1	EST_HUMAN	601157633F1 NIH MGC 21 Homo sapiens cDNA clone IMAGE:3504272 5'
44	5254	10368	1.4	2.00E-38	AL163248.2	NT	Homo sapiens chromosome 21 segment HS21C048
1358	8486	11652	0.9	2.00E-38	5902097	NT	Homo sapiens SMT3 (suppressor of mit two 3, yeast) homolog 2 (SMT3H2), mRNA
							zw30d01.r1 Soares ovary tumor NbHOT Homo sapiens cDNA clone IMAGE:770785 5' similar to SW:MA12_RABIT P45701 MANNOSYL-OLIGOSACCHARIDE ALPHA-1,2-
							MANNOSIDASE :
1627	6753	11922	0.6	2.00E-38	AA437353.1	EST_HUMAN	zw30d01.r1 Soares ovary tumor NbHOT Homo sapiens cDNA clone IMAGE:770785 5' similar to SW:MA12_RABIT P45701 MANNOSYL-OLIGOSACCHARIDE ALPHA-1,2-
							MANNOSIDASE :
1627	6753	11923	0.6	2.00E-38	AA437353.1	EST_HUMAN	zw30d01.r1 Soares fetal lung NBHL18W Homo sapiens cDNA clone IMAGE:300174 5'
2560	7673	12875	0.7	2.00E-38	W07055.1	EST_HUMAN	to SW:MA12_RABIT P45701 MANNOSYL-OLIGOSACCHARIDE ALPHA-1,2-
							MANNOSIDASE :
1077	6215		0.8	1.00E-38	AA401570.1	EST_HUMAN	zw30d01.r1 Soares fetal lung NBHL18W Homo sapiens cDNA clone IMAGE:300174 5'
1954	7071	12268	0.9	1.00E-38	4885288	NT	contains element MER19 repetitive element :
1973	7088	12290	1.0	1.00E-38	7661869	NT	contains element MER19 repetitive element :
2016	7129	12329	0.8	1.00E-38	7662129	NT	contains element MER19 repetitive element :
2445	7544	12753	0.6	1.00E-38	AF270831.1	NT	Homo sapiens KIAA0443 gene product (KIAA0443), mRNA
4063	9190	14275	1.4	1.00E-38	AB037863.1	NT	Homo sapiens cyclin K (CCNK) gene, exon 7
							Homo sapiens mRNA for KIAA1442 protein, partial cds
							Homo sapiens low density lipoprotein receptor-related protein 6 (LRP6) mRNA, and translated products
4223	9347	14428	0.8	1.00E-38	4505016	NT	Homo sapiens chromosome 21 segment HS21C003
4229	9353	14434	1.3	1.00E-38	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
4229	9353	14435	1.3	1.00E-38	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
4483	9613	14705	1.2	1.00E-38	8922543	NT	Homo sapiens hypothetical protein FLJ10600 (FLJ10600), mRNA
							Homo sapiens ATPase, H+ transporting, lysosomal (vacuolar proton pump) 16kD (ATP6C) mRNA
48	5258	10374	1.8	8.00E-39	4502312	NT	Homo sapiens estrogen receptor-binding fragment-associated gene 9 (EBAG9) mRNA
1372	6500	11866	0.6	8.00E-39	4758229	NT	Homo sapiens estrogen receptor-binding fragment-associated gene 9 (EBAG9) mRNA
							wh53f10.x1 NC1_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2384491 3' similar to TR:P87890 P87890 POL. PROTEIN :
1768	6908		1.1	8.00E-39	AI823404.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C027
2047	7160	12384	2.0	7.00E-39	AL163227.2	NT	Homo sapiens chromosome 21 segment HS21C027
							Homo sapiens X-linked anhidrotic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions
891	6134	11289	1.3	5.00E-39	AF003528.1	NT	flanking repeat regions
							at36b04.x1 Baitaid colon HPLRB7 Homo sapiens cDNA clone IMAGE:2374063 3' similar to TR:Q15408 Q15408 NEUTRAL PROTEASE LARGE SUBUNIT :contains LTR.11 LTR7
2957	8108	13214	5.1	5.00E-39	AI750154.1	EST_HUMAN	repetitive element :
536	5701	10623	3.6	4.00E-39	AB015610.1	NT	Chlorococcus aethiops mRNA for ribosomal protein S4X, complete cds
3525	8686	13770	1.0	4.00E-39	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
							hm1c16 Regional genomic DNA specific cDNA library Homo sapiens cDNA clone CR12-1
41	5251	10362	3.8	3.00E-39	AA631949.1	EST_HUMAN	

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Table 4

2061	7173	1.0	4.00E-40	AF003528.1	NT	Homo sapiens X-linked anhidrotic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions
4291	9415	7.9	4.00E-40	7662117	NT	Homo sapiens KIAA0433 protein (KIAA0433), mRNA
1673	6797	0.5	3.00E-40	7705948	NT	Homo sapiens rec (LOC51201), mRNA
2485	7582	0.6	3.00E-40	BE386406.1	EST_HUMAN	601273576F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3614635 5'
4040	9168	1.0	3.00E-40	A1925849.1	EST_HUMAN	wh1207.x1 NCI_CGAP_Kid1 Homo sapiens cDNA clone IMAGE:2380549 3'
322	5505	4.3	2.00E-40	A1223036.1	EST_HUMAN	ig52h08.x1 Scores 16515 NHT Homo sapiens cDNA clone IMAGE:1838847 3'
777	5929	0.9	2.00E-40	AW303868.1	EST_HUMAN	h24e10.x1 NCI_CGAP_U4 Homo sapiens cDNA clone IMAGE:2761098 3' similar to SW:RS5_MOUSE P97461.40S RIBOSOMAL PROTEIN S5.;
1633	6759	0.7	2.00E-40	AW684809.1	EST_HUMAN	EST376877 MAGE resequences, MAGH Homo sapiens cDNA
1633	6759	0.7	2.00E-40	AW684809.1	EST_HUMAN	EST376877 MAGE resequences, MAGH Homo sapiens cDNA
1892	7009	0.8	2.00E-40	4506186	NT	Homo sapiens proteasome (prosome, macropain) subunit, alpha type, 7 (PSMA7) mRNA, and translated products
1892	7009	0.8	2.00E-40	4506186	NT	Homo sapiens proteasome (prosome, macropain) subunit, alpha type, 7 (PSMA7) mRNA, and translated products
2026	7139	1.1	2.00E-40	A1968562.1	EST_HUMAN	w60a11.x1 NCI_CGAP_G06 Homo sapiens cDNA clone IMAGE:2514716 3' similar to TR:Q91829 Q91829 ZINC FINGER PROTEIN.;
2123	7233	0.9	2.00E-40	5453592	NT	Homo sapiens adenylyl cyclase-associated protein 2 (CAP2) mRNA
2333	7436	0.9	2.00E-40	A1277892.1	NT	Homo sapiens partial TTN gene for titin
2658	7747	1.1	2.00E-40	BE275932.1	EST_HUMAN	601121567F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3345784 5'
3087	8236	3.6	2.00E-40	5453592	NT	Homo sapiens adenylyl cyclase-associated protein 2 (CAP2) mRNA
3913	6759	6.4	2.00E-40	AW964909.1	EST_HUMAN	EST376877 MAGE resequences, MAGH Homo sapiens cDNA
3913	6759	6.4	2.00E-40	AW964909.1	EST_HUMAN	EST376877 MAGE resequences, MAGH Homo sapiens cDNA
4807	9917	1.5	2.00E-40	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080
4807	9917	1.5	2.00E-40	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080
865	6013	0.8	1.00E-40	AA225889.1	EST_HUMAN	nc08a09.s1 NCI_CGAP_P1 Homo sapiens cDNA clone IMAGE:1007608
2653	7742	0.7	1.00E-40	BE018348.1	EST_HUMAN	bb78a10.y1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3048570 5' similar to TR:Q9Z158 Q9Z158 SYNTAXIN 17.;
3256	8405	1.8	1.00E-40	4507142	NT	Homo sapiens sorting nexin 3 (SNX3) mRNA
4505	9624	6.3	1.00E-40	4508012	NT	Homo sapiens zinc finger protein 200 (ZNF200) mRNA, and translated products
4892	9999	0.9	1.00E-40	7705778	NT	Homo sapiens CGI-65 protein (LOC51103), mRNA
811	7800	0.8	7.00E-41	A1934364.1	EST_HUMAN	wp041004.x1 NCI_CGAP_Kid1 Homo sapiens cDNA clone IMAGE:2463895 3'
811	7800	0.8	7.00E-41	A1934364.1	EST_HUMAN	wp041004.x1 NCI_CGAP_Kid1 Homo sapiens cDNA clone IMAGE:2463895 3'
279	5466	0.6	6.00E-41	AB037163.1	NT	Homo sapiens DISC5 mRNA, complete cds
2064	7176	0.8	6.00E-41	7667042	NT	Homo sapiens Down syndrome candidate region 1 (DSCR1), mRNA
1761	6882	1.3	5.00E-41	T62628.1	EST_HUMAN	yc03e10.s1 Streptococcus pneumoniae (9332/10) Homo sapiens cDNA clone IMAGE:79626 3'
1957	7074	1.8	5.00E-41	AW843784.1	EST_HUMAN	CM4-CND044-210100-084-804 CND044 Homo sapiens cDNA
4018	9147	1.0	5.00E-41	4885636	NT	Homo sapiens target of myb1 (chicken) homolog (TOM1), mRNA
385	5554	0.7	4.00E-41	BE156318.1	EST_HUMAN	QV0-HT0367-150200-114-p09 HT0367 Homo sapiens cDNA

Table 4

1388	6515	11681	3.4	4.00E-41	AI027117.1	EST_HUMAN	ow45e06.s1 Soares_parityroid_tumor_NbHPA Homo sapiens cDNA clone IMAGE:1649794 3' similar to TR:000597 000597 CYTOCHROME C-LIKE POLYPEPTIDE; contains LTR5.b1 LTR5 repetitive element;
1388	6515	11682	3.4	4.00E-41	AI027117.1	EST_HUMAN	ow45e06.s1 Soares_parityroid_tumor_NbHPA Homo sapiens cDNA clone IMAGE:1649794 3' similar to TR:000597 000597 CYTOCHROME C-LIKE POLYPEPTIDE; contains LTR5.b1 LTR5 repetitive element;
1404	6531	11702	0.8	4.00E-41	AB008661.1	NT	Homo sapiens gene for activin receptor type IIb, complete cds
1618	6744	11912	3.1	4.00E-41	AI500406.1	EST_HUMAN	trn8cd4.x1 NCI CGAP Bm25 Homo sapiens cDNA clone IMAGE:2165958 3' similar to contains OFR.b1 OFR repetitive element;
2859	8010	13110	3.0	4.00E-41	AJ229041.1	NT	Homo sapiens 959 kb contig between AML1 and CBR1 on chromosome 21q22; segment 1/3
2859	8010	13111	3.0	4.00E-41	AJ229041.1	NT	Homo sapiens 959 kb contig between AML1 and CBR1 on chromosome 21q22; segment 1/3
4052	9179	14262	1.9	4.00E-41	X92685.1	NT	H.sapiens DNase I hypersensitive site (HSS-3) enhancer element
932	6079	11236	0.6	3.00E-41	AB030178.1	NT	Homo sapiens PAD-H19 mRNA for peptidylarginine deiminase type II, complete cds
4240	9365	14446	3.1	3.00E-41	AB026896.1	NT	Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)
5047	10147	11837	0.9	3.00E-41	AB037748.1	NT	Homo sapiens mRNA for KIAA1327 protein, partial cds
1782	6667	11837	2.6	2.00E-41	U43701.1	NT	Human ribosomal protein L23a mRNA, complete cds
1915	7032	12220	0.8	2.00E-41	AA331940.1	EST_HUMAN	EST35818 Embryo, 8 week 1 Homo sapiens cDNA 5' end
2172	7281	12494	1.0	2.00E-41	AJ271366.1	NT	Homo sapiens mRNA for putative adaptor protein (GRB10 gene)
2221	7328	12542	1.5	2.00E-41	X89631.1	NT	G.gorilla DNA for ZNF80 gene homolog
2798	6667	11837	1.9	2.00E-41	U43701.1	NT	Human ribosomal protein L23a mRNA, complete cds
4521	9640	14731	1.1	2.00E-41	AL163267.2	NT	Homo sapiens chromosome 21 segment HS21C067
4521	9640	14732	1.1	2.00E-41	AL163267.2	NT	Homo sapiens chromosome 21 segment HS21C067
4465	9585	14681	4.6	1.00E-41	6678468	NT	Mus musculus tubulin alpha 6 (Tuba6), mRNA
455	5621	10748	1.8	8.00E-42	AF003530.1	NT	Homo sapiens homeobox protein CDX4 (CDX4) gene, complete cds and flanking repeat regions
2062	7174	12381	1.3	8.00E-42	AB026898.1	NT	Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)
636	5795	10918	4.1	7.00E-42	AF052051.1	NT	ORCTL4 genes, complete cds
636	5795	10919	4.1	7.00E-42	AF052051.1	NT	Homo sapiens glutathione transferase A4 gene, exon 1
916	6062		0.6	7.00E-42	AL163285.2	NT	Homo sapiens chromosome 21 segment HS21C085
1812	6931	12118	1.2	6.00E-42	AF012872.1	NT	Homo sapiens phosphatidylinositol 4-kinase 230 (p4K230) mRNA, complete cds
1812	6931	12119	1.2	6.00E-42	AF012872.1	NT	Homo sapiens phosphatidylinositol 4-kinase 230 (p4K230) mRNA, complete cds
2244	7350		1.3	6.00E-42	AW236656.1	EST_HUMAN	xp2808.x1 NCI CGAP HN10 Homo sapiens cDNA clone IMAGE:2741799 3' similar to contains L1.11 L1 repetitive element;
4936	10042		1.0	6.00E-42	AI284770.1	EST_HUMAN	qu24109.x1 NCI CGAP B12 Homo sapiens cDNA clone IMAGE:1965761 similar to contains Alu repetitive element;
131	5327		1.9	5.00E-42	AJ271735.1	NT	Alu repetitive element;
431	5598	10728	1.2	5.00E-42	BE217913.1	EST_HUMAN	Homo sapiens Xq pseudautosomal region, segment 1/2
							h31e11.x1 NCI CGAP LU24 Homo sapiens cDNA clone IMAGE:3175052 3'



Table 4

478	5844	1.0	5.00E-42	5730038	NT	Homo sapiens SET domain and mariner transposase fusion gene (SETMAR) mRNA
479	5645	1.3	5.00E-42	5730038	NT	Homo sapiens SET domain and mariner transposase fusion gene (SETMAR) mRNA
4884	9992	1.1	5.00E-42	AI541305.1	EST_HUMAN	pect.2-4-F08.r ecionom Homo sapiens cDNA 5'
736	5890	3.0	4.00E-42	AF050086.1	NT	Homo sapiens MHC class 1 region
736	5890	3.0	4.00E-42	AF050086.1	NT	Homo sapiens MHC class 1 region
1050	6189	0.9	4.00E-42	AF189011.1	NT	Homo sapiens ribonuclease III (RN3) mRNA, complete cds
4100	9226	1.8	4.00E-42	X55417.1	NT	H.sapiens PROS-27 mRNA
4156	9282	4.5	4.00E-42	4508496	NT	Homo sapiens regulatory factor X, 4 (influences HLA class II expression) (RFx4) mRNA
4480	9600	10.3	4.00E-42	4508008	NT	Homo sapiens zinc finger protein 177 (ZNF177) mRNA
98	5306	1.0	3.00E-42	AA486105.1	EST_HUMAN	ab14e10.s1 StrataGene lung (#937210) Homo sapiens cDNA clone IMAGE:840810 3' similar to contains THR12 THR repetitive element;
2361	7463	1.4	2.00E-42	AW898344.1	EST_HUMAN	RC3-NN0070-270400-011-h10 NN0070 Homo sapiens cDNA
2375	7477	0.8	2.00E-42	AW250059.1	EST_HUMAN	2819293.3pHme NIH MGC_7 Homo sapiens cDNA clone IMAGE:2819293 3'
717	5870	1.1	1.00E-42	X57147.1	NT	Human endogenous retrovirus pHE.1 (ERV9)
1026	6166	1.0	1.00E-42	AW295809.1	EST_HUMAN	U1-H-B1t-afn-e-04-U1.s1 NC1_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2721871 3'
1085	6223	1.1	1.00E-42	AJ251818.1	NT	Homo sapiens partial C9 gene for complement component C9, exon 1
1085	6223	1.1	1.00E-42	AJ251818.1	NT	Homo sapiens partial C9 gene for complement component C9, exon 1
1085	6223	1.1	1.00E-42	AJ251818.1	NT	Homo sapiens NADH-ubiquinone oxidoreductase AGGG subunit precursor homolog mRNA, nuclear gene encoding mitochondrial protein, complete cds
1222	7910	4.4	1.00E-42	AF067166.1	NT	Homo sapiens NADH-ubiquinone oxidoreductase AGGG subunit precursor homolog mRNA, nuclear gene encoding mitochondrial protein, complete cds
1222	7910	4.4	1.00E-42	AF067166.1	NT	Homo sapiens PDNP1 gene, exon 17
1222	7910	4.4	1.00E-42	AF067166.1	NT	Homo sapiens PDNP1 gene, exon 17
1986	7101	0.9	1.00E-42	AF110296.1	NT	Homo sapiens major histocompatibility complex, class II, DM alpha (HLA-DMA) mRNA
2497	7594	0.7	1.00E-42	5174458	NT	Homo sapiens origin recognition complex, subunit 5 (yeast homolog)-like (ORCSL) mRNA, and translated products
2935	8086	8.9	1.00E-42	4505524	NT	Homo sapiens KIAA0255 gene product (KIAA0255), mRNA
3647	8786	2.2	1.00E-42	7662027	NT	Homo sapiens KIAA0255 gene product (KIAA0255), mRNA
3849	8985	1.0	1.00E-42	AL163267.2	NT	Homo sapiens chromosome 21 segment HS21C067
4153	9279	1.7	1.00E-42	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080
4489	9609	0.9	1.00E-42	AW813617.1	EST_HUMAN	RC3-ST0197-161099-012-a03 ST0197 Homo sapiens cDNA
4640	9754	2.9	1.00E-42	5603122	NT	Homo sapiens proteasome inhibitor (Pi31), mRNA
4640	9754	2.9	1.00E-42	5603122	NT	Homo sapiens proteasome inhibitor (Pi31), mRNA
4669	9781	5.4	1.00E-42	4506758	NT	Homo sapiens ryanodine receptor 3 (RYR3) mRNA
4769	9880	1.2	1.00E-42	AB033114.1	NT	Homo sapiens mRNA for KIAA1268 protein, partial cds
5048	10148	1.0	1.00E-42	4501912	NT	Homo sapiens a disintegrin and metalloproteinase domain 23 (ADAM23) mRNA
5048	10148	1.0	1.00E-42	4501912	NT	Homo sapiens a disintegrin and metalloproteinase domain 23 (ADAM23) mRNA
665	5840	1.5	8.00E-43	8923276	NT	Homo sapiens hypothetical protein FLJ20297 (FLJ20297), mRNA
665	5840	1.5	8.00E-43	8923276	NT	Homo sapiens hypothetical protein FLJ20297 (FLJ20297), mRNA
665	5840	1.5	8.00E-43	8923276	NT	Homo sapiens hypothetical protein FLJ20297 (FLJ20297), mRNA
685	5840	1.5	8.00E-43	8923276	NT	Homo sapiens hypothetical protein FLJ20297 (FLJ20297), mRNA
3589	8728	6.1	7.00E-43	AW246442.1	EST_HUMAN	2822251.5pHme NIH MGC_7 Homo sapiens cDNA clone IMAGE:2822251 5'

Table 4

1320	6449		3.7	6.00E-43	AA91890.1	EST_HUMAN	ne72406.s1 NCI_CGAP_Ew1 Homo sapiens cDNA clone IMAGE:309803 similar to gp1:05095 60S RIBOSOMAL PROTEIN L30 (HUMAN);
137	5333		0.7	5.00E-43	AL163213.2	NT	Homo sapiens chromosome 21 segment HS21C013
494	5659	10781	1.0	5.00E-43	AA382780.1	EST_HUMAN	EST196033 Testis 1 Homo sapiens cDNA 5' end
957	7865	11260	1.7	4.00E-43	AF003528.1	NT	Homo sapiens X-linked anhidrotic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions
714	5866	11006	3.3	3.00E-43	AA083568.1	EST_HUMAN	zn09109.s1 Striatogene hNT neuron (#937233) Homo sapiens cDNA clone IMAGE:546977 3' similar to TR:G1136285 G1136285 UDP-GALNAC:POLYPEPTIDE N-ACETYL GALACTOSAMINYLTRANSFERASE. [1];
1195	6327		1.0	3.00E-43	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
1669	6793	11969	0.5	3.00E-43	X97869.1	NT	H.sapiens gene encoding La autoantigen
3524	8665	13769	1.1	3.00E-43	S69002.1	NT	AML1-EV1-1=AML1-EV1-1 fusion protein (rearranged translocation) [human, leukemic cell line SKH1, mRNA Nidant, 5838 nt]
4193	9319	14404	1.0	3.00E-43	AA548154.1	EST_HUMAN	ms5506.s1 NCI_CGAP_P77 Homo sapiens cDNA clone IMAGE:1017419
177	5370		1.5	2.00E-43	AI190764.1	EST_HUMAN	q661c09.x1 Soares Testis, NHT Homo sapiens cDNA clone IMAGE:1733968 3' similar to contains PTR7 13 PTR7 PTR7 repetitive element;
1630	6756	11926	1.1	1.00E-43	AF154536.1	NT	Homo sapiens Ras-like GTP-binding protein (RAB27A) gene, exons 1b and 2
1630	6756	11927	1.1	1.00E-43	AF154536.1	NT	Homo sapiens Ras-like GTP-binding protein (RAB27A) gene, exons 1b and 2
1678	6802	11982	1.2	1.00E-43	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
872	6020	11180	2.0	8.00E-44	AI222985.1	EST_HUMAN	q123q01.x1 Soares NFL_T GBC S1 Homo sapiens cDNA clone IMAGE:1845552 3'
872	6020	11181	2.0	8.00E-44	AI222985.1	EST_HUMAN	q123q01.x1 Soares NFL_T GBC S1 Homo sapiens cDNA clone IMAGE:1845552 3'
643	5802		0.9	7.00E-44	RO6035.1	EST_HUMAN	y689601.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:124920 5'
2187	7296	12510	1.2	7.00E-44		5031886 NT	Homo sapiens LIM domain-containing preferred translocation partner in lipoma (LPP) mRNA
2937	8086	13195	2.2	7.00E-44	AF048729.1	NT	Homo sapiens minisatellite ms32 repeat region
2937	8086	13196	2.2	7.00E-44	AF048729.1	NT	Homo sapiens minisatellite ms32 repeat region
3786	8923	14017	2.3	7.00E-44	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
4148	9274	14353	1.2	7.00E-44	AF231919.1	NT	Homo sapiens chromosome 21 unknown mRNA
4148	9274	14354	1.2	7.00E-44	AF231919.1	NT	Homo sapiens chromosome 21 unknown mRNA
300	5486		0.9	5.00E-44	AI289880.1	NT	Homo sapiens KIAA0851 gene (partial), X73 gene and LZTFL1 gene
329	5510		0.7	5.00E-44	AI289880.1	NT	Homo sapiens KIAA0851 gene (partial), X73 gene and LZTFL1 gene
3366	8511	13618	2.9	4.00E-44	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103
1746	6868		1.1	3.00E-44		6912477 NT	Homo sapiens karyopherin alpha 6 (importin alpha 7) (KPNA6), mRNA
3059	8210	13309	5.1	3.00E-44	AA169851.1	EST_HUMAN	zp18b05.r1 Striatogene fetal retina 937202 Homo sapiens cDNA clone IMAGE:509777 5'
3396	8538	13844	1.5	3.00E-44	AA663268.1	EST_HUMAN	ae92b04.s1 Striatogene schizy brain S11 Homo sapiens cDNA clone IMAGE:1020367 3'
3396	8538	13845	1.5	3.00E-44	AA663268.1	EST_HUMAN	ae92b04.s1 Striatogene schizy brain S11 Homo sapiens cDNA clone IMAGE:1020367 3'
861	6029		1.4	2.00E-44	W28189.1	EST_HUMAN	43-65 Human retina cDNA randomly primed sublibrary Homo sapiens cDNA
1033	6173	11325	0.9	2.00E-44		4826865 NT	Homo sapiens DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 1 (DDX1) mRNA

Table 4

1033	6173	11326	0.9	2.00E-44	4826865	NT	Homo sapiens DEAD/4 (Asp-Glu-Ala-Asp/His) box polypeptide 1 (DDX1) mRNA
1189	6321	11477	1.6	2.00E-44	5803200	NT	Homo sapiens transmembrane trafficking protein (TMP21), mRNA
1189	6321	11478	1.6	2.00E-44	5803200	NT	Homo sapiens transmembrane trafficking protein (TMP21), mRNA
1290	6419	11584	1.0	2.00E-44	AF133568.1	NT	Homo sapiens RAB38 (RAB38) mRNA, complete cds
1346	6474	11640	0.5	2.00E-44	BE465325.1	EST_HUMAN	hw14g06.x1 NCI CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3182938 3' similar to SW:OXYB_HUMAN P22059 OXYSTEROL-BINDING PROTEIN.
2105	7216	12426	0.7	2.00E-44	AF070651.1	NT	Homo sapiens tissue-type bone marrow zinc finger protein 4 mRNA, complete cds
2529	7625	12826	1.1	2.00E-44	D25303.1	NT	Human mRNA for integrin alpha subunit, complete cds
2567	7660		1.2	2.00E-44	5901933	NT	Homo sapiens adaptor-related protein complex 4, sigma 1 subunit (CLAPS4), mRNA
3425	8567	13679	1.4	2.00E-44	D87875.1	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
4468	9588	14684	1.8	2.00E-44	AW664379.1	EST_HUMAN	PM4-SN0018-120500-003-804 SN0016 Homo sapiens cDNA
46	5256	10371	1.2	1.00E-44	7657334	NT	Homo sapiens Missense/NIK-related kinase (MINIK), mRNA
46	5256	10372	1.2	1.00E-44	7657334	NT	Homo sapiens Missense/NIK-related kinase (MINIK), mRNA
566	5727	10844	0.6	1.00E-44	AW853132.1	EST_HUMAN	RC1-CT0249-030300-026-112 CT0249 Homo sapiens cDNA
1179	6312		0.5	1.00E-44	AW984803.1	EST_HUMAN	RC1-BN0039-110300-012-401 BN0039 Homo sapiens cDNA
1555	6682		2.0	1.00E-44	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103
2177	7286	12497	1.3	1.00E-44	AAA34554.1	EST_HUMAN	zms53402.r1 Soares, total, fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:773763 5' similar to contains THR13 THR repetitive element;
2177	7286	12498	1.3	1.00E-44	AAA34554.1	EST_HUMAN	zms53402.r1 Soares, total, fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:773763 5' similar to contains THR13 THR repetitive element;
2237	7938	12556	1.1	1.00E-44	AA398099.1	EST_HUMAN	z188g11.r1 Soares, testis_NHT Homo sapiens cDNA clone IMAGE:729476 5'
2732	7916	13021	1.4	1.00E-44	AF196779.1	NT	Homo sapiens transcription factor IGHM enhancer 3, JM11 protein, JM4 protein, JM5 protein, T54 protein, JM10 protein, A4 differentiation-dependent protein, triple LIM domain protein 6, and synapophysin genes, complete cds; and L-type calcium channel a2>
3664	8803		5.1	1.00E-44	AA455889.1	EST_HUMAN	aa01cd9.s1 Soares, NHMPU, S1 Homo sapiens cDNA clone IMAGE:811964 3'
5061	10159	15234	0.8	1.00E-44	AJ130785.1	NT	Homo sapiens alpha satellite DNA, M1 monomer type
5081	10159	15235	0.8	1.00E-44	AJ130785.1	NT	Homo sapiens alpha satellite DNA, M1 monomer type
4476	9596	14691	1.7	9.00E-45	8922391	NT	Homo sapiens hypothetical protein FLJ10379 (FLJ10379), mRNA
4476	9596	14692	1.7	9.00E-45	8922391	NT	Homo sapiens hypothetical protein FLJ10379 (FLJ10379), mRNA
2477	7575	12777	1.4	8.00E-45	5174718	NT	Homo sapiens TRK-fused gene (NOTE: non-standard symbol and name) (TFG) mRNA
5015	10117	15188	7.5	8.00E-45	5174718	NT	Homo sapiens TRK-fused gene (NOTE: non-standard symbol and name) (TFG) mRNA
3896	9031		5.3	6.00E-45	AW157670.1	EST_HUMAN	au83h07.x1 Schneller fetal brain 00004 Homo sapiens cDNA clone IMAGE:2782909 3'
874	6022		1.1	5.00E-45	AL163203.2	NT	similar to SW:R13A_HUMAN P40429 60S RIBOSOMAL PROTEIN L13A;
3173	8322	13436	2.0	5.00E-45	A1523766.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C003
1127	6263	11415	3.1	4.00E-45	X95826.1	NT	ig94i07.x1 NCI CGAP CLL1 Homo sapiens cDNA clone IMAGE:2116453 3' similar to SW:PAX1_MOUSE P09084 PAIRED BOX PROTEIN PAX-1;
2246	7352	12559	0.7	4.00E-45	BE265622.1	EST_HUMAN	H. sapiens ART4 gene
1190	6322		0.9	3.00E-45	AW500307.1	EST_HUMAN	601194440F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3538425 5'
							UH-HF-BN0-akg-d-02-0-UI.r1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3077019 5'

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Table 4

4666	9778	14876	1.1	3.00E-46	Z73660.1	NT	H.sapiens Ig lambda light chain variable region gene (7C.11.2) germ-line; Ig-Light-Lambda; VLambda
819	5969	11126	2.0	2.00E-46	AA68646.1	EST_HUMAN	ne06a08.s1 NC1_CGAP_Co3 Homo sapiens cDNA clone IMAGE:880408 3' similar to contains THR.b2 THR repetitive element;
1542	6669		1.3	2.00E-46	AA678246.1	EST_HUMAN	z127a11.s1 Soares_fetal_liver_spleen_1NF.LS.S1 Homo sapiens cDNA clone IMAGE:431996 3'
1623	6749	11917	0.9	2.00E-46	U78027.1	NT	Homo sapiens Bruton's tyrosine kinase (BTK), alpha-D-galactosidase A (GLA), L44-like ribosomal protein (L44L) and FTP3 (FTP3) genes, complete cds
4199	9325	14412	1.0	2.00E-46	AF016191.1	NT	Rattus norvegicus podocytin channel (eng3) mRNA, complete cds
4899	10006	15087	1.2	2.00E-46	AA399286.1	EST_HUMAN	z159a02.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:726650 5' similar to SW:RSP1_MOUSE C01730 RSP-1 PROTEIN.;
1213	6343	11502	1.8	1.00E-46	4502694	NT	Homo sapiens cell division cycle 10 (homologous to CDC10 of S. cerevisiae) (CDC10) mRNA
2236	7343	12555	1.7	1.00E-46	AW878516.1	EST_HUMAN	EST390625 IMAGE resequenced, MAGP Homo sapiens cDNA
2351	7453	12660	0.9	1.00E-46	H97330.1	EST_HUMAN	EST48b095 WAT11 Homo sapiens cDNA clone 48b095
3211	8359	13468	2.8	1.00E-46	AA631912.1	EST_HUMAN	np78b02.s1 NC1_CGAP_P2 Homo sapiens cDNA clone IMAGE:1132395 similar to gb:XT6717 H.sapiens MT-11 mRNA. (HUMAN);
4772	9882		2.6	1.00E-46	AB023197.1	NT	Homo sapiens mRNA for KIAA0980 protein, partial cds
749	5901		1.5	9.00E-47	AJ271735.1	NT	Homo sapiens Xq pseudautosomal region, segment 1/2
4848	9955	15044	2.6	9.00E-47	AW770928.1	EST_HUMAN	h193a04.x1 NC1_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3009534 3' similar to TR:O76703 O75703 HYPOTHETICAL_12.4 KD PROTEIN.;
1766	6887	12071	5.1	8.00E-47	Y18538.1	NT	Homo sapiens HLA-C gene, exon 5, individual 18323
1766	6887	12072	5.1	8.00E-47	Y18536.1	NT	Homo sapiens HLA-C gene, exon 5, individual 18323
2684	7771	12971	0.6	8.00E-47	5453955	NT	Homo sapiens protein phosphatase 2, regulatory subunit B (B56), epsilon isoform (PPP2R5E) mRNA
2689	8141	13244	1.7	8.00E-47	AJ229043.1	NT	Homo sapiens 959 kb contig between AML1 and CBR1 on chromosome 21q22, segment 3/3
693	5948	10983	2.0	6.00E-47	7705390	NT	Homo sapiens H91620p protein (H91620p) mRNA
2501	7598	12798	1.1	6.00E-47	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
1379	6508	11672	1.2	4.00E-47	4557556	NT	Homo sapiens E1A binding protein p300 (EP300) mRNA
171	7882		0.6	3.00E-47	BE385682.1	EST_HUMAN	601278193r1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3618934 5'
801	5952	11103	1.8	3.00E-47	N57483.1	EST_HUMAN	yy54b04.s1 Soares_multiple_sclerosis_2NbhMSP Homo sapiens cDNA clone IMAGE:277327 3'
930	6077	11235	3.0	3.00E-47	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
1984	7099	12302	0.5	3.00E-47	AB007899.1	NT	Homo sapiens KIAA0439 mRNA, partial cds
3235	8383	13489	5.1	3.00E-47	AA304095.1	EST_HUMAN	EST16895 Aorta endothelial cells, TNF alpha-treated Homo sapiens cDNA 5' end similar to similar to metalloproteinase 1
3865	9021		5.0	3.00E-47	U93161.1	NT	Homo sapiens nuclear dual-specificity phosphatase (SBF1) mRNA, partial cds
4265	9390	14473	1.0	3.00E-47	IM12959.1	NT	Human T-cell receptor active alpha-chain mRNA from JM cell line, complete cds
142	5338	10468	1.5	2.00E-47	4505318	NT	Homo sapiens myosin phosphatase, target subunit 2 (MYPT2), mRNA
952	6096	11254	0.7	2.00E-47	AL163209.2	NT	Homo sapiens chromosome 21 segment HS21C009

Table 4

952	6098	11255	0.7	2.00E-47	AL163209.2	NT	Homo sapiens chromosome 21 segment HS21C009
1548	6675		1.2	2.00E-47	AI989279.1	EST_HUMAN	wg98b02.x1 NCI CGAP GC8 Homo sapiens cDNA clone IMAGE:247985 3'
1575	6701	11870	1.2	2.00E-47	7662109	NT	Homo sapiens KIAA0426 gene product (KIAA0426), mRNA
1654	6779	11952	1.6	2.00E-47	AA524514.1	EST_HUMAN	ng43h12.s1 NCI CGAP C03 Homo sapiens cDNA clone IMAGE:937607 3'
2185	7294	12506	0.8	2.00E-47	AF060568.1	NT	Homo sapiens promyelocytic leukemia zinc finger protein (PLZF) gene, complete cds
2620	7710	12910	0.6	2.00E-47	AA077092.1	EST_HUMAN	7B07G09 Chromosome 7 Fetal Brain cDNA Library Homo sapiens cDNA clone 7B07G09
4251	9376	14456	1.7	2.00E-47	4504866	NT	Homo sapiens ring finger protein (C3HC4 type) 8 (RNF8), mRNA
4287	9412	14499	1.8	2.00E-47	AA569592.1	EST_HUMAN	n123g07.s1 NCI CGAP P1 Homo sapiens cDNA clone IMAGE:914652
4287	9412	14500	1.8	2.00E-47	AA569592.1	EST_HUMAN	n123g07.s1 NCI CGAP P1 Homo sapiens cDNA clone IMAGE:914652
4406	9526	14616	2.1	2.00E-47	5174648	NT	Homo sapiens Rev/Rex activation domain binding protein-related (RAB-R) mRNA
4707	9819	14916	1.1	2.00E-47	AW985166.1	EST_HUMAN	EST377239 IMAGE resequences, MAGI Homo sapiens cDNA
1383	6510	11674	1.6	1.00E-47	AI333429.1	EST_HUMAN	qp99h03.x1 Soares_fetal_lung_NbHL19W Homo sapiens cDNA clone IMAGE:1931189 3'
3749	8887	13975	0.8	1.00E-47	BE280477.1	EST_HUMAN	601155321F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3138893 5'
3749	8887	13976	0.8	1.00E-47	BE280477.1	EST_HUMAN	601155321F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3138893 5'
5008	10110	15180	2.6	1.00E-47	AW813906.1	EST_HUMAN	RC3-ST0197-130400-017A02 ST0197 Homo sapiens cDNA
1595	6721	11890	0.9	9.00E-48	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
1230	6360		0.5	8.00E-48	4501900	NT	Homo sapiens aminocyclase 1 (ACY1), mRNA
1231	6360		1.5	8.00E-48	4501900	NT	Homo sapiens aminocyclase 1 (ACY1), mRNA
3096	8247	13350	3.6	8.00E-48	AW768477.1	EST_HUMAN	h61b103.x1 NCI CGAP Lym12 Homo sapiens cDNA clone IMAGE:3001133 3' similar to gb:X64707 BREAST BASIC CONSERVED PROTEIN 1 (HUMAN);
3096	8247	13351	3.6	8.00E-48	AW768477.1	EST_HUMAN	gb:X64707 BREAST BASIC CONSERVED PROTEIN 1 (HUMAN);
482	5648		1.4	7.00E-48	AB033035.1	NT	g61b103.x1 NCI CGAP Lym12 Homo sapiens cDNA clone IMAGE:3001133 3' similar to gb:X64707 BREAST BASIC CONSERVED PROTEIN 1 (HUMAN);
483	5648		4.6	7.00E-48	AB033035.1	NT	g61b103.x1 NCI CGAP Lym12 Homo sapiens cDNA clone IMAGE:3001133 3' similar to gb:X64707 BREAST BASIC CONSERVED PROTEIN 1 (HUMAN);
1482	6609	11782	1.1	7.00E-48	6912719	NT	g61b103.x1 NCI CGAP Lym12 Homo sapiens cDNA clone IMAGE:3001133 3' similar to gb:X64707 BREAST BASIC CONSERVED PROTEIN 1 (HUMAN);
1620	6746	11914	1.3	7.00E-48	5730038	NT	g61b103.x1 NCI CGAP Lym12 Homo sapiens cDNA clone IMAGE:3001133 3' similar to gb:X64707 BREAST BASIC CONSERVED PROTEIN 1 (HUMAN);
1551	6678	11846	0.8	6.00E-48	AF163441.1	NT	g61b103.x1 NCI CGAP Lym12 Homo sapiens cDNA clone IMAGE:3001133 3' similar to gb:X64707 BREAST BASIC CONSERVED PROTEIN 1 (HUMAN);
3269	10295	13521	1.4	5.00E-48	4828891	NT	g61b103.x1 NCI CGAP Lym12 Homo sapiens cDNA clone IMAGE:3001133 3' similar to gb:X64707 BREAST BASIC CONSERVED PROTEIN 1 (HUMAN);
1498	6624		1.3	4.00E-48	AA157453.1	EST_HUMAN	z055c04.s1 Striatum pancreas (#937208) Homo sapiens cDNA clone IMAGE:590790 3'
1933	7050	12242	6.9	3.00E-48	4885170	NT	similar to contains L1.13 L1 repetitive element;
1933	7050	12243	6.9	3.00E-48	4885170	NT	similar to contains L1.13 L1 repetitive element;
3579	8718	13816	0.9	3.00E-48	AW664531.1	EST_HUMAN	Homo sapiens chromosome X open reading frame 6 (CXORF6) mRNA
39	5248	10359	1.2	2.00E-48	AA631940.1	EST_HUMAN	Homo sapiens chromosome X open reading frame 6 (CXORF6) mRNA
1752	6874	12054	0.9	2.00E-48	AA348396.1	EST_HUMAN	h114b12.x1 NCI CGAP GU1 Homo sapiens cDNA clone IMAGE:2972255 3' similar to SW:DCRB_HUMAN P56655 DOWN SYNDROME CRITICAL REGION PROTEIN B.;
1752	6874	12055	0.9	2.00E-48	AA348396.1	EST_HUMAN	h114b12.x1 NCI CGAP GU1 Homo sapiens cDNA clone IMAGE:2972255 3' similar to SW:DCRB_HUMAN P56655 DOWN SYNDROME CRITICAL REGION PROTEIN B.;

Table 4

4431	9552	14846	1.4	2.00E-48	BE245065.1	EST_HUMAN	TCBAP1D3842 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project=TCBA Homo sapiens cDNA clone TCBAP3842
50	5259	10376	0.9	1.00E-48	7706534	NT	Homo sapiens desipalin resistance-associated overexpressed protein (LOC51747), mRNA
855	6004	11164	2.4	1.00E-48	4502166	NT	Homo sapiens amyloid beta (A4) precursor protein (protease nexin-II, Alzheimer disease) (APP), mRNA
1274	6404	11564	1.1	1.00E-48	5032032	NT	Homo sapiens RNA binding motif protein 6 (RBM6) mRNA
1876	6994	12180	16.0	1.00E-48	AL163302.2	NT	Homo sapiens chromosome 21 segment HS21C102
3443	8585	13699	1.2	1.00E-48	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
5082	10180	15260	1.1	1.00E-48	M10976.1	NT	Human endogenous retroviral DNA (4-1), complete retroviral segment
134	5557	10689	1.5	7.00E-49	5729990	NT	Homo sapiens proteasome (prosome, macropain) 26S subunit, ATPase, 4 (PSMC4) mRNA
134	5557	10690	1.5	7.00E-49	5729990	NT	Homo sapiens proteasome (prosome, macropain) 26S subunit, ATPase, 4 (PSMC4) mRNA
388	5557	10689	0.6	7.00E-49	5729990	NT	Homo sapiens proteasome (prosome, macropain) 26S subunit, ATPase, 4 (PSMC4) mRNA
388	5557	10690	0.6	7.00E-49	5729990	NT	Homo sapiens proteasome (prosome, macropain) 26S subunit, ATPase, 4 (PSMC4) mRNA
389	5557	10689	0.7	7.00E-49	5729990	NT	Homo sapiens proteasome (prosome, macropain) 26S subunit, ATPase, 4 (PSMC4) mRNA
389	5557	10690	0.7	7.00E-49	5729990	NT	Homo sapiens proteasome (prosome, macropain) 26S subunit, ATPase, 4 (PSMC4) mRNA
1202	6334	11490	1.4	7.00E-49	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
2129	7239	12447	0.9	7.00E-49	TT5294.1	EST_HUMAN	yc89b07.r1 Soares Infant brain 1N1B Homo sapiens cDNA clone IMAGE:23223 5' similar to SP-ACUA_PENCH P36333 ACETYL-COENZYME A SYNTHETASE :
4550	9669	14759	1.0	7.00E-49	IO60811	SWISSPROT	HYPOTHETICAL PROTEIN DJ845024.3
190	5384	10511	4.0	6.00E-49	AW731740.1	EST_HUMAN	ba55g05.x1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:2900504 3' similar to gb:xi17206 40S RIBOSOMAL PROTEIN S4 (HUMAN); gb:M20632 Mouse LLRep3 protein mRNA from a repetitive element, complete (MOUSE):
4935	10041	15113	1.0	6.00E-49	AW801688.1	EST_HUMAN	IL5-UM0068-080400-057-c10 UM0068 Homo sapiens cDNA
695	5850	10984	1.2	5.00E-49	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
695	5850	10985	1.2	5.00E-49	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
1753	6875	12056	0.7	5.00E-49	AA172121.1	EST_HUMAN	z229c07.r1 Stratiogene neuroepithelium (#837231) Homo sapiens cDNA clone IMAGE:610860 5' similar to TR:G233226 G233226 RTVL-H PROTEIN : contains LTR7.13
2721	7805	13009	1.9	5.00E-49	U17714.1	NT	IMAGE:610860 5' similar to TR:G233226 G233226 RTVL-H PROTEIN : contains LTR7.13
514	5678	10796	13.0	4.00E-49	AW189533.1	EST_HUMAN	LTR7 LTR7 repetitive element :
548	5711	10830	0.9	3.00E-49	X68988.1	NT	Homo sapiens putative tumor suppressor ST13 (ST13) mRNA, complete cds
2611	7701		0.7	3.00E-49	AA016131.1	EST_HUMAN	X08801.x1 NCL_CGAP_U14 Homo sapiens cDNA clone IMAGE:2675593 3' similar to WP:BC0350.2B CE06703 :
							H sapiens mRNA for acetyl-CoA carboxylase
							za31c05.r1 Soares refina N264HR Homo sapiens cDNA clone IMAGE:360584 5' similar to contains L1.13 L1 repetitive element :

Table 4

4909	10016	15098	2.1	3.00E-49	U46999.1	NT	Human type IV collagen (COL4A6) gene, exon 40
645	5804		0.9	2.00E-49	BE166990.1	EST_HUMAN	MR3-HT0487-150200-113-g01 HT0487 Homo sapiens cDNA
3185	8334	13446	1.4	2.00E-49	N26446.1	EST_HUMAN	ly23d06.r1 Soares melanocyte 2NBHM Homo sapiens cDNA clone IMAGE:262571.5'
3521	8662	13767	0.9	2.00E-49	AF026564.1	NT	Homo sapiens RNA binding protein II (RBMII) gene, complete cds
							oz88d02.x1 Soares_senescent fibroblasts, NbHSF Homo sapiens cDNA clone IMAGE:1682403.3 similar to gb:U31470 RAS-LIKE PROTEIN TC10 (HUMAN); contains Alu repetitive element; contains element MER22 repetitive element;
4693	9805	14905	1.1	2.00E-49	A167357.1	EST_HUMAN	Homo sapiens DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 11 (S.cerevisiae CHL1-like helicase) (DDX11) mRNA
80	5286	10413	0.6	1.00E-49	4758135	NT	Homo sapiens DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 11 (S.cerevisiae CHL1-like helicase) (DDX11) mRNA
80	5286	10414	0.6	1.00E-49	4758135	NT	Homo sapiens DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 11 (S.cerevisiae CHL1-like helicase) (DDX11) mRNA
1760	8881	12063	0.9	1.00E-49	BE255216.1	EST_HUMAN	601115769F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3356273.5'
4923	10030		1.1	9.00E-50	AF101475.1	NT	Homo sapiens glycine N-methyltransferase (GNMT) gene, complete cds
163	5358	10483	0.9	8.00E-50	AL163202.2	NT	Homo sapiens chromosome 21 segment HS21C002
702	5857	10892	0.6	8.00E-50	X95097.2	NT	Homo sapiens mRNA for VIP receptor 2
702	5857	10893	0.6	8.00E-50	X95097.2	NT	Homo sapiens mRNA for VIP receptor 2
1016	6156		1.2	8.00E-50	AF000573.1	NT	Homo sapiens homogenisate 1,2-dioxygenase gene, complete cds
1727	6850	12029	0.9	8.00E-50	4501890	NT	Homo sapiens actinin, alpha 1 (ACTN1) mRNA
2324	7427	12637	1.1	8.00E-50	Y16641.1	NT	Rattus norvegicus mRNA for hnRNP protein, partial
2432	7531	12736	1.4	8.00E-50	7706394	NT	Homo sapiens p47 (LOC51674), mRNA
2432	7531	12737	1.4	8.00E-50	7706394	NT	Homo sapiens p47 (LOC51674), mRNA
2666	7753	12853	0.6	8.00E-50	4826658	NT	Homo sapiens capping protein (actin filament) muscle Z-line, beta (CAPZB), mRNA
603	5761	10881	1.0	7.00E-50	BE089591.1	EST_HUMAN	Q10-BT0703-280400-211-608 BT0703 Homo sapiens cDNA
4002	9133		10.0	5.00E-50	8822586	NT	Homo sapiens hypohelical protein FLJ10675 (FLJ10675), mRNA
899	6046		1.3	4.00E-50	AA601143.1	EST_HUMAN	no54e09.s1 NCI CGAP_S51 Homo sapiens cDNA clone IMAGE:1104520.3 similar to gb:X53741_mai FIBULIN-1, ISOFORM A PRECURSOR (HUMAN);
1896	7013		0.9	3.00E-50	M18048.1	NT	Human endogenous retrovirus RTVL-H2
3259	8406	13513	1.1	3.00E-50	AA746142.1	EST_HUMAN	ob03060.s1 NCI CGAP_K43 Homo sapiens cDNA clone IMAGE:1322627.3'
							CMVA5 Human cardiac muscle expression library Homo sapiens cDNA clone 4151935 similar to CMVA5 Cardiomypathy associated gene 5
3692	8831	13924	4.6	3.00E-50	AW755254.1	EST_HUMAN	CMVA5 Human cardiac muscle expression library Homo sapiens cDNA clone 4151935 similar to CMVA5 Cardiomypathy associated gene 5
761	5913		1.7	2.00E-50	AF055066.1	NT	Homo sapiens MHC class 1 region
1063	6201	11355	1.6	2.00E-50	4557752	NT	Homo sapiens MHC class 1 region
1425	6552	11729	6.5	2.00E-50	AF138303.1	NT	Homo sapiens midline 1 (Opitz/BBB syndrome) (MID1) mRNA
235	5426	10550	1.0	1.00E-50	BE007080.1	EST_HUMAN	Homo sapiens decorin D mRNA, complete cds, alternatively spliced
235	5426	10551	1.0	1.00E-50	BE007080.1	EST_HUMAN	PM3-BN0137-290300-002-g11 BN0137 Homo sapiens cDNA
454	5620	10747	0.7	1.00E-50	AL163209.2	NT	PM3-BN0137-290300-002-g11 BN0137 Homo sapiens cDNA
2314	7417		3.3	1.00E-50	AJ271735.1	NT	Homo sapiens chromosome 21 segment HS21C009
1476	6605		8.2	9.00E-51	Z12962.1	NT	Homo sapiens Xq pseudautosomal region; segment 1/2
26	5237	10342	0.6	8.00E-51	AA775999.1	EST_HUMAN	H.sapiens mRNA for homologue to yeast ribosomal protein L41
4467	9587	14683	4.9	8.00E-51	AA610842.1	EST_HUMAN	aa82g10.s1 Stralagene schizo brain S11 Homo sapiens cDNA clone IMAGE:970722.3'
							no88e09.s1 NCI CGAP_Lut1 Homo sapiens cDNA clone IMAGE:1142440.3 similar to gb:X12671_mai HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN A1 (HUMAN);



Table 4

3245	8392	13489	1.4	7.00E-51	AW889218.1	EST_HUMAN	QV4-NT0028-200400-180-d05 NT0028 Homo sapiens cDNA
3317	8462	13574	0.8	7.00E-51	AW274720.1	EST_HUMAN	xb34803.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2695564 3' similar to TR:Q92340 Q92340 ATYPICAL PKC SPECIFIC BINDING PROTEIN.;
3541	8682	13762	7.4	7.00E-51	7662109	NT	Homo sapiens KIAA0428 gene product (KIAA0428), mRNA
4076	9203	14289	1.3	7.00E-51	AL079828.1	EST_HUMAN	DKFZp434B2229_r1 434 (synonym: hhes3) Homo sapiens cDNA clone DKFZp434B2229 5'
4076	9203	14290	1.3	7.00E-51	AL079828.1	EST_HUMAN	DKFZp434B2229_r1 434 (synonym: hhes3) Homo sapiens cDNA clone DKFZp434B2229 5'
4254	9379	14459	2.4	7.00E-51	AW295603.1	EST_HUMAN	U1-H-BW0-aip-b-05-0-U1.s1 NCI_CGAP_Sub6 Homo sapiens cDNA clone IMAGE:2729817 3'
1836	7053	12246	1.9	6.00E-51	7657266	NT	Homo sapiens KIAA0929 protein Mx2 interacting nuclear target (MINT) homolog (KIAA0929), mRNA
3428	8570	13682	12.9	6.00E-51	7657266	NT	Homo sapiens KIAA0929 protein Mx2 interacting nuclear target (MINT) homolog (KIAA0929), mRNA
774	5926	11075	3.7	5.00E-51	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21G003
786	5937	11089	1.5	5.00E-51	4507500	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1), mRNA
975	7904	11277	1.4	5.00E-51	AL133204.1	NT	Novel human gene mapping to chromosome X
1590	6716	11886	0.8	5.00E-51	5031890	NT	Homo sapiens 26S proteasome-associated pad1 homolog (POH1), mRNA
2548	7644	12843	4.2	5.00E-51	AL007558.1	NT	Homo sapiens mRNA for nucleoporin 155
3863	8999	14098	1.1	5.00E-51	M30938.1	NT	Human Ku (p70/p80) subunit mRNA, complete cds
3863	8999	14098	1.1	5.00E-51	M30938.1	NT	Human Ku (p70/p80) subunit mRNA, complete cds
5004	10107	15175	2.3	5.00E-51	AB037832.1	NT	Homo sapiens mRNA for KIAA1411 protein, partial cds
130	5326	10458	0.9	3.00E-51	AI567348.1	EST_HUMAN	t81c09.x1 NCI_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2224720 3' similar to gb:M26326 KERATIN, TYPE I CYTOSKELETAL 18 (HUMAN);
613	5771	10891	0.6	3.00E-51	W79058.1	EST_HUMAN	zdf7h04.r1 Soares_fetal_heart_NbHH19W Homo sapiens cDNA clone IMAGE:346615 5'
613	5771	10892	0.6	3.00E-51	W79058.1	EST_HUMAN	zdf7h04.r1 Soares_fetal_heart_NbHH19W Homo sapiens cDNA clone IMAGE:346615 5'
1159	6294	11449	1.4	3.00E-51	AI567348.1	EST_HUMAN	t81c09.x1 NCI_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2224720 3' similar to gb:M26326 KERATIN, TYPE I CYTOSKELETAL 18 (HUMAN);
4232	9356	14438	2.1	3.00E-51	AL159142.1	NT	Novel human gene mapping to chromosome 22
362	5540	10671	0.6	2.00E-51	4507798	NT	Homo sapiens ubiquitin protein ligase E3A (human papilloma virus E6-associated protein, Angelman syndrome) (UBE3A), mRNA
673	5829	10956	1.1	2.00E-51	BE391063.1	EST_HUMAN	601285684F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3607463 5'
673	5829	10957	1.1	2.00E-51	BE391063.1	EST_HUMAN	601285684F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3607463 5'
673	5829	10957	1.1	2.00E-51	BE391063.1	EST_HUMAN	601285684F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3607463 5'
1662	6786	11863	0.8	2.00E-51	AA233352.1	EST_HUMAN	z30a05.r1 Stratagene NT2 neuronal precursor 937230 Homo sapiens cDNA clone IMAGE:664880 5' similar to TR:G233226 G233226 RTVL-H PROTEIN. ; contains LTR7.13 LTR repetitive element.;
3672	8811	13905	2.2	2.00E-51	AI492415.1	EST_HUMAN	z27g03.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2131732 3'
4392	9514	14603	1.0	2.00E-51	AW137826.1	EST_HUMAN	U1-H-B1-adj-d-02-0-U1.s1 NCI_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2716851 3'

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Table 4

109	5312	10437	1.5	1.00E-51	4503528	NT	Homo sapiens eukaryotic translation initiation factor 4A, isoform 1 (EIF4A1) mRNA
4309	9432	14521	1.0	1.00E-51	4759071	NT	Homo sapiens small inducible cytokine subfamily A (Cys-Cys), member 15 (SCYA15) mRNA
4309	9432	14522	1.0	1.00E-51	4759071	NT	Homo sapiens small inducible cytokine subfamily A (Cys-Cys), member 15 (SCYA15) mRNA
146	5342	10471	2.5	8.00E-52	AA720574.1	EST_HUMAN	nm21g02.s1 NCI_CGAP_C03 Homo sapiens cDNA clone IMAGE:1241138 3' similar to contains THR.L3 THR repetitive element;
1481	6608	11781	1.3	8.00E-52	X84900.1	NT	H. sapiens mRNA for laminin-5, alpha3b chain
1170	6304		0.9	6.00E-52	BE072409.1	EST_HUMAN	QV3-B70537-271299-049-d07 BT0537 Homo sapiens cDNA
1686	6792	11968	0.8	6.00E-52	AF109907.1	NT	Homo sapiens S164 gene, partial cds; PS1 and hypothetical protein genes, complete cds; and S171 gene, partial cds
751	5903	11049	0.6	5.00E-52	AW009208.1	EST_HUMAN	wt79a10.x1 NCI_CGAP_C03 Homo sapiens cDNA clone IMAGE:2504154 3' similar to TR:O43789 O43789 OLFACTORY RECEPTOR;
751	5903	11050	0.6	5.00E-52	AW009208.1	EST_HUMAN	wt79a10.x1 NCI_CGAP_C03 Homo sapiens cDNA clone IMAGE:2504154 3' similar to TR:O43789 O43789 OLFACTORY RECEPTOR;
4340	9463	14553	2.1	5.00E-52	Z78898.1	NT	H. sapiens flow-sorted chromosome 8 HindIII fragment, SC6pA18H7
1639	6765	11934	0.9	4.00E-52	AF257318.1	NT	Homo sapiens SH3-containing protein SH3GLB1 mRNA, complete cds
1748	6870	12048	8.6	4.00E-52	4758843	NT	Homo sapiens nucleoporin 155KD (NUP155) mRNA
2706	7791		20.5	4.00E-52	AF047677.1	NT	Homo sapiens dystrophin (DMD) gene, deletion breakpoints 1-3 in intron 5
3850	8986	14086	0.8	4.00E-52	4507500	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA
577	5737	10853	1.5	3.00E-52	Z20083.1	EST_HUMAN	HSAABBJOK.S, Human foetal Adrenals tissue Homo sapiens cDNA
487	5652	10776	0.6	2.00E-52	AA601246.1	EST_HUMAN	no14g09.s1 NCI_CGAP_Phe1 Homo sapiens cDNA clone IMAGE:1100704 3' similar to TR:E29140 E29140 SPALT PROTEIN;
550	5713	10831	1.4	2.00E-52	M10976.1	NT	Human endogenous retroviral DNA (4-1), complete retroviral segment
550	5713	10832	1.4	2.00E-52	M10976.1	NT	Human endogenous retroviral DNA (4-1), complete retroviral segment
2450	7549	12758	0.6	2.00E-52	BE207576.1	EST_HUMAN	bb66b07.y1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3030421 5' similar to gb:XI6483 Mus musculus mRNA for Zp1-1 zinc finger protein (MOUSE);
522	5686	10808	1.4	1.00E-52	AA634445.1	EST_HUMAN	zu75h12.s1 Soares testis NHT Homo sapiens cDNA clone IMAGE:743879 3'
1349	8477	11643	3.0	1.00E-52	4504026	NT	Homo sapiens glutamate-aminolipase (glutamine synthase) (GLUL) mRNA
2489	7586		1.2	1.00E-52	4502238	NT	Homo sapiens arylsulfinatase D (ARSD), transcript variant 1, mRNA
3021	8173	13273	1.4	1.00E-52	S61070.1	NT	pol reverse transcriptase homolog (retroviral element) [human, endogenous retroviral element RTV-L-Hp1, Genomic, 660 nt]
3723	8860	13952	1.0	9.00E-53	4506064	NT	Homo sapiens protein kinase, cAMP-dependent, regulatory, type II, beta (PRKAR2B) mRNA
4293	9417	14507	1.0	9.00E-53	AF001446.1	NT	Homo sapiens core binding factor alpha1 subunit (CBFA1) gene, exon 3
4966	10069	15143	0.9	9.00E-53	7661713	NT	Homo sapiens precised osteoblast protein (GS3786), mRNA
4009	9140	14222	2.2	5.00E-53	4758543	NT	Homo sapiens heterogeneous nuclear ribonucleoprotein C (C1/C2) (HNRPC) mRNA
43	5253	10366	0.7	4.00E-53	AL163285.2	NT	Homo sapiens chromosome 21 segment HS21C085
43	5253	10367	0.7	4.00E-53	AL163285.2	NT	Homo sapiens chromosome 21 segment HS21C085
4715	9827	14919	1.1	4.00E-53	7705414	NT	Homo sapiens hook1 protein (HOOK1), mRNA

Table 4

2625	7715	12916	0.9	3.00E-53	AB026898.1	NT	Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)
3670	8809	13903	1.3	3.00E-53	AW050836.1	EST_HUMAN	IL2-JM0081-240300-055-C03 UM0081 Homo sapiens cDNA 3'
4486	9606	14699	1.2	3.00E-53	AW803563.1	EST_HUMAN	QV3-810381-270100-073-d08 BT0381 Homo sapiens cDNA
4833	9941	15030	0.9	3.00E-53	BE069344.1	EST_HUMAN	EST77525 Pancreas tumor III Homo sapiens cDNA 5' end
450	5616		1.5	2.00E-53	AA366556.1	EST_HUMAN	Homo sapiens Brulon's tyrosine kinase (BTK), alpha-D-galactosidase A (GLA), L44-like ribosomal protein (L44L), and FTP3 (FTP3) genes, complete cds
2279	7385	12592	1.1	2.00E-53	U78027.1	NT	Homo sapiens ATPase, H+ transporting, lysosomal (vacuolar proton pump) 31kD, Vacuolar proton-ATPase, subunit E, V-ATPase, subunit E (ATP6E), mRNA
2490	7587		3.8	2.00E-53	4502316	NT	Homo sapiens core-binding factor, runt domain, alpha subunit 2; translocated to, 1; cyclin D-related (CBFA2T1) mRNA
2694	7781	12978	6.9	2.00E-53	4757915	NT	Homo sapiens core-binding factor, runt domain, alpha subunit 2; translocated to, 1; cyclin D-related (CBFA2T1) mRNA
2694	7781	12978	6.9	2.00E-53	4757915	NT	Homo sapiens core-binding factor, runt domain, alpha subunit 2; translocated to, 1; cyclin D-related (CBFA2T1) mRNA
2694	7781	12978	6.9	2.00E-53	4757915	NT	Homo sapiens core-binding factor, runt domain, alpha subunit 2; translocated to, 1; cyclin D-related (CBFA2T1) mRNA
3207	8355	13465	1.2	2.00E-53	AF083822.1	NT	Homo sapiens dihydropyridine receptor alpha 2 subunit (CACNA2D1) gene, exon 6
3970	9102	14185	2.1	2.00E-53	M61873.1	NT	Human Krueppel-related DNA-binding protein (TF34) gene, partial cds
4390	9512	14600	1.1	2.00E-53	4506962	NT	Homo sapiens SKAP55 homologue (SKAP-HOM) mRNA
5091	10189	15267	1.1	2.00E-53	AL163261.2	NT	Homo sapiens chromosome 21 segment HS21C081
5091	10189	15267	1.1	2.00E-53	AL163261.2	NT	Homo sapiens chromosome 21 segment HS21C081
5091	10189	15267	1.1	2.00E-53	AL163261.2	NT	Homo sapiens chromosome 21 segment HS21C081
1429	6556	11732	0.9	1.00E-53	AJ271736.1	NT	Homo sapiens Xq pseudautosomal region; segment 2/2
3364	8507	13615	1.0	1.00E-53	AB026898.1	NT	Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)
5152	10247	15319	0.8	9.00E-54	4507500	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA
5152	10247	15320	0.8	9.00E-54	4507500	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA
200	5394	10520	1.1	8.00E-54	BE386785.1	EST_HUMAN	601272863F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3614031 5'
1784	6914	12100	1.3	8.00E-54	4504610	NT	Homo sapiens insulin-like growth factor 2 receptor (IGF2R) mRNA
4629	9743	14839	1.3	8.00E-54	4507848	NT	Homo sapiens ubiquitin specific protease 13 (isopeptidase T-3) (USP13) mRNA
4629	9743	14840	1.3	8.00E-54	4507848	NT	Homo sapiens ubiquitin specific protease 13 (isopeptidase T-3) (USP13) mRNA
5030	9743	14839	1.1	8.00E-54	4507848	NT	Homo sapiens ubiquitin specific protease 13 (isopeptidase T-3) (USP13) mRNA
5030	9743	14840	1.1	8.00E-54	4507848	NT	Homo sapiens ubiquitin specific protease 13 (isopeptidase T-3) (USP13) mRNA
379	5585	10718	1.3	7.00E-54	AA812537.1	EST_HUMAN	a179c12.s1 Soares_testis_NHT Homo sapiens cDNA clone 1377046 3' similar to contains MER30.13 MER30 repetitive element;
1789	6909	12095	0.6	7.00E-54	Y16645.1	NT	Homo sapiens mRNA for monocyte chemotactic protein-2
2158	7267	12477	1.7	7.00E-54	NZ7177.1	EST_HUMAN	yw66d12.s1 Soares_gliacenta_80bweeks_2NBHP8069V Homo sapiens cDNA clone IMAGE:257399 3' similar to contains LTR7.b3 LTR7 repetitive element;
22	5231	10334	0.5	8.00E-54	AB003618.1	NT	Homo sapiens DNA for MICB, exon 4, 5 and partial cds
1833	6852	12137	0.9	8.00E-54	4505052	NT	Homo sapiens lymphocyte antigen 75 (LY75) mRNA, and translated products
1833	6852	12138	0.9	8.00E-54	4505052	NT	Homo sapiens lymphocyte antigen 75 (LY75) mRNA, and translated products
3246	8393	13500	0.8	6.00E-54	88922148	NT	Homo sapiens hypothetical protein DKFZp434M035 (DKFZp434M035), mRNA
3923	9057	14144	2.4	6.00E-54	4502872	NT	Homo sapiens chloride channel 6 (CLCN6) mRNA

Table 4

4774	9884	1.7	6.00E-54	Y09846.1	NT	H.sapiens shc pseudogene, p86 isoform
4930	9884	1.3	6.00E-54	Y09846.1	NT	H.sapiens shc pseudogene, p86 isoform
2104	7215	0.8	5.00E-54	P51523	SWISSPROT	ZINC FINGER PROTEIN 84 (ZINC FINGER PROTEIN HPF2)
176	5369	36.0	4.00E-54	AF110103.1	NT	Tupia belangeri beta-actin mRNA, partial cds
						EST17696 Jurkat T-cells VI Homo sapiens cDNA 5' end similar to glyceraldehyde-3-phosphate dehydrogenase
940	6087	14.0	4.00E-54	AA308764.1	EST_HUMAN	Human mRNA for KIAA0077 gene, partial cds
1764	6885	1.2	4.00E-54	D38521.1	NT	Human mRNA for KIAA0077 gene, partial cds
1764	6885	1.2	4.00E-54	D38521.1	NT	Human mRNA for KIAA0077 gene, partial cds
3168	8317	1.2	4.00E-54	AI935086.1	EST_HUMAN	wd28d11.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2329269 3' similar to TR:O02711 Q02711 PRO-POL-DUTPASE POLYPROTEIN;
88	5294	1.7	3.00E-54	AA313487.1	EST_HUMAN	EST185371 Colon carcinoma (HCC) cell line Homo sapiens cDNA 5' end
2522	7618	0.9	3.00E-54	AL110383.1	EST_HUMAN	DKFZP434E0731_r1 434 (synonym: hhes3) Homo sapiens cDNA clone DKFZP434E0731 5'
2563	7676	0.9	3.00E-54	AI908757.1	EST_HUMAN	IL-BT189-180389-007 BT189 Homo sapiens cDNA
626	5785	2.1	2.00E-54	5031900	NT	Homo sapiens killer cell lectin-like receptor subfamily G, member 1 (KLRG1), mRNA
1342	6470	0.7	2.00E-54	4507184	NT	Homo sapiens nuclear antigen Sp100 (SP100) mRNA
1529	6656	0.6	2.00E-54	AA655008.1	EST_HUMAN	nt78a09.s1 NCI_CGAP_P193 Homo sapiens cDNA clone IMAGE:1204600 similar to contains element L1 repetitive element;
2493	7589	1.3	2.00E-54	AW163175.1	EST_HUMAN	au92g03.y1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2783764 5'
2556	7650	0.7	2.00E-54	AL163210.2	NT	similar to SW:CU1_HUMAN_Q13616 CULLIN HOMOLOG 1;
2865	8016	1.7	2.00E-54	AW057524.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C010
3501	8643	4.1	2.00E-54	AA532925.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C001
4110	9236	2.0	2.00E-54	4502642	NT	Homo sapiens chromosome 21 segment HS21C001
4343	9466	1.1	2.00E-54	AL163201.2	NT	Homo sapiens chromosome 21 segment HS21C001
4780	9890	1.5	2.00E-54	AF083823.1	NT	Homo sapiens peptidylarginine deiminase type III (LOC51702), mRNA
5156	10251	0.8	2.00E-54	Y07829.2	NT	Homo sapiens dihydropyridine receptor alpha 2 subunit (CACNA2D1) gene, exon 7
1294	6423	14.6	8.00E-55	Y07829.2	NT	Homo sapiens RFB30 gene for RING finger protein
1297	6426	0.8	8.00E-55	Y07829.2	NT	Homo sapiens RFB30 gene for RING finger protein
1065	6203	1.2	7.00E-55	R09346.1	EST_HUMAN	yl26a04.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:127998 5' similar to SP:C561 BOVIN P10897 CYTOCHROME;
1732	6855	1.1	5.00E-55	AA704971.1	EST_HUMAN	z195b09.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:462617 3'
1732	6855	1.1	5.00E-55	AA704971.1	EST_HUMAN	z195b09.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:462617 3'
49	7880	1.4	4.00E-55	AW957894.1	EST_HUMAN	EST370084 IMAGE_resequences, IMAGE Homo sapiens cDNA
656	5813	12.0	4.00E-55	4826973	NT	Homo sapiens RNA binding motif protein, Y chromosome, family 1, member A1 (RBMV1A1) mRNA
1422	6550	0.7	4.00E-55	7861713	NT	Homo sapiens predicted osteoblast protein (GS3786), mRNA

Table 4

1422	6550	11726	0.7	4.00E-55	7661713	NT	Homo sapiens predicted osteoblast protein (GS3786), mRNA
1979	7094	12295	0.6	4.00E-55	4506180	NT	Homo sapiens proteasome (prosome, macropain) subunit, alpha type, 2 (PSMA2) mRNA
1979	7094	12295	0.6	4.00E-55	4506180	NT	Homo sapiens proteasome (prosome, macropain) subunit, alpha type, 2 (PSMA2) mRNA
1979	7094	12296	0.6	4.00E-55	4506180	NT	Homo sapiens proteasome (prosome, macropain) subunit, alpha type, 2 (PSMA2) mRNA
2039	7152	12356	2.8	4.00E-55	4503314	NT	Homo sapiens diacylglycerol kinase, gamma (90K) (DGKG) mRNA
2039	7152	12357	2.8	4.00E-55	4503314	NT	Homo sapiens diacylglycerol kinase, gamma (90K) (DGKG) mRNA
2262	7388	12578	1.3	4.00E-55	4507794	NT	Homo sapiens ubiquitin-conjugating enzyme E2 variant 1 (UBE2V1) mRNA
2545	7641	12578	1.0	4.00E-55	AL271735.1	NT	Homo sapiens Xq pseudautosomal region, segment 1/2
3242	8389	13496	1.4	4.00E-55	AL183300.2	NT	Homo sapiens chromosome 21 segment HS21C100
373	5549	10682	0.8	2.00E-55	X57147.1	NT	Human endogenous retrovirus PHE.1 (ERV9)
539	5702	10915	0.9	2.00E-55	M10976.1	NT	Human endogenous retrovirus PHE.1 (ERV9)
633	5792	10915	1.1	2.00E-55	4507296	NT	Human endogenous retrovirus PHE.1 (ERV9)
1813	6932	12120	0.8	2.00E-55	7019494	NT	Homo sapiens putative protein O-mannosyltransferase (POMT2), mRNA
1813	6932	12121	0.8	2.00E-55	7019494	NT	Homo sapiens putative protein O-mannosyltransferase (POMT2), mRNA
2828	8079	13188	0.8	2.00E-55	4507798	NT	Homo sapiens ubiquitin protein ligase E3A (human papilloma virus E6-associated protein, Angelman syndrome) (UBE3A) mRNA
3141	8280	13396	2.9	2.00E-55	BE070016.1	EST_HUMAN	MR1-BT0405-080300-001-c04 BT0405 Homo sapiens cDNA
3141	8290	13397	2.9	2.00E-55	BE070016.1	EST_HUMAN	MR1-BT0405-080300-001-c04 BT0405 Homo sapiens cDNA
91	6297	10423	0.5	1.00E-55	4505060	NT	Homo sapiens mannose-6-phosphate receptor (calion dependent) (M6PR) mRNA
182	5376	10501	4.1	1.00E-55	U09823.1	NT	Oryzodius carinatus New Zealand white elongation factor 1 alpha (Rabellaz) mRNA, complete cds
574	5734	11420	1.2	1.00E-55	AB020710.1	NT	RC-BT091-200199-072 BT091 Homo sapiens cDNA
1132	6288	11420	1.2	1.00E-55	AB020710.1	NT	Homo sapiens mRNA for KIAA0903 protein, partial cds
1907	7024	12212	0.9	1.00E-55	BE277861.1	EST_HUMAN	60112016F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:2967027 5'
1907	7024	12213	0.9	1.00E-55	BE277861.1	EST_HUMAN	60112016F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:2967027 5'
2277	7383	12603	0.8	1.00E-55	5803174	NT	Homo sapiens SMA3 (SMA3), mRNA
2280	7673	12603	1.0	1.00E-55	AF000990.1	NT	Homo sapiens testis-specific Testis Transcript Y 1 (TTY1) mRNA, partial cds
2470	7568	12770	12.0	1.00E-55	AL278305.1	NT	Homo sapiens HLA-A*0101 gene for MHC class I antigen, exons 1-8
2507	7603	12803	1.7	1.00E-55	AB007866.2	NT	Homo sapiens mRNA for KIAA0406 protein, partial cds
2507	7603	12804	1.7	1.00E-55	AB007866.2	NT	Homo sapiens mRNA for KIAA0406 protein, partial cds
2568	7661	12863	1.4	1.00E-55	LS4057.1	NT	Homo sapiens CLP mRNA, partial cds
2670	7757	12957	1.6	1.00E-55	AW027307.1	EST_HUMAN	wf3a10x1 Soares, thymus, NIH-Tth Homo sapiens cDNA clone IMAGE:2513082 3' similar to WP-Y47H9C.2 CE20263 :
2670	7757	12958	1.6	1.00E-55	AW027307.1	EST_HUMAN	wf3a10x1 Soares, thymus, NIH-Tth Homo sapiens cDNA clone IMAGE:2513082 3' similar to WP-Y47H9C.2 CE20263 :
3363	8506	13614	1.2	1.00E-55	W28189.1	EST_HUMAN	43c5 Human telomerase cDNA randomly primed sublibrary Homo sapiens cDNA
3907	9042	14129	3.5	1.00E-55	AL163267.2	NT	Homo sapiens chromosome 21 segment HS21C067
4197	9323	14410	1.0	1.00E-55	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
4721	9833	14924	1.0	1.00E-55	AB037163.1	NT	Homo sapiens DSCR5b mRNA, complete cds
4721	9833	14925	1.0	1.00E-55	AB037163.1	NT	Homo sapiens DSCR5b mRNA, complete cds

Table 4

5081	10179	15259	1.2	1.00E-55	8923125	NT	Homo sapiens hypothetical protein FLJ20126 (FLJ20126), mRNA
2703	7789	12989	1.9	7.00E-56	H19934.1	EST_HUMAN	Ym2g03.r1 Soares adult brain N2b5H855V Homo sapiens cDNA clone IMAGE:173044 5' similar to contains THR repetitive element:
4261	9386	14470	1.1	6.00E-56	R96413.1	EST_HUMAN	yq37e01.r1 Soares fetal liver spleen 1NfLS Homo sapiens cDNA clone IMAGE:197976 5'
1666	6790	11966	0.8	5.00E-56	AW997712.1	EST_HUMAN	RC3-BN0053-170200-011-H01 BN0053 Homo sapiens cDNA
25	5234	10337	2.1	4.00E-56	AF141349.1	NT	Homo sapiens beta-tubulin mRNA, complete cds
25	5234	10338	2.1	4.00E-56	AF141349.1	NT	Homo sapiens beta-tubulin mRNA, complete cds
2676	7763	12863	1.5	4.00E-56	4507728	NT	Homo sapiens tubulin, beta polypeptide (TUBB) mRNA
2676	7763	12864	1.5	4.00E-56	4507728	NT	Homo sapiens tubulin, beta polypeptide (TUBB) mRNA
2781	5679	10800	1.0	4.00E-56	AF003528.1	NT	Homo sapiens X-linked anhidrotic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions
3138	8287	13394	1.1	4.00E-56	AW293688.1	EST_HUMAN	UL-H-BI2-ano-d-07-Q-U.s1 NCI_CGAP_Sub4 Homo sapiens cDNA clone IMAGE:2727588 3'
1318	6447	11613	9.9	3.00E-56	8924029	NT	Homo sapiens hypothetical protein PRO1304 (PRO1304), mRNA
2103	7214	12424	2.7	3.00E-56	6912697	NT	Homo sapiens oncogene TC21 (TC21), mRNA
3086	8237	13336	1.6	3.00E-56	AA325826.1	EST_HUMAN	EST28889 Cerebellum II Homo sapiens cDNA 5' end
3086	8237	13337	1.6	3.00E-56	AA325826.1	EST_HUMAN	EST28889 Cerebellum II Homo sapiens cDNA 5' end
3761	8899		1.4	3.00E-56	AF050686.1	NT	Homo sapiens MHC class 1 region
4327	9450	14538	4.1	3.00E-56	AL163268.2	NT	Homo sapiens chromosome 21 segment HS21C068
4470	9580	14686	2.1	3.00E-56	5902085	NT	Homo sapiens superkiller viralicidic activity 2 (S. cerevisiae homolog)-like (SKIV2L), mRNA
513	5677		1.0	2.00E-56	AA199818.1	EST_HUMAN	zq52a08.s1 Striatogene neuroepithelium (#937231) Homo sapiens cDNA clone
716	7897	11008	1.2	2.00E-56	BE064386.1	EST_HUMAN	IMAGE:645206 3'
716	7897	11009	1.2	2.00E-56	BE064386.1	EST_HUMAN	RC4-BT0310-110300-015-f10 BT0310 Homo sapiens cDNA
2334	7437	12845	1.0	2.00E-56	4585863	NT	Homo sapiens phosphodiesterase 6A, cGMP-specific, rod, alpha (PDE6A), mRNA
2334	7437	12846	1.0	2.00E-56	4585863	NT	Homo sapiens phosphodiesterase 6A, cGMP-specific, rod, alpha (PDE6A), mRNA
2959	8110	13216	0.9	2.00E-56	AB037835.1	NT	Homo sapiens mRNA for KIAA1414 protein, partial cds
984	6109		1.4	1.00E-56	AF190930.1	NT	Macaca fascicularis protein tyrosine phosphatase (PRL-1) mRNA, complete cds
3622	8761	13853	1.8	1.00E-56	AW589833.1	EST_HUMAN	hg23c11.x1 NCI_CGAP GC6 Homo sapiens cDNA clone IMAGE:2946452 3'
3622	8761	13854	1.8	1.00E-56	AW589833.1	EST_HUMAN	hg23c11.x1 NCI_CGAP GC6 Homo sapiens cDNA clone IMAGE:2946452 3'
4963	10066	15138	1.5	1.00E-56	AI905162.1	EST_HUMAN	QV-BT077-130189-079 BT077 Homo sapiens cDNA
609	5767		0.7	9.00E-57	AW860885.1	EST_HUMAN	QV-OT0033-070300-152-H03 OT0033 Homo sapiens cDNA
4109	9235	14318	1.2	9.00E-57	4758279	NT	Homo sapiens EphA4 (EPHA4) mRNA
4109	9235	14319	1.2	9.00E-57	4758279	NT	Homo sapiens EphA4 (EPHA4) mRNA
13	5221	10322	0.5	8.00E-57	8823349	NT	Homo sapiens hypothetical protein FLJ20371 (FLJ20371), mRNA
294	5480	10611	1.0	8.00E-57	AW816405.1	EST_HUMAN	QV-A-ST0234-181199-037-05 ST0234 Homo sapiens cDNA
866	6014	11174	2.0	8.00E-57	AW264599.1	EST_HUMAN	x05d10.x1 NCI_CGAP Bm53 Homo sapiens cDNA clone IMAGE:2759251 3' similar to gb-U05875 INTERFERON-GAMMA RECEPTOR BETA CHAIN PRECURSOR (HUMAN);
1774	6895	12083	0.6	8.00E-57	AA496109.1	EST_HUMAN	zr51b12.r1 Soares testis NHT Homo sapiens cDNA clone IMAGE:757151 5'

Table 4

3335	8479	13592	1.0	8.00E-57	4758279	NT	Homo sapiens EPHA4 (EPHA4) mRNA
3335	8478	13593	1.0	8.00E-57	4758279	NT	Homo sapiens EPHA4 (EPHA4) mRNA
5107	10203	15282	1.0	8.00E-57	AA971001.1	EST_HUMAN	op67h2.s1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1561939 3'
2592	7684	12885	0.7	7.00E-57	7657592	NT	Homo sapiens smg GDS-ASSOCIATED PROTEIN (SMAP) mRNA
2592	7684	12886	0.7	7.00E-57	7657592	NT	Homo sapiens smg GDS-ASSOCIATED PROTEIN (SMAP) mRNA
3212	8360	13469	0.9	7.00E-57	7242158	NT	Homo sapiens NME7 (NME7) mRNA
3212	8360	13470	0.9	7.00E-57	7242158	NT	Homo sapiens NME7 (NME7) mRNA
3233	8361	13488	6.5	7.00E-57	6005979	NT	Homo sapiens Kruppel-like factor 8 (KLF8) mRNA
3801	8938	14032	2.2	7.00E-57	AF012872.1	NT	Homo sapiens phosphatidylinositol 4-kinase 230 (p4K230) mRNA, complete cds
3801	8938	14033	2.2	7.00E-57	AF012872.1	NT	Homo sapiens phosphatidylinositol 4-kinase 230 (p4K230) mRNA, complete cds
3694	8833	13925	1.2	4.00E-57	AB026898.1	NT	Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)
787	5938	11090	0.8	3.00E-57	4507798	NT	Homo sapiens ubiquitin protein ligase E3A (human papilloma virus E6-associated protein, Angelman syndrome) (UBE3A) mRNA
1309	6437		3.9	3.00E-57	AA230279.1	EST_HUMAN	nc1307.s1 NCI_CGAP_P1 Homo sapiens cDNA clone IMAGE:1008037 similar to
2342	7444	12651	1.0	3.00E-57	AA348335.1	EST_HUMAN	SW:RS10_HUMAN P46783 40S RIBOSOMAL PROTEIN S10.;
3514	8655	13762	1.2	3.00E-57	AF232708.1	NT	EST54770 Hippocampus II Homo sapiens cDNA 5' end
3639	8778		115.9	3.00E-57	AW863964.1	EST_HUMAN	Homo sapiens cell-line tsA201a chloride ion current inducer protein (Cln) gene, complete cds
2699	7785	12985	1.2	2.00E-57	AA045419.1	EST_HUMAN	RC3-C10254-110300-027-d10 CT0254 Homo sapiens cDNA
3392	8534		2.9	2.00E-57	AL163204.2	NT	ak02b02.s1 Soares_parathyroid_tumor_NbHPA Homo sapiens cDNA clone IMAGE:1404747 3' similar to contains Alu repetitive elementcontains element MER22 repetitive element ;
3504	8646	13755	0.8	2.00E-57	R07702.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C004
3504	8646	13756	0.8	2.00E-57	R07702.1	EST_HUMAN	ye98h01.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:125809 5'
4409	9529	14618	6.9	2.00E-57	AL163283.2	NT	ye98h01.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:125809 5'
2184	7293	12505	1.1	1.00E-57	AW503208.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C083
638	5797	10921	0.9	8.00E-58	AI798376.1	EST_HUMAN	U1-HF-BND-8K1-g-07-Q-U1.1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3078348 5'
638	5797	10922	0.9	8.00E-58	AI798376.1	EST_HUMAN	U1-HF-BND-8K1-g-07-Q-U1.1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3078348 5'
2945	8096		2.8	8.00E-58	7706132	NT	TR:O15475 O15475 UNNAMED HERV-H PROTEIN ;
3382	8525	13631	4.2	7.00E-58	BE263616.1	EST_HUMAN	TR:O15475 O15475 UNNAMED HERV-H PROTEIN ;
3382	8525	13632	4.2	7.00E-58	BE263616.1	EST_HUMAN	TR:O15475 O15475 UNNAMED HERV-H PROTEIN ;
2207	7316	12529	0.9	6.00E-58	BE395061.1	EST_HUMAN	TR:O15475 O15475 UNNAMED HERV-H PROTEIN ;
2871	8022	13124	1.2	6.00E-58	BE242150.1	EST_HUMAN	TCAP1E1219 Pediatric acute myelogenous leukemia cell (FAB M1) Baylor-HGSC project=TCAP Homo sapiens cDNA clone TCAP1219

Table 4

2871	8022	13125	1.2	6.00E-58	BE242150.1	EST_HUMAN	TCAP1E1219 Pediatric acute myelogenous leukemia cell (FAB M1) Baylor-HGSC
297	5483	10613	1.0	5.00E-58	4507334	NT	project=TCAP Homo sapiens cDNA clone TCAP1219
1176	6310	11464	1.5	5.00E-58	AW797948.1	EST_HUMAN	Homo sapiens synapjanin 1 (SYNJ1), mRNA
1176	6310	11465	1.5	5.00E-58	AW797948.1	EST_HUMAN	CM3-UM0043-240300-127-e07 UM0043 Homo sapiens cDNA
1177	6310	11464	1.0	5.00E-58	AW797948.1	EST_HUMAN	CM3-UM0043-240300-127-e07 UM0043 Homo sapiens cDNA
1177	6310	11465	1.0	5.00E-58	AW797948.1	EST_HUMAN	CM3-UM0043-240300-127-e07 UM0043 Homo sapiens cDNA
3281	8426	13534	3.6	5.00E-58	AA988183.1	EST_HUMAN	cg8607.s1 NCI CGAP Lu5 Homo sapiens cDNA clone IMAGE:1603908.3
369	5547	10679	6.1	4.00E-58	4502302	NT	Homo sapiens ATP synthase, H <sup>+</sup> transporting, mitochondrial F1 complex, O subunit (oligomycin sensitivity conferring protein) (ATP5O), mRNA
779	5931	11080	0.5	4.00E-58	4504634	NT	Homo sapiens interleukin 10 receptor, beta (IL10RB), mRNA
1452	6579	11753	1.2	4.00E-58	4503648	NT	Homo sapiens coagulation factor IX (plasma thromboplastic component, Christmas disease, hemophilia B) (F9), mRNA
2531	7627	12829	1.0	4.00E-58	AF265555.1	NT	Homo sapiens ubiquitin-conjugating BIR-domain enzyme APOLLON mRNA, complete cds
2590	7683	12883	1.0	4.00E-58	U36251.1	NT	Human beta-prime-adaptin (BAM22) gene, exon 3
3283	8428	13536	1.1	4.00E-58	D16470.1	NT	Human mRNA, Xq terminal portion
3680	8819	13912	2.1	4.00E-58	5031660	NT	Homo sapiens EGF-like repeats and discoidin-like domains 3 (EDIL3), mRNA
332	5513		1.2	3.00E-58	R17879.1	EST_HUMAN	yg10602.t1 Soares infant brain 1N18 Homo sapiens cDNA clone IMAGE:31693.5
1367	6495	11661	0.9	3.00E-58	4758981	NT	Homo sapiens peptide YY (PYY) mRNA
925	6072	11230	2.8	2.00E-58	AF068624.1	NT	Homo sapiens 5-aminolevulinic synthase 2 (ALAS2) gene, complete cds
1040	6180	11333	0.5	2.00E-58	AW881145.1	EST_HUMAN	QVQ-OT0033-010400-182-e07 OT0033 Homo sapiens cDNA
							bp080807.y1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2823733.5 similar to gp:x88391 60S RIBOSOMAL PROTEIN L6 (HUMAN); gp:x81987 M.musculus mRNA (for TAX responsive element binding protein (MOUSE);
1266	6397		4.1	2.00E-58	BE208632.1	EST_HUMAN	Human complement component C5 mRNA, 3'end
705	5660	10995	0.9	1.00E-58	M65134.1	NT	Homo sapiens NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 9 (22kD, 922)
1052	6191	11343	1.9	1.00E-58	6274549	NT	(NDUFEB9), mRNA
1305	6434	11569	0.7	1.00E-58	AW957182.1	EST_HUMAN	EST369252 MAGE resequences, MAGD Homo sapiens cDNA
1305	6434	11600	0.7	1.00E-58	AW957182.1	EST_HUMAN	EST369252 MAGE resequences, MAGD Homo sapiens cDNA
1375	6503	11668	1.1	1.00E-58	ALJ238093.1	NT	Homo sapiens partial AF4 gene, exons 2 to 7 and Alu repeat elements
1641	6767	11938	2.0	1.00E-58	BE466132.1	EST_HUMAN	hy1008.x1 NCI CGAP GC6 Homo sapiens cDNA clone IMAGE:3196935.3
2771	7655	13059	1.0	1.00E-58	4759169	NT	Homo sapiens steroid regulatory element binding transcription factor 2 (SREBF2) mRNA
3493	8634	13747	1.0	1.00E-58	4758081	NT	Homo sapiens chondroclon sulfate proteoglycan 2 (versican) (CSPG2) mRNA
3493	8634	13748	1.0	1.00E-58	4758081	NT	Homo sapiens chondroclon sulfate proteoglycan 2 (versican) (CSPG2) mRNA
3659	8798	13892	0.8	1.00E-58	4507628	NT	Homo sapiens transition protein 1 (during histone to protamine replacement) (TNP1), mRNA
4627	9741	14836	0.9	1.00E-58	M65963.1	NT	Human pithomone converting enzyme (NEC2) gene, exon 4
4695	10002	15085	4.9	1.00E-58	AI141083.1	EST_HUMAN	oz43h01.x1 Soares NihHAFu S1 Homo sapiens cDNA clone IMAGE:1678129.3
2182	7291	12503	9.9	8.00E-59	4507378	NT	Homo sapiens TATA box binding protein (TBP) mRNA
3088	8239	13339	6.2	5.00E-59	AI807484.1	EST_HUMAN	wf48c11.x1 Soares NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2358836.3



Table 4

3338	8482	3.9	5.00E-59	AL159142.1	NT	Novel human gene mapping to chromosome 22
4559	9677	5.9	5.00E-59	X83497.1	NT	H sapiens DNA for ZNF80-linked ERV9 long terminal repeat
776	5928	0.8	4.00E-59	D80006.1	NT	Human mRNA for KIAA0184 gene, partial cds
4685	9797	1.2	4.00E-59	4508758	NT	Human sapiens ryanodine receptor 3 (RYR3) mRNA
4685	9797	1.2	4.00E-59	4508758	NT	Human sapiens ryanodine receptor 3 (RYR3) mRNA
9	5217	2.0	3.00E-59	AW965524.1	EST_HUMAN	EST377582 MAGE resequences, MAGE. Homo sapiens cDNA
221	5413	1.4	3.00E-59	7662247	NT	Homo sapiens KIAA0680 gene product (KIAA0680), mRNA
1682	6806	3.6	3.00E-59	4505860	NT	Homo sapiens plasmalogen activator, tissue (PLATa) mRNA
1682	6806	3.6	3.00E-59	4505860	NT	Homo sapiens plasmalogen activator, tissue (PLATa) mRNA
2082	7194	2.8	3.00E-59	AF249745.1	NT	Homo sapiens chromosome 2q22 RhoGEF mRNA, complete cds
2082	7194	2.8	3.00E-59	AF249745.1	NT	Homo sapiens chromosome 2q22 RhoGEF mRNA, complete cds
3090	8241	3.7	3.00E-59	4502014	NT	Homo sapiens A kinase (PRKA) anchor protein 1 (AKAP1), mRNA
3090	8241	3.7	3.00E-59	4502014	NT	Homo sapiens A kinase (PRKA) anchor protein 1 (AKAP1), mRNA
3753	8891	1.2	3.00E-59	4508044	NT	Homo sapiens zona pellucida glycoprotein 2 (sperm receptor) (ZP2) mRNA
4683	9795	1.1	3.00E-59	4756329	NT	Homo sapiens Testis-specific XK-related protein on Y (XKRY) mRNA
4734	9845	1.9	3.00E-59	7427522	NT	Homo sapiens protein tyrosine phosphatase, receptor type, T (PTPRT), mRNA
157	5353	1.2	1.00E-59	BE296411.1	EST_HUMAN	601176757F1 NIH MGC_17 Homo sapiens cDNA clone IMAGE:3531927 5'
						caash11.s1 NC_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1309029 3' similar to
						TR:Q13537 Q13537 MER37 TRANSDUCIBLE ELEMENT, COMPLETE CONSENSUS
2575	7668	0.9	1.00E-59	AA748468.1	EST_HUMAN	SEQUENCE:.
1455	6582	1.0	8.00E-60	4759159	NT	Homo sapiens small nuclear ribonucleoprotein D3 polypeptide (18kD) (SNRPD3) mRNA
2125	7235	1.0	8.00E-60	5174656	NT	Homo sapiens differentiation-related gene 1 (nickel-specific induction protein) (RTP) mRNA
2125	7235	1.0	8.00E-60	5174656	NT	Homo sapiens differentiation-related gene 1 (nickel-specific induction protein) (RTP) mRNA
2125	7235	1.0	8.00E-60	5174656	NT	Homo sapiens differentiation-related gene 1 (nickel-specific induction protein) (RTP) mRNA
737	5891	2.3	7.00E-60	AF055066.1	NT	Homo sapiens MHC class 1 region
738	5891	11.0	7.00E-60	AF055066.1	NT	Homo sapiens MHC class 1 region
798	5849	1.2	7.00E-60	4504634	NT	Homo sapiens interleukin 10 receptor, beta (IL10RB), mRNA
2081	7193	0.6	7.00E-60	AF077188.1	NT	Homo sapiens cullin 4A (CUL4A) mRNA, complete cds
4088	9214	2.6	7.00E-60	4505488	NT	Homo sapiens ornithine decarboxylase 1 (ODC1) mRNA
78	5284	0.7	5.00E-60	AI807917.1	EST_HUMAN	wf52c07.x1 Soares NFL_T GBC_S1 Homo sapiens cDNA clone IMAGE:2359212 3'
78	5284	0.7	5.00E-60	AI807917.1	EST_HUMAN	wf52c07.x1 Soares NFL_T GBC_S1 Homo sapiens cDNA clone IMAGE:2359212 3'
2188	7297	0.9	4.00E-60	AW503208.1	EST_HUMAN	UI-HF-BNO-akt-g-07-Q-UL1 NIH MGC_50 Homo sapiens cDNA clone IMAGE:3076348 5'
2188	7297	0.9	4.00E-60	AW503208.1	EST_HUMAN	UI-HF-BNO-akt-g-07-Q-UL1 NIH MGC_50 Homo sapiens cDNA clone IMAGE:3076348 5'
2942	8093	1.1	4.00E-60	AA299037.1	EST_HUMAN	EST11498 Uleus Homo sapiens cDNA 5' end similar to reovirus-related pol
1826	6945	0.8	3.00E-60	6031190	NT	Homo sapiens profilin (PRB) mRNA
4354	9476	2.1	3.00E-60	AI271735.1	NT	Homo sapiens Xq pseudautosomal region: segment 1/2
1405	6532	1.0	2.00E-60	Z11694.1	NT	H. sapiens 41kDa protein kinase related to rat ERK2
1691	6815	1.3	2.00E-60	M24603.1	NT	Human bcr protein mRNA, 5' end
3839	8975	0.8	2.00E-60	AF231919.1	NT	Homo sapiens chromosome 21 unknown mRNA
511	5675	0.5	1.00E-60	BE178586.1	EST_HUMAN	PM3-HT0605-270200-001-806 HT0605 Homo sapiens cDNA

Table 4

2739	7823	13027	0.7	1,00E-60	L41825.1	NT	Homo sapiens CYP17 gene, 5' end
4874	9891	15065	1.1	1,00E-60	AL163285.2	NT	Homo sapiens chromosome 21 segment HS21C085
2635	7724	12927	1.4	8,00E-61	AW006478.1	EST_HUMAN	wf05b10.x1 NCI CGAP Co3 Homo sapiens cDNA clone IMAGE:2506555 3'
2635	7724	12928	1.4	8,00E-61	AW006478.1	EST_HUMAN	wf05b10.x1 NCI CGAP Co3 Homo sapiens cDNA clone IMAGE:2506555 3'
2921	8072		1.7	8,00E-61	X57147.1	NT	Homo sapiens endogenous retrovirus pHE 1 (ERV9)
122	5320	10450	0.9	7,00E-61	7706670	NT	Homo sapiens PXR2b protein (PXR2b), mRNA
122	5320	10451	0.9	7,00E-61	7706670	NT	Homo sapiens PXR2b protein (PXR2b), mRNA
123	5320	10450	0.9	7,00E-61	7706670	NT	Homo sapiens PXR2b protein (PXR2b), mRNA
123	5320	10451	0.9	7,00E-61	7706670	NT	Homo sapiens PXR2b protein (PXR2b), mRNA
265	5452	10577	0.7	6,00E-61	BE409310.1	EST_HUMAN	6013009338F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3635480 5'
784	5945	11098	0.6	6,00E-61	BE409310.1	EST_HUMAN	6013009338F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3635480 5'
1289	6428	11592	3.5	6,00E-61	AF119860.1	NT	Homo sapiens PRO2014 mRNA, complete cds
1612	6738	11908	1.0	6,00E-61	BE257400.1	EST_HUMAN	6011092338F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3350145 5'
1628	6754	11924	0.8	6,00E-61	AA596033.1	EST_HUMAN	nm6h09.s1 NCI CGAP Lart Homo sapiens cDNA clone IMAGE:1088897 3'
1655	6760	11953	0.6	5,00E-61	4506008	NT	Homo sapiens protein phosphatase 1, regulatory subunit 10 (PPP1R10) mRNA
3000	8152	13252	1.9	5,00E-61	AL163279.2	NT	Homo sapiens chromosome 21 segment HS21C079
3114	8263	13367	0.8	5,00E-61	AB020632.1	NT	Homo sapiens mRNA for KIAA0825 protein, partial cds
3161	8310	13422	1.9	5,00E-61	4502166	NT	Homo sapiens amyloid beta (A $\beta$ ) precursor protein (protease nexin-II, Alzheimer disease) (APP), mRNA
3899	9034		1.7	5,00E-61	AJ229041.1	NT	Homo sapiens 959 kb contig between AML1 and CBR1 on chromosome 21q22; segment 1/3
1424	6561		1.3	4,00E-61	W28189.1	EST_HUMAN	43c5 Human retina cDNA randomly primed sublibrary Homo sapiens cDNA
4119	9245	14329	1.1	3,00E-61	BE396279.1	EST_HUMAN	601309785F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3631220 5'
490	5655	10778	0.5	2,00E-61	8922828	NT	Homo sapiens hypothetical protein FLJ11026 (FLJ11026), mRNA
1194	6326	11482	1.4	2,00E-61	BE168410.1	EST_HUMAN	OV3-HT0513-060400-147-d01 HT0513 Homo sapiens cDNA
1194	6326	11483	1.4	2,00E-61	BE168410.1	EST_HUMAN	OV3-HT0513-060400-147-d01 HT0513 Homo sapiens cDNA
1642	6768	11939	1.3	2,00E-61	NS3039.1	EST_HUMAN	iy53d11.s1 Soares fetal liver spleen TNF $\alpha$ Homo sapiens cDNA clone IMAGE:246453 3'
2109	7220	12429	0.5	2,00E-61	4758003	NT	similar to gbL125444.60S RIBOSOMAL PROTEIN L35A (HUMAN);
2604	7694		1.2	2,00E-61	BE384973.1	EST_HUMAN	Homo sapiens calmagin (CLGN), mRNA
428	5595		0.9	1,00E-61	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
756	5908	11056	1.3	1,00E-61	5453829	NT	Homo sapiens origin recognition complex, subunit 2 (yeast homolog)-like (ORC2L) mRNA
1377	6505	11670	1.1	1,00E-61	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
1731	6854		1.0	1,00E-61	U32657.1	NT	Human polymorphic trinucleotide repeat in X-linked retinitis pigmentosa (RP3) gene region
1814	6933	12122	1.6	1,00E-61	6005983	NT	Homo sapiens zona pellucida glycoprotein 3A (sperm receptor) (ZP3A), mRNA
2150	7260	12467	0.5	1,00E-61	AW827281.1	EST_HUMAN	xt11b09.y1 NCI CGAP Lf5 Homo sapiens cDNA clone IMAGE:2693369 5' similar to
2804	7956	13085	1.7	1,00E-61	BE386363.1	EST_HUMAN	contains element MSR1 repetitive element;
3330	8474	13587	0.9	1,00E-61	7682319	NT	601273513F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3614667 5'
							Homo sapiens KIAA0806 gene product (KIAA0806), mRNA

Table 4

3671	8910	13904	1.5	1.00E-61	BE174455.1	EST_HUMAN	QVZ-HT0577-140300-077-g08 HT0577 Homo sapiens cDNA
4339	9462	14551	1.0	1.00E-61	4759249	NT	Homo sapiens TRAF family member-associated NFKB activator (TANK) mRNA
4339	9462	14552	1.0	1.00E-61	4759249	NT	Homo sapiens TRAF family member-associated NFKB activator (TANK) mRNA
4751	9862	14954	7.6	1.00E-61	AW298181.1	EST_HUMAN	U1-H-BWO-aj-b-08-0-U1.s1 NCL_CGAP_Sub6 Homo sapiens cDNA clone IMAGE:2732871.3
4751	9862	14954	7.6	1.00E-61	AW298181.1	EST_HUMAN	U1-H-BWO-aj-b-08-0-U1.s1 NCL_CGAP_Sub6 Homo sapiens cDNA clone IMAGE:2732871.3
4751	9862	14955	7.6	1.00E-61	AW298181.1	EST_HUMAN	U1-H-BWO-aj-b-08-0-U1.s1 NCL_CGAP_Sub6 Homo sapiens cDNA clone IMAGE:2732871.3
4878	9885	15067	0.9	1.00E-61	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
4451	9671	14670	0.8	8.00E-62	AA830420.1	EST_HUMAN	oc66h11.s1 NCL_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1354725.3 similar to SW:POL_MLVRK_P31796 POL POLYPROTEIN ;
4451	9671	14670	0.8	8.00E-62	AA830420.1	EST_HUMAN	NUCLEOLAR TRANSCRIPTION FACTOR 1 (UPSTREAM BINDING FACTOR 1) (UBF-1) (AUTOANTIGEN NOR-90)
3462	8603	13716	0.8	7.00E-62	P17480	SWISSPROT	Human zinc finger protein ZNF131 mRNA, partial cds
2869	8120		1.1	6.00E-62	U09410.1	NT	Human zinc finger protein ZNF131 mRNA, partial cds
410	5578	10715	1.5	5.00E-62	A1950528.1	EST_HUMAN	W51607.x1 NCL_CGAP_Lu28 Homo sapiens cDNA clone IMAGE:2547204.3 similar to SW:GG95_HUMAN_Q08379 GOLGIN-95, contains element MER22 repetitive element ;
2356	7458	12664	1.2	5.00E-62	AJ271735.1	NT	Homo sapiens Xq pseudautosomal region; segment 1/2
2356	7458	12665	1.2	5.00E-62	AJ271735.1	NT	Homo sapiens Xq pseudautosomal region; segment 1/2
3372	8515	13622	2.2	5.00E-62	4506758	NT	Homo sapiens gamma/beta receptor 3 (RYR3) mRNA
4233	9357	14439	1.7	5.00E-62	AA431093.1	EST_HUMAN	zw78609.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:782344.3 similar to SW:NRDC_RAT_P47245 NARLDYSIN ;
822	5972	11129	1.2	4.00E-62	AW161479.1	EST_HUMAN	aw71d03.y1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2781701.5 similar to gb:M37104 ATP SYNTHASE COUPLING FACTOR 6, MITOCHONDRIAL
822	5972	11130	1.2	4.00E-62	AW161479.1	EST_HUMAN	aw71d03.y1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2781701.5 similar to gb:M37104 ATP SYNTHASE COUPLING FACTOR 6, MITOCHONDRIAL
823	5972	11128	1.6	4.00E-62	AW161479.1	EST_HUMAN	aw71d03.y1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2781701.5 similar to gb:M37104 ATP SYNTHASE COUPLING FACTOR 6, MITOCHONDRIAL
823	5972	11130	1.6	4.00E-62	AW161479.1	EST_HUMAN	aw71d03.y1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2781701.5 similar to gb:M37104 ATP SYNTHASE COUPLING FACTOR 6, MITOCHONDRIAL
1446	6573		0.9	4.00E-62	AA311281.1	EST_HUMAN	EST_182043 Jurkat T-cells V Homo sapiens cDNA 5' end
2409	7508	12715	1.4	4.00E-62	A1827900.1	EST_HUMAN	EST_182043 Jurkat T-cells V Homo sapiens cDNA 5' end
2409	7508	12716	1.4	4.00E-62	A1827900.1	EST_HUMAN	EST_182043 Jurkat T-cells V Homo sapiens cDNA 5' end
2821	7972	13074	1.1	4.00E-62	L10391.1	NT	EST_182043 Jurkat T-cells V Homo sapiens cDNA 5' end
3353	8497		6.6	4.00E-62	4557887	NT	EST_182043 Jurkat T-cells V Homo sapiens cDNA 5' end
4947	10052		2.0	4.00E-62	AJ243213.1	NT	EST_182043 Jurkat T-cells V Homo sapiens cDNA 5' end
68	5275	10400	1.1	3.00E-62	4557794	NT	EST_182043 Jurkat T-cells V Homo sapiens cDNA 5' end

Table 4

3008	8160	13260	1.0	3,00E-62	AB040909.1	NT	Homo sapiens mRNA for KIAA1476 protein, partial cds
3008	8160	13261	1.0	3,00E-62	AB040909.1	NT	Homo sapiens mRNA for KIAA1476 protein, partial cds
3640	8779	13872	1.9	3,00E-62	X52858.1	NT	Human cyclophilin-related processed pseudogene
1211	6342	11501	0.5	2,00E-62	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
1028	6168	11323	1.2	1,00E-62	AF248540.1	NT	Homo sapiens intersecin 2 (SH3D1B) mRNA, complete cds
1526	6653	11820	2.5	1,00E-62	L78810.1	NT	Homo sapiens ADP/ATP carrier protein (ANT-2) gene, complete cds
1758	6879	12060	1.0	1,00E-62	AA623207.1	EST_HUMAN	a70611, r1 Soares, JNHMPu_S1 Homo sapiens cDNA clone IMAGE:1047404 5' similar to WP:K01H12.1 CE03453:
2884	8035	13136	1.1	1,00E-62	AL039044.1	EST_HUMAN	DKFZ566F104_r1 566 (synonym: htkd2) Homo sapiens cDNA clone DKFZp566F104 5'
4426	9547	14640	1.3	1,00E-62	8923201	NT	Homo sapiens hypothetical protein FLJ20212 (FLJ20212), mRNA
335	5516	10641	0.7	9,00E-63	AW616405.1	EST_HUMAN	CV4-ST0234-181199-037-f05 ST0234 Homo sapiens cDNA
2297	7401		0.6	9,00E-63	C18159.1	EST_HUMAN	C18159 Human placenta cDNA (TFJlwara) Homo sapiens cDNA clone GEN-558C10 5'
3955	9088	14170	7.4	9,00E-63	AB002348.2	NT	Homo sapiens mRNA for KIAA0350 protein, partial cds
3955	9088	14171	7.4	9,00E-63	AB002348.2	NT	Homo sapiens mRNA for KIAA0350 protein, partial cds
2296	7400	12609	0.6	8,00E-63	4557734	NT	Homo sapiens monamine oxidase A (MAOA), nuclear gene encoding mitochondrial protein, mRNA
2322	7425	12634	0.8	8,00E-63	5031810	NT	Homo sapiens IL2-inducible T-cell kinase (ITK), mRNA
3415	8557	13666	3.8	8,00E-63	AF198349.1	NT	Gallus gallus Dact2 protein (Dact2) mRNA, complete cds
3415	8557	13667	3.8	8,00E-63	AF198349.1	NT	Gallus gallus Dact2 protein (Dact2) mRNA, complete cds
4168	9284	14375	3.4	8,00E-63	AL163288.2	NT	Homo sapiens chromosome 21 segment HS21C068
913	6059		0.6	7,00E-63	AI872137.1	EST_HUMAN	wms5g11.x1 NC1_CGAP_U12 Homo sapiens cDNA clone IMAGE:2439908 3'
3279	8424	13533	1.0	4,00E-63	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C078
1893	7010	12198	0.7	3,00E-63	AB018260.1	NT	Homo sapiens mRNA for KIAA0717 protein, partial cds
2753	7837	13038	1.3	3,00E-63	J00310.1	NT	Human Mel-RNA-1 gene 1
2791	6349	11510	3.1	3,00E-63	6005963	NT	Homo sapiens zinc finger protein 144 (Mzf-18) (ZNF144), mRNA
4445	9565	14661	3.2	3,00E-63	AW954734.1	EST_HUMAN	EST368804 MAGE reassquences, MAGEC Homo sapiens cDNA
184	5378	10504	1.1	2,00E-63	U07804.1	NT	Human DNA topoisomerase I mRNA, partial cds
191	5385	10512	0.6	2,00E-63	4885228	NT	Homo sapiens eyes absent (Drosophila) homolog 2 (EYA2), mRNA
489	5654		1.4	2,00E-63	4557624	NT	Homo sapiens glutamate-cysteine ligase (gamma-glutamylcysteine synthetase), catalytic (72.8kD) (GLCLC) mRNA
809	5960	11115	1.8	2,00E-63	7657042	NT	Homo sapiens Down syndrome candidate region 1 (DSCR1), mRNA
1547	6674	11844	0.9	2,00E-63	AB030388.1	NT	Homo sapiens RHCE mRNA for Rh blood CE group antigen polypeptide, complete cds
1547	6674	11845	0.9	2,00E-63	AB030388.1	NT	Homo sapiens RHCE mRNA for Rh blood CE group antigen polypeptide, complete cds
3119	8288	13373	1.7	2,00E-63	4502166	NT	Homo sapiens amyloid beta (A4) precursor protein (protease nexin-II, Alzheimer disease) (APP), mRNA
3248	8395	13502	1.8	2,00E-63	AF109718.1	NT	Homo sapiens chromosome 3 subtelomeric region
3631	8968	14067	1.9	2,00E-63	L39891.1	NT	Homo sapiens poly/cystic kidney disease-associated protein (PKD1) gene, complete cds
4760	9871	14966	1.1	2,00E-63	AF111167.2	NT	Homo sapiens jun dimerization protein gene, partial cds; cfos gene, complete cds; and unknown gene

Table 4

4246	9371	14450	2.9	1.00E-63	F08485.1	EST_HUMAN	HSCZVD111 normalized infant brain cDNA Homo sapiens cDNA clone c-zvd11
4246	9371	14451	2.9	1.00E-63	F08485.1	EST_HUMAN	HSCZVD111 normalized infant brain cDNA Homo sapiens cDNA clone c-zvd11
1307	6436	11602	0.6	9.00E-64	H30687.1	EST_HUMAN	y078602.r1 Soares adult brain N2b4HB55Y Homo sapiens cDNA clone IMAGE:184034 5'
1307	6436	11603	0.6	9.00E-64	H30687.1	EST_HUMAN	y078602.r1 Soares adult brain N2b4HB55Y Homo sapiens cDNA clone IMAGE:184034 5'
1030	6170		2.7	8.00E-64	BE280796.1	EST_HUMAN	601155232F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3139038 5'
4874	9786		5.2	8.00E-64	AL163213.2	NT	Homo sapiens chromosome 21 segment HS21C013
3486	8627		1.0	7.00E-64	BE394321.1	EST_HUMAN	601311455F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3633204 5'
4625	9739	14835	2.4	7.00E-64	4507490	NT	Homo sapiens thymal oligopeptidase 1 (THOP1) mRNA
4625	9739	14836	2.4	7.00E-64	4507490	NT	Homo sapiens thymal oligopeptidase 1 (THOP1) mRNA
1692	6816	11995	0.6	6.00E-64	A1651992.1	EST_HUMAN	wb51e07.x1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:2309220 3' similar to gb:M15182 BETA-GLUCURONIDASE PRECURSOR (HUMAN);
1692	6816	11996	0.6	6.00E-64	A1651992.1	EST_HUMAN	wb51e07.x1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:2309220 3' similar to gb:M15182 BETA-GLUCURONIDASE PRECURSOR (HUMAN);
2675	7762	12962	1.1	6.00E-64	BE252937.1	EST_HUMAN	601117529F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3367986 5'
3084	8235	13333	3.7	6.00E-64	AW026445.1	EST_HUMAN	wv13e03.x1 NCI_CGAP_Bm23 Homo sapiens cDNA clone IMAGE:2529436 3'
3084	8235	13334	3.7	6.00E-64	AW026445.1	EST_HUMAN	wv13e03.x1 NCI_CGAP_Bm23 Homo sapiens cDNA clone IMAGE:2529436 3'
803	5854	11106	0.8	5.00E-64	AF231919.1	NT	Homo sapiens chromosome 21 unknown mRNA
803	5854	11107	0.8	5.00E-64	AF231919.1	NT	Homo sapiens chromosome 21 unknown mRNA
1402	6529	11699	0.9	5.00E-64	L40933.1	NT	Homo sapiens phosphoglucomutase-related protein (PGMRP) gene, complete cds
1402	6529	11700	0.9	5.00E-64	L40933.1	NT	Homo sapiens phosphoglucomutase-related protein (PGMRP) gene, complete cds
1683	6607	11989	0.8	5.00E-64	U89358.1	NT	Human I(3)mb protein homolog mRNA, complete cds
2796	6592	11767	1.0	5.00E-64	7662205	NT	Homo sapiens KIAA0618 gene product (KIAA0618), mRNA
2796	6592	11768	1.0	5.00E-64	7662205	NT	Homo sapiens KIAA0618 gene product (KIAA0618), mRNA
3876	9012	14107	5.6	5.00E-64	AF017433.1	NT	Homo sapiens putative transcription factor CR53 (CR53) mRNA, partial cds
2151	7261	12468	1.4	3.00E-64	C18895.1	EST_HUMAN	C18895 Human placenta cDNA (TFu1wara) Homo sapiens cDNA clone GEN:569E02 5'
1072	8210	11363	0.9	2.00E-64	AA609940.1	EST_HUMAN	a09408.s1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:1031151 3'
1376	6504	11669	1.3	2.00E-64	4757701	NT	Homo sapiens eIF4E-like cap-binding protein (4EHP) mRNA
2478	7576		0.6	2.00E-64	A1927030.1	EST_HUMAN	w087b01.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2462281 3' similar to contains element L1 repetitive element;
2484	7581	12784	1.1	2.00E-64	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
2484	7581	12785	1.1	2.00E-64	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
3101	8251	13355	2.6	2.00E-64	4504068	NT	Homo sapiens glutamic-oxaloacetic transaminase 2, mitochondrial (asparagine aminotransferase 2) (GOT2), nuclear gene encoding mitochondrial protein, mRNA
3719	8856	13948	1.3	2.00E-64	AW958145.1	EST_HUMAN	EST370215 IMAGE (resequences), IMAGE Homo sapiens cDNA
3719	8856	13949	1.3	2.00E-64	AW958145.1	EST_HUMAN	EST370215 IMAGE (resequences), IMAGE Homo sapiens cDNA
258	5446	10571	0.6	1.00E-64	AF231919.1	NT	Homo sapiens chromosome 21 unknown mRNA
1740	6863	12040	2.1	1.00E-64	A1929419.1	EST_HUMAN	au60c01.x1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2519136 3' similar to gb:l21696_cds1 PROTHYMOSIN ALPHA (HUMAN); contains element MSF1 repetitive element;

Table 4

3466	8607	13720	5.6	1.00E-64	AF196779.1	NT	Homo sapiens transcription factor IGHM enhancer 3, JM11 protein, JM4 protein, JM5 protein, T54 protein, JM10 protein, A4 differentiation-dependent protein, triple LIM domain protein 6, and synapophysin genes, complete cds; and L-type calcium channel $\alpha$ -
3536	8677	13780	1.3	1.00E-64	AF228527.1	NT	Homo sapiens TRIAD3 mRNA, partial cds
3536	8677	13781	1.3	1.00E-64	AF228527.1	NT	Homo sapiens TRIAD3 mRNA, partial cds
4142	9268		2.7	1.00E-64	8922772	NT	Homo sapiens hypothetical protein FLJ10923 (FLJ10923), mRNA
1598	6725	11895	0.5	9.00E-65	8922772	NT	Homo sapiens hypothetical protein FLJ10923 (FLJ10923), mRNA
2230	7337	12549	0.9	9.00E-65	X89211.1	NT	H. sapiens DNA for endogenous retroviral like element
2230	7337	12550	0.9	9.00E-65	X89211.1	NT	H. sapiens DNA for endogenous retroviral like element
1880	6998		3.0	6.00E-65	AA50929.1	EST_HUMAN	n86d10.s1 NCI CGAP P-11 Homo sapiens cDNA clone IMAGE:999379 similar to gbK03002.60S RIBOSOMAL PROTEIN L32 (HUMAN);
615	5773	10894	0.9	5.00E-65	AF064604.1	NT	Homo sapiens KE03 protein mRNA, partial cds
1331	6460	11626	0.6	5.00E-65	7661951	NT	Homo sapiens KIAA0156 gene product (KIAA0156), mRNA
1331	6460	11627	0.6	5.00E-65	7661951	NT	Homo sapiens KIAA0156 gene product (KIAA0156), mRNA
2110	7221	12430	1.0	5.00E-65	AB033768.1	NT	Homo sapiens hPAD-colony10 mRNA for peptidylarginine deiminase type I, complete cds
2338	7438	12648	1.0	5.00E-65	BE31673.1	EST_HUMAN	601142861F1 NIH_MGC_14 Homo sapiens cDNA clone IMAGE:3506774.5
3217	8365	13476	1.9	5.00E-65	4507648	NT	Homo sapiens ubiquitin specific protease 13 (isopeptidase T-3) (USP13), mRNA
3217	8365	13477	1.9	5.00E-65	4507648	NT	Homo sapiens ubiquitin specific protease 13 (isopeptidase T-3) (USP13), mRNA
186	5380	10507	1.1	4.00E-65	AL120419.1	EST_HUMAN	DKFZP761G108.t1 761 (synonym: hamy2) Homo sapiens cDNA clone DKFZP761G108.5
728	5682	11023	0.5	4.00E-65	AI268468.1	EST_HUMAN	qna46a01.x1 Soares_placenta_8109weeks_2NbhP8109W Homo sapiens cDNA clone IMAGE:1691800.3
728	5682	11024	0.5	4.00E-65	AI268468.1	EST_HUMAN	qna46a01.x1 Soares_placenta_8109weeks_2NbhP8109W Homo sapiens cDNA clone IMAGE:1691800.3
1062	6200	11354	0.8	4.00E-65	4826735	NT	IMAGE:1891800.3
1470	6597	11772	3.0	4.00E-65	4506636	NT	IMAGE:1891800.3
2288	7393	12600	1.0	4.00E-65	BE221469.1	EST_HUMAN	Homo sapiens fragile X mental retardation, autosomal homolog 1 (FXR1), mRNA
2288	7393	12601	1.0	4.00E-65	BE221469.1	EST_HUMAN	Homo sapiens ribosomal protein L34 (RPL34), mRNA
5138	10233	15307	1.0	4.00E-65	9055269	NT	Homo sapiens ribosomal protein L34 (RPL34), mRNA
5138	10233	15308	1.0	4.00E-65	9055269	NT	Homo sapiens ribosomal protein L34 (RPL34), mRNA
1212	7868		1.8	3.00E-65	X78932.1	NT	Homo sapiens ribosomal protein L34 (RPL34), mRNA
1780	6901	12089	1.1	3.00E-65	AI000692.1	EST_HUMAN	H. sapiens HZF9 mRNA for zinc finger protein
3239	8386	13494	1.4	3.00E-65	4504950	NT	ov23f03.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1638173.3 similar to contains element MSR1 repetitive element;
3660	8799	13893	1.0	3.00E-65	AI000692.1	EST_HUMAN	ov23f03.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1638173.3 similar to contains element MSR1 repetitive element;

Table 4

4551	9670	14760	1.4	3.00E-65	6912385	NT	Homo sapiens rab8 GTPase activating protein (GAP and centrosome-associated) (GAPCEN), mRNA
528	5682	10814	1.3	1.00E-65	7657495	NT	Homo sapiens putative Rab5 GDP/GTP exchange factor homologue (RABEX5), mRNA
1994	7110	12313	0.9	1.00E-65	AB040946.1	NT	Homo sapiens mRNA for KIAA1513 protein, partial cds
3326	8470	13584	0.9	1.00E-65	BE468881.1	EST_HUMAN	h224a08.x1 NC1 CGAP GC8 Homo sapiens cDNA clone IMAGE:3208888.3
3917	8051	14138	2.1	1.00E-65	4504082	NT	Homo sapiens glypican 4 (GPC4) mRNA
3917	9051	14139	2.1	1.00E-65	4504082	NT	Homo sapiens glypican 4 (GPC4) mRNA
4112	9238	14321	2.4	1.00E-65	AW028340.1	EST_HUMAN	w09cd9.x1 NC1 CGAP Gas4 Homo sapiens cDNA clone IMAGE:2543152.3
4112	9238	14322	2.4	1.00E-65	AW028340.1	EST_HUMAN	w09cd9.x1 NC1 CGAP Gas4 Homo sapiens cDNA clone IMAGE:2543152.3
4415	9535	14624	1.1	1.00E-65	AW136725.1	EST_HUMAN	U1-H-B11-adm-a-11-Q-U1.s1 NC1 CGAP Sub3 Homo sapiens cDNA clone IMAGE:2717108.3
4415	9535	14625	1.1	1.00E-65	AW136725.1	EST_HUMAN	U1-H-B11-adm-a-11-Q-U1.s1 NC1 CGAP Sub3 Homo sapiens cDNA clone IMAGE:2717108.3
65	5273	10396	0.5	9.00E-66	AL160311.1	NT	Novel human gene mapping to chromosome 22
65	5273	10397	0.5	9.00E-66	AL160311.1	NT	Novel human gene mapping to chromosome 22
1332	6461	11628	0.9	9.00E-66	5031980	NT	Homo sapiens 26S proteasome-associated pad1 homolog (POH1) mRNA
1332	6461	11628	0.9	9.00E-66	5031980	NT	Homo sapiens 26S proteasome-associated pad1 homolog (POH1) mRNA
1468	6595	12779	1.5	9.00E-66	M87299.1	NT	Human transposon-like element, partial
2460	7578	12779	1.0	9.00E-66	8823943	NT	Homo sapiens transcription factor NRF (NRF), mRNA
2460	7578	12780	1.0	9.00E-66	8823943	NT	Homo sapiens transcription factor NRF (NRF), mRNA
3826	8963	14061	0.9	9.00E-66	M72393.1	NT	Human calcium-dependent phospholipid-binding protein (PLA2) mRNA, complete cds
3826	8963	14062	0.9	9.00E-66	M72393.1	NT	Human calcium-dependent phospholipid-binding protein (PLA2) mRNA, complete cds
4591	9705	14798	0.9	8.00E-66	AA424304.1	EST_HUMAN	zv90005.t1 Soares NIHMPu S1 Homo sapiens cDNA clone IMAGE:767048.5
4269	9394	14476	1.2	6.00E-66	A1924653.1	EST_HUMAN	w057n07.x1 NC1 CGAP Lu19 Homo sapiens cDNA clone IMAGE:2449597.3 similar to
4269	9394	14477	1.2	6.00E-66	A1924653.1	EST_HUMAN	w057n07.x1 NC1 CGAP Lu19 Homo sapiens cDNA clone IMAGE:2449597.3 similar to
4269	9394	14478	1.2	6.00E-66	A1924653.1	EST_HUMAN	w057n07.x1 NC1 CGAP Lu19 Homo sapiens cDNA clone IMAGE:2449597.3 similar to
1344	6472	11639	0.8	5.00E-66	BE064410.1	EST_HUMAN	RC4-BT031-141189-011-h06 BT0311 Homo sapiens cDNA
773	5925	11074	0.8	4.00E-66	6679816	NT	Mus musculus fragile X mental retardation syndrome 1 homolog (Fmr1), mRNA
2235	7342	12554	0.7	4.00E-66	X89211.1	NT	H. sapiens DNA for endogenous retroviral like element
2425	7524		1.3	4.00E-66	AJ223364.1	NT	Homo sapiens germ-line DNA upstream of Jkappa locus
1408	6535	11707	8.9	3.00E-66	4502098	NT	Homo sapiens solute carrier family 25 (mitochondrial carrier, adenine nucleotide translocator), member 5 (SLC25A5), nuclear gene encoding mitochondrial protein, mRNA
1408	6535	11708	8.9	3.00E-66	4502098	NT	Homo sapiens solute carrier family 25 (mitochondrial carrier, adenine nucleotide translocator), member 5 (SLC25A5), nuclear gene encoding mitochondrial protein, mRNA

Table 4

1939	7056	12249	0.8	3.00E-66	N55323.1	EST_HUMAN	yz27g12.r1 Soares, multiple sclerosis_2NBHMSP Homo sapiens cDNA clone IMAGE:284326 5' similar to SW-H2B1_TIGCA P35068 HISTONE H2B.1/H2B.2. [2] PIR:B56612:
1939	7056	12250	0.8	3.00E-66	N55323.1	EST_HUMAN	yz27g12.r1 Soares, multiple sclerosis_2NBHMSP Homo sapiens cDNA clone IMAGE:284326 5' similar to SW-H2B1_TIGCA P35068 HISTONE H2B.1/H2B.2. [2] PIR:B56612:
1939	7056	12251	0.8	3.00E-66	N55323.1	EST_HUMAN	yz27g12.r1 Soares, multiple sclerosis_2NBHMSP Homo sapiens cDNA clone IMAGE:284326 5' similar to SW-H2B1_TIGCA P35068 HISTONE H2B.1/H2B.2. [2] PIR:B56612:
3079	8230	13329	5.5	3.00E-66	7682223	NT	Homo sapiens KIAA0649 gene product (KIAA0649), mRNA
45	5255	10369	1.0	2.00E-66	7657334	NT	Homo sapiens Mismatch/NIK-related kinase (MINK), mRNA
45	5255	10370	1.0	2.00E-66	7657334	NT	Homo sapiens Mismatch/NIK-related kinase (MINK), mRNA
416	5205	10306	0.9	2.00E-66	4505524	NT	Homo sapiens origin recognition complex, subunit 5 (yeast homolog)-like (ORC5L), mRNA, and translated products
416	5205	10307	0.9	2.00E-66	4505524	NT	Homo sapiens origin recognition complex, subunit 5 (yeast homolog)-like (ORC5L), mRNA, and translated products
1784	6904	12092	0.7	2.00E-66	AL163301.2	NT	Homo sapiens chromosome 21 segment HS21C101
2944	8095	13201	1.0	2.00E-66	X65859.1	NT	H. sapiens pseudogene for the low affinity IL-8 receptor
3975	9107	14189	0.9	2.00E-66	AF108389.1	NT	Homo sapiens sodium/calcium exchanger isoform NaCa3 (NCX1) mRNA, complete cds
4556	9674	14765	12.7	2.00E-66	AJ133267.2	NT	Homo sapiens HLA-B gene for human leucocyte antigen B
4556	9674	14766	12.7	2.00E-66	AJ133267.2	NT	Homo sapiens HLA-B gene for human leucocyte antigen B
4829	9937		0.8	8.00E-67	M78158.1	EST_HUMAN	EST1750 Subtracted Hippocampus, Striatum (cat. #936205) Homo sapiens cDNA clone HHCPN31 similar to L1 repetitive element
376	5582	10716	2.1	7.00E-67	AW162232.1	EST_HUMAN	auf5d02.x1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2782083.3 similar to gb:M37104 ATP SYNTHASE COUPLING FACTOR 6, MITOCHONDRIAL PRECURSOR (HUMAN);
1360	6488	11654	1.0	7.00E-67	AA363416.1	EST_HUMAN	EST16812 Testis (Homo sapiens cDNA 5' end similar to similar to C. elegans hypothetical protein, cosmid ZK353
1535	6661	11828	1.0	7.00E-67	W65947.1	EST_HUMAN	IMAGE:416049 5'
1535	6661	11829	1.0	7.00E-67	W65947.1	EST_HUMAN	IMAGE:416049 5'
1988	7103	12305	1.1	7.00E-67	7657243	NT	IMAGE:416049 5'
1988	7103	12306	1.1	7.00E-67	7657243	NT	IMAGE:416049 5'
2779	5582	10716	2.4	7.00E-67	AW162232.1	EST_HUMAN	IMAGE:416049 5'
547	5710	10829	1.3	6.00E-67	X68868.1	NT	IMAGE:416049 5'
778	5930	11078	0.5	6.00E-67	Z17227.1	NT	IMAGE:416049 5'
1252	6361	11540	0.9	6.00E-67	Y14320.1	NT	IMAGE:416049 5'
3131	8280	13388	1.2	6.00E-67	4506434	NT	IMAGE:416049 5'



Table 4

3391	8533	13638	1.2	6.00E-67	4507332	NT	Homo sapiens Synapsin III (SYN3) mRNA, and translated products
3391	8533	13639	1.2	6.00E-67	4507332	NT	Homo sapiens Synapsin III (SYN3) mRNA, and translated products
4035	8163	14246	1.3	6.00E-67	AL163201.2	NT	Homo sapiens chromosome 21 segment HS21C001
4035	8163	14247	1.3	6.00E-67	AL163201.2	NT	Homo sapiens chromosome 21 segment HS21C001
4607	9721	14815	3.4	6.00E-67	7657020	NT	Homo sapiens DKFZP434P211 protein (DKFZP434P211). mRNA
4607	9721	14816	3.4	6.00E-67	7657020	NT	Homo sapiens DKFZP434P211 protein (DKFZP434P211). mRNA
5125	9988		2.1	6.00E-67	4507848	NT	Homo sapiens ubiquitin specific protease 13 (isopeptidase T-3) (USP13) mRNA
3184	8333	13445	2.5	5.00E-67	AF009660.1	NT	Homo sapiens T cell receptor beta locus, TCRBV7S3A2 to TCRBV12S2 region
1306	6435	11601	0.6	4.00E-67	R90819.1	EST_HUMAN	Yn0241.1 Soares adult brain N264HB59Y Homo sapiens cDNA clone IMAGE:167253 5'
2782	5775	10897	0.9	3.00E-67	AA333768.1	EST_HUMAN	EST37803 Embryo, 9 week Homo sapiens cDNA 5' end
3407	8549	13657	1.1	3.00E-67	BE064410.1	EST_HUMAN	RC4-BT0311-141199-011-H06 BT0311 Homo sapiens cDNA
4596	9710	14802	3.1	3.00E-67	AW869159.1	EST_HUMAN	MR3-SN0068-040500-008-f01 SN0068 Homo sapiens cDNA
180	5374	10499	0.7	2.00E-67	BE348354.1	EST_HUMAN	hw16g09x1 NCI CGAP Lu24 Homo sapiens cDNA clone IMAGE:3163136 3' similar to
827	5976	11136	2.0	2.00E-67	AW816405.1	EST_HUMAN	WP-F23H11.9 CE08617 ;
1089	8227		0.6	2.00E-67	AF167460.1	NT	QV4-ST0234-181189-037-f05 ST0234 Homo sapiens cDNA
1841	6956	12146	0.5	2.00E-67	BE303037.1	EST_HUMAN	Homo sapiens double stranded RNA activated protein kinase (PKR) gene, exons 2a, 2, 3, and 4
1841	6956	12147	0.5	2.00E-67	BE303037.1	EST_HUMAN	ba72g05.y1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:2905976 5' similar to
2381	7483	12685	1.2	2.00E-67	4758795	NT	TR:094892 Q94892 KIAA0798 PROTEIN. ;
3422	8564	13676	3.9	2.00E-67	AA625755.1	EST_HUMAN	ba72g05.y1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:2805976 5' similar to
3921	8055	14142	2.3	2.00E-67	AL163300.2	NT	TR:094892 Q94892 KIAA0798 PROTEIN. ;
4716	8828		1.1	2.00E-67	AA418535.1	EST_HUMAN	ba72g05.y1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:745392 3'
253	5441	10568	1.5	1.00E-67	4502166	NT	z919g01.s1 Soares testis NHT Homo sapiens cDNA clone IMAGE:745392 3'
3794	8931	14024	5.0	8.00E-68	AA209456.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C100
3794	8931	14025	5.0	8.00E-68	AA209456.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C100
1849	6967		0.8	6.00E-68	AW503842.1	EST_HUMAN	z919g01.s1 Soares testis NHT Homo sapiens cDNA clone IMAGE:767296 5'
56	5285	10386	0.9	5.00E-68	AA304324.1	EST_HUMAN	z919g01.s1 Soares testis NHT Homo sapiens cDNA clone IMAGE:767296 5'
56	5285	10387	0.9	5.00E-68	AA304324.1	EST_HUMAN	z919g01.s1 Soares testis NHT Homo sapiens cDNA clone IMAGE:767296 5'
57	5265	10386	1.0	5.00E-68	AA304324.1	EST_HUMAN	z919g01.s1 Soares testis NHT Homo sapiens cDNA clone IMAGE:767296 5'
57	5265	10387	1.0	5.00E-68	AA304324.1	EST_HUMAN	z919g01.s1 Soares testis NHT Homo sapiens cDNA clone IMAGE:767296 5'
785	7864	11087	0.9	5.00E-68	AF231919.1	NT	z919g01.s1 Soares testis NHT Homo sapiens cDNA clone IMAGE:767296 5'
785	7864	11088	0.9	5.00E-68	AF231919.1	NT	z919g01.s1 Soares testis NHT Homo sapiens cDNA clone IMAGE:767296 5'
802	5953	11104	1.3	5.00E-68	AF231919.1	NT	z919g01.s1 Soares testis NHT Homo sapiens cDNA clone IMAGE:767296 5'
802	5953	11105	1.3	5.00E-68	AF231919.1	NT	z919g01.s1 Soares testis NHT Homo sapiens cDNA clone IMAGE:767296 5'

Table 4

3108	8258	13362	2.6	5.00E-68	AB037852.1	NT	Homo sapiens mRNA for KIAA1431 protein, partial cds
4900	10007		17.2	4.00E-68	PO4406	SWISSPROT	GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, LIVER
3611	8750	13844	5.6	3.00E-68	AF236082.1	NT	Mus musculus G-protein coupled receptor GPR73 (Gpr73) mRNA, complete cds
2832	7983		12.3	2.00E-68	DD0522.1	NT	Cricetus longicaudatus mRNA for EF-1 alpha, complete cds
4563	9699	14793	1.7	2.00E-68	AB008681.1	NT	Homo sapiens gene for activin receptor type IIB, complete cds
72	5278	10405	1.3	1.00E-68	4505222	NT	Homo sapiens meningioma (disrupted in balanced translocation) 1 (MNI1) mRNA
293	5479	10610	3.2	1.00E-68	AW616405.1	EST_HUMAN	QV4-ST0234-181199-037-05 ST0234 Homo sapiens cDNA
2205	7314	12526	1.3	1.00E-68	AF119860.1	NT	Homo sapiens PRO2014 mRNA, complete cds
2205	7314	12527	1.3	1.00E-68	AF119860.1	NT	Homo sapiens PRO2014 mRNA, complete cds
2728	7812	13018	1.0	1.00E-68	AW451832.1	EST_HUMAN	U1-H-B13-alk-f-01-Q-U1.s1 NCI_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:2737272 3'
3928	9062	14149	1.0	1.00E-68	BE296032.1	EST_HUMAN	601177002F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3532344 5'
4954	10059	15130	1.0	1.00E-68	AA897343.1	EST_HUMAN	a47g12.s1 Scores_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1460518 3'
19	5228	10329	0.6	9.00E-69	5031976	NT	Homo sapiens pre-B-cell colony-enhancing factor (PBEF) mRNA
19	5228	10330	0.6	9.00E-69	5031976	NT	Homo sapiens pre-B-cell colony-enhancing factor (PBEF) mRNA
1011	6151	11304	0.6	9.00E-69	5031980	NT	Homo sapiens 26S proteasome-associated pad1 homolog (POH1) mRNA
1011	6151	11305	0.6	9.00E-69	5031980	NT	Homo sapiens 26S proteasome-associated pad1 homolog (POH1) mRNA
4037	9165	14250	0.8	9.00E-69	4757867	NT	Homo sapiens v-rel murine sarcoma viral oncogene homolog B1 (BRAF) mRNA
3340	8484		1.2	8.00E-69	AJ237744.1	NT	Homo sapiens RIB1R1 gene (partial), exon 12
509	5673		0.6	4.00E-69	AI873630.1	EST_HUMAN	wm26h11.x1 NCI_CGAP_U14 Homo sapiens cDNA clone IMAGE:2437125 3'
380	5586	10719	1.0	3.00E-69	BE258012.1	EST_HUMAN	601110371F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3351352 5'
596	5754	10872	0.6	3.00E-69	AF221712.1	NT	Homo sapiens Smad- and Olf-interacting zinc finger protein mRNA, partial cds
							yd08a02.r1 Scores Infant brain 11NB Homo sapiens cDNA clone IMAGE:24880 5' similar to SF-A48636 A48836 SPEGF III/EGF REPEAT-CONTAINING FIBROPELIN-LIKE PROTEIN SEA URCHIN:
1536	6662		1.4	3.00E-69	T80514.1	EST_HUMAN	Homo sapiens lymphatic vessel endothelial hyaluronan receptor 1 (LYVE-1) mRNA
2325	7428		0.9	3.00E-69	5729910	NT	Homo sapiens lymphatic vessel endothelial hyaluronan receptor 1 (LYVE-1) mRNA
3990	9122	14208	0.9	3.00E-69	AI765888.1	EST_HUMAN	wb6g08.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2385758 3'
124	5566	10702	1.0	2.00E-69	AF160252.1	NT	Homo sapiens KIAA0553 protein gene, complete cds; and alpha1b protein gene, partial cds
124	5566	10703	1.0	2.00E-69	AF160252.1	NT	Homo sapiens KIAA0553 protein gene, complete cds; and alpha1b protein gene, partial cds
398	5566	10702	1.7	2.00E-69	AF160252.1	NT	Homo sapiens KIAA0553 protein gene, complete cds; and alpha1b protein gene, partial cds
398	5566	10703	1.7	2.00E-69	AF160252.1	NT	Homo sapiens KIAA0553 protein gene, complete cds; and alpha1b protein gene, partial cds
1842	6860	12148	1.2	2.00E-69	BE297857.1	EST_HUMAN	601109444F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3350074 5'
2813	7984		2.7	2.00E-69	AA431157.1	EST_HUMAN	zw71g02.r1 Scores_testis_NHT Homo sapiens cDNA clone IMAGE:781682 5'
1675	6799	11977	0.9	1.00E-69	AF053768.1	NT	Rattus norvegicus brain specific contactin-binding protein CBP90 mRNA, partial cds
2284	7939	12597	0.6	8.00E-70	AA230303.1	EST_HUMAN	nc13612.r1 NCI_CGAP_P1 Homo sapiens cDNA clone IMAGE:1008023
4277	8402	14486	2.2	8.00E-70	L77566.1	NT	Homo sapiens DGS-1 mRNA, 3' end
1771	8692	12078	0.7	7.00E-70	AI497807.1	EST_HUMAN	hm89101.x1 NCI_CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2165305 3'

Table 4

1771	6892	12080	0.7	7.00E-70	AA497807.1	EST_HUMAN	Im8901.x1 NCI CGAP Brm25 Homo sapiens cDNA clone IMAGE:2165305.3'
1886	7006	12192	0.6	7.00E-70	AA282955.1	EST_HUMAN	Z15h04.l1 NCI CGAP GC81 Homo sapiens cDNA clone IMAGE:713239.5'
2018	7131		1.3	7.00E-70	5031868	NT	Homo sapiens tumor suppressor deleted in oral cancer-related 1 (DOC-IR) mRNA
4132	8258	14338	3.9	7.00E-70	4757723	NT	Homo sapiens adenylate cyclase 3 (ADCY3) mRNA
							Homo sapiens amyloid beta (A4) precursor protein (protease nexin-II, Alzheimer disease) (APP) mRNA
853	8002	11162	0.7	6.00E-70	4502166	NT	Human Ku (p70p69) subunit mRNA, complete cds
2090	7201	12406	1.4	6.00E-70	M30938.1	NT	Human Ku (p70p69) subunit mRNA, complete cds
2461	7560	12764	1.0	6.00E-70	8923899	NT	Homo sapiens CMP-N-acetylneuraminic acid synthase (LOC55907), mRNA
2505	7945	12800	0.7	5.00E-70	7662307	NT	Homo sapiens KIAA0792 gene product (KIAA0792), mRNA
2505	7945	12801	0.7	5.00E-70	7662307	NT	Homo sapiens KIAA0792 gene product (KIAA0792), mRNA
1571	6697	11864	0.9	3.00E-70	BE071796.1	EST_HUMAN	RC0-BT0522-071299-011-a12 BT0522 Homo sapiens cDNA
1571	6697	11865	0.9	3.00E-70	BE071796.1	EST_HUMAN	RC0-BT0522-071299-011-a12 BT0522 Homo sapiens cDNA
							yy07a10.l1 Soares melanocyte 2NbhM Homo sapiens cDNA clone IMAGE:270522.5' similar to SW:ID3H_RAT P29266 3-HYDROXYISOBUTYRATE DEHYDROGENASE PRECURSOR ;
674	5830	10958	4.5	2.00E-70	NA2161.1	EST_HUMAN	yy07a10.l1 Soares melanocyte 2NbhM Homo sapiens cDNA clone IMAGE:270522.5' similar to SW:ID3H_RAT P29266 3-HYDROXYISOBUTYRATE DEHYDROGENASE PRECURSOR ;
							qx51h01.x1 NCI CGAP Pan1 Homo sapiens cDNA clone IMAGE:2004913.3'
674	5830	10959	4.5	2.00E-70	NA2161.1	EST_HUMAN	qx51h01.x1 NCI CGAP Pan1 Homo sapiens cDNA clone IMAGE:2004913.3'
689	5844	10981	0.7	2.00E-70	AI246899.1	EST_HUMAN	Homo sapiens hypothetical protein FLJ20758 (FLJ20758), mRNA
1004	6144	11298	0.6	2.00E-70	8923869	NT	Homo sapiens hypothetical protein FLJ20758 (FLJ20758), mRNA
1167	6301	11456	0.7	2.00E-70	7661983	NT	Homo sapiens KIAA0193 gene product (KIAA0193), mRNA
1167	6301	11457	0.7	2.00E-70	7661983	NT	Homo sapiens KIAA0193 gene product (KIAA0193), mRNA
1387	6514	11680	1.0	2.00E-70	BE467311.1	EST_HUMAN	hz66c12.x1 NCI CGAP Lu24 Homo sapiens cDNA clone IMAGE:3212768.3'
1708	6831	12011	0.8	2.00E-70	AL163202.2	NT	Homo sapiens chromosome 21 segment HS21C002
							z46g04.l1 Soares retina N264HR Homo sapiens cDNA clone IMAGE:380214.5' similar to SW:GAG_HTLIA P03345 GAG POLYPROTEIN ;
2272	7378		1.3	2.00E-70	AA054010.1	EST_HUMAN	EST373895 MAGG resequences, MAGG Homo sapiens cDNA
2344	7446	12653	2.9	2.00E-70	AW961822.1	EST_HUMAN	EST373895 MAGG resequences, MAGG Homo sapiens cDNA
2344	7446	12654	2.9	2.00E-70	AW961822.1	EST_HUMAN	EST373895 MAGG resequences, MAGG Homo sapiens cDNA
3983	9095	14180	4.0	2.00E-70	M69181.1	NT	Human nonmuscle myosin heavy chain-B (MYH10) mRNA, partial cds
							Homo sapiens transglutaminase 3 (E polypeptide, protein-glutamine-gamma-glutamyltransferase) (TGMS3) mRNA
3347	8491		3.0	1.00E-70	4507476	NT	glutaminyltransferase) (TGMS3) mRNA
3469	8610	13722	1.0	9.00E-71	AW936999.1	EST_HUMAN	GM3-DT0032-151299-055-h12 DT0032 Homo sapiens cDNA
1743	8866	12044	0.6	8.00E-71	AA594019.1	EST_HUMAN	m28607.s1 NCI CGAP Gatl Homo sapiens cDNA clone IMAGE:1085220.3'
							TCBAP2E0520 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project=TCBA Homo sapiens cDNA clone TCBAP0520
3717	8854	13946	0.9	7.00E-71	BE244676.1	EST_HUMAN	project=TCBA Homo sapiens cDNA clone TCBAP0520
1818	6937	12127	1.0	6.00E-71	7705404	NT	Homo sapiens heme-binding protein (HEBP), mRNA
1818	6937	12128	1.0	6.00E-71	7705404	NT	Homo sapiens heme-binding protein (HEBP), mRNA
2576	7669		0.8	6.00E-71	BE266255.1	EST_HUMAN	601191652F1 NIH_MGC 7 Homo sapiens cDNA clone IMAGE:3535549.5'
2163	7272	12483	1.3	5.00E-71	AF056322.1	NT	Homo sapiens SP100-HMG nuclear autoantigen (SP100) mRNA, complete cds
4030	9158	14242	1.4	5.00E-71	AW816405.1	EST_HUMAN	QV4-ST0234-181199-037-f05 ST0234 Homo sapiens cDNA
5144	10239	15314	3.2	5.00E-71	AIB29496.1	EST_HUMAN	w18h10.x1 NCI CGAP U11 Homo sapiens cDNA clone IMAGE:2425315.3'

Table 4

97	5304	10431	1.1	4.00E-71	4507592	NT	Homo sapiens tumor necrosis factor (ligand) superfamily, member 10 (TNFSF10) mRNA
347	5528	10655	39.0	4.00E-71	AF157626.1	NT	Equus caballus glyceraldehyde-3-phosphate dehydrogenase mRNA, partial cds
347	5528	10656	39.0	4.00E-71	AF157626.1	NT	Equus caballus glyceraldehyde-3-phosphate dehydrogenase mRNA, partial cds
2850	8001	13098	0.9	4.00E-71	7705414	NT	Homo sapiens hook1 protein (HOOK1), mRNA
2850	8001	13099	0.9	4.00E-71	7705414	NT	Homo sapiens hook1 protein (HOOK1), mRNA
2850	8001	13099	0.9	4.00E-71	7705414	NT	Homo sapiens plasminogen (PLG) mRNA
2857	8008	13107	1.6	4.00E-71	4505880	NT	Homo sapiens SP100-HMG nuclear autoantigen (SP100) mRNA, complete cds
4330	9453	14541	3.4	4.00E-71	AF056322.1	NT	Homo sapiens SP100-HMG nuclear autoantigen (SP100) mRNA, complete cds
4913	10020	15099	5.0	4.00E-71	7657602	NT	Homo sapiens putative home-binding protein (SOUL), mRNA
1210	6341	11500	0.9	2.00E-71	AL163206.2	NT	Homo sapiens chromosome 21 segment HS21C006
622	5781	10903	0.7	1.00E-71	AU077927.1	EST_HUMAN	oy15603.s1 Soares_senescent_fibroblasts_NbHSF Homo sapiens cDNA clone IMAGE:1665916 3' similar to contains LOR1.b2 LOR1 repetitive element;
926	6073	11231	0.7	1.00E-71	7706281	NT	Homo sapiens neuronal cell death-related protein (LOC51616), mRNA
1084	6222	11373	1.4	1.00E-71	AF205890.1	NT	Homo sapiens disabled-2 gene, exons 2 through 15 and complete cds
1317	6446	11612	3.8	1.00E-71	AF012872.1	NT	Homo sapiens phosphatidylinositol 4-kinase 230 (p4K230) mRNA, complete cds
2036	7149	12353	1.2	1.00E-71	AB017007.1	NT	Homo sapiens PMS2L16 mRNA, partial cds
2036	7149	12354	1.2	1.00E-71	AB017007.1	NT	Homo sapiens PMS2L16 mRNA, partial cds
2661	7750	12948	1.8	1.00E-71	7657153	NT	Homo sapiens hairy/enhancer-cell-split related with YRPW motif-like (HEYL), mRNA
3457	8598	13711	1.2	1.00E-71	AF118666.1	NT	Homo sapiens inorganic pyrophosphatase mRNA, complete cds
3546	8687	13786	4.7	1.00E-71	AF246219.1	NT	Homo sapiens SNARE protein kinase SNARK mRNA, complete cds
3546	8687	13789	4.7	1.00E-71	AF246219.1	NT	Homo sapiens SNARE protein kinase SNARK mRNA, complete cds
3597	8736	13830	0.9	1.00E-71	BE122850.1	EST_HUMAN	02_15 Human Epidermal Keratinocyte Subtraction Library- Upregulated Transcripts Homo sapiens cDNA clone 02_15 5' similar to Homo sapiens chromosome 19
3597	8736	13831	0.9	1.00E-71	BE122850.1	EST_HUMAN	02_15 Human Epidermal Keratinocyte Subtraction Library- Upregulated Transcripts Homo sapiens cDNA clone 02_15 5' similar to Homo sapiens chromosome 19
3681	8820	13913	1.9	1.00E-71	AF218904.1	NT	Homo sapiens attractin precursor (ATRN) gene, exon 19
4370	9492	14582	1.9	1.00E-71	D28476.1	NT	Homo sapiens attractin precursor (ATRN) gene, exon 19
401	5569	10705	1.2	9.00E-72	AI857635.1	EST_HUMAN	wk95g03.x1 NCI_CGAP_Lu19 Homo sapiens cDNA clone IMAGE:2423188 3' similar to TR:O86705 O86705 HYPOTHETICAL 38.6 KD PROTEIN; contains Alu repetitive element;
401	5569	10706	1.2	9.00E-72	AI857635.1	EST_HUMAN	wk95g03.x1 NCI_CGAP_Lu19 Homo sapiens cDNA clone IMAGE:2423188 3' similar to TR:O86705 O86705 HYPOTHETICAL 38.6 KD PROTEIN; contains Alu repetitive element;
4023	9151	14232	5.2	7.00E-72	4501866	NT	Homo sapiens aconitase 2, mitochondrial (ACO2), nuclear gene encoding mitochondrial protein, mRNA
4023	9151	14233	5.2	7.00E-72	4501866	NT	Homo sapiens aconitase 2, mitochondrial (ACO2), nuclear gene encoding mitochondrial protein, mRNA
4023	9151	14234	5.2	7.00E-72	4501866	NT	Homo sapiens aconitase 2, mitochondrial (ACO2), nuclear gene encoding mitochondrial protein, mRNA
1122	6259		0.9	5.00E-72	L11645.1	NT	Homo sapiens alpha-tubulin mRNA, complete cds
211	5404	10528	1.1	4.00E-72	8922990	NT	Homo sapiens hypothetical protein FLJ1316 (FLJ1316), mRNA

Table 4

865	6033	4.9	3.00E-72	AA723823.1	EST_HUMAN	ah3a206.s1 Soares testis_NHT Homo sapiens cDNA clone 1310280.3'
1139	6275	2.1	3.00E-72	U16306.1	NT	Human chondroitin sulfate proteoglycan versican V0 splice-variant precursor peptide mRNA, complete cds
1139	6275	2.1	3.00E-72	U16306.1	NT	Human chondroitin sulfate proteoglycan versican V0 splice-variant precursor peptide mRNA, complete cds
3037	8189	10.5	3.00E-72	AL229043.1	NT	Homo sapiens 959 kb contig between AML1 and CBR1 on chromosome 21q22, segment 3/3
3241	8386	2.6	3.00E-72	8923548	NT	Homo sapiens hypothetical protein FLJ20585 (FLJ20585), mRNA
3750	8888	2.5	3.00E-72	S77589.1	NT	TCR V delta 2-C alpha =T-cell receptor delta and C alpha fusion gene (alternatively spliced, splice junction) [human, precursor B-cell line REH, mRNA Partial, 211 nt]
4835	8943	0.9	3.00E-72	AI654337.1	EST_HUMAN	wb31a08.x1 NCI_CGAP GC8 Homo sapiens cDNA clone IMAGE:2307254.3'
2030	7143	0.9	1.00E-72	AA846225.1	EST_HUMAN	al83d02.s1 Soares_papillary_thyroid_tumor_NbHPA Homo sapiens cDNA clone IMAGE:1387395
1443	6570	1.2	9.00E-73	AW374968.1	EST_HUMAN	3'
5102	10196	1.0	9.00E-73	AW867850.1	EST_HUMAN	MRO-CT0063-071099-002-h11 CT0063 Homo sapiens cDNA
1022	6181	1.0	8.00E-73	AW071755.1	EST_HUMAN	MRO-SN0040-050500-002-001 SN0040 Homo sapiens cDNA
1399	6526	1.1	8.00E-73	AI024877.1	EST_HUMAN	MR0-SN0040-050500-002-001 SN0040 Homo sapiens cDNA
1118	6255	0.8	7.00E-73	8923290	NT	ws55c06.x1 NCI_CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2501098.3' similar to
3261	8408	1.1	7.00E-73	AL163206.2	NT	TR-O59050 Q59050 HYPOTHETICAL PROTEIN MJ1656.;
4863	9970	1.6	7.00E-73	AL163282.2	NT	TR-O59050 Q59050 HYPOTHETICAL PROTEIN MJ1656.;
152	5348	0.8	6.00E-73	AL163218.2	NT	ov39h08.x1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:1639743.3'
1247	6376	1.4	3.00E-73	FO0548.1	EST_HUMAN	Homo sapiens hypothetical protein FLJ20309 (FLJ20309), mRNA
1247	6376	1.4	3.00E-73	FO0548.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C082
1247	6376	1.4	3.00E-73	FO0548.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C082
833	5982	0.6	2.00E-73	AF139697.1	NT	Homo sapiens chromosome 21 segment HS21C018
1902	7020	0.5	2.00E-73	AW888081.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C018
2251	7357	1.1	2.00E-73	U01317.1	NT	Homo sapiens chromosome 21 segment HS21C018
3144	8293	3.5	2.00E-73	4502582	NT	HSB10E082 STRATAGENE Human skeletal muscle cDNA library, cat. #936215. Homo sapiens cDNA clone 10E08
3503	8645	1.0	2.00E-73	7669539	NT	HSB10E082 STRATAGENE Human skeletal muscle cDNA library, cat. #936215. Homo sapiens cDNA clone 10E08
3503	8645	1.0	2.00E-73	7669539	NT	transcript variant 3, mRNA
2434	7533	0.9	1.00E-73	AF198349.1	NT	Homo sapiens Parkinson disease (autosomal recessive, juvenile) 2, parkin (PARK2), transcript variant 3, mRNA
2073	7185	1.0	9.00E-74	AW054828.1	EST_HUMAN	Gallus gallus Dact2 protein (Dact2) mRNA, complete cds
723	5877	1.4	8.00E-74	4557426	NT	ws60d04.x1 NCI_CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2501575.3' similar to
1906	7023	1.1	7.00E-74	AI001689.1	NT	TR-Q13541 Q13541 4E-BINDING PROTEIN 1.;
3286	8431	1.0	7.00E-74	AL163266.2	NT	Homo sapiens CD38-like 4 (CD39L4) mRNA
						Homo sapiens NKG2D gene, exon 10
						Homo sapiens chromosome 21 segment HS21C046

Table 4

1106	6244	11397	0.9	6.00E-74	AF109907.1	NT	Homo sapiens S164 gene, partial cds; P51 and hypothetical protein genes, complete cds; and S171 gene, partial cds
1609	6736	11905	1.0	6.00E-74	AW263177.1	EST_HUMAN	h78g07.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2700636 3'
2268	7374	12582	3.6	6.00E-74	BE388260.1	EST_HUMAN	60128352.F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3605453 5'
2268	7374	12583	3.6	6.00E-74	BE388260.1	EST_HUMAN	60128352.F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3605453 5'
2834	7985	13085	1.4	6.00E-74	AW014039.1	EST_HUMAN	U1-H-B10-aah-h-03-Q-U1.s1 NCI_CGAP_Sub1 Homo sapiens cDNA clone IMAGE:2709365 3'
2834	7985	13086	1.4	6.00E-74	AW014039.1	EST_HUMAN	U1-H-B10-aah-h-03-Q-U1.s1 NCI_CGAP_Sub1 Homo sapiens cDNA clone IMAGE:2709365 3'
3652	8791	13884	2.6	6.00E-74	BE048846.1	EST_HUMAN	h54611.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3132332 3'
3652	8791	13885	2.6	6.00E-74	BE048846.1	EST_HUMAN	h54611.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3132332 3'
4826	9934	15024	1.2	6.00E-74	H09912.1	EST_HUMAN	ym05g03.r1 Soares Infant brain 1N1B Homo sapiens cDNA clone IMAGE:46895 5'
887	6035	11193	0.9	5.00E-74	AW020986.1	EST_HUMAN	d17c09.y1 Morton Fetal Cochlea Homo sapiens cDNA clone IMAGE:2483704 5'
2689	7756		5.2	5.00E-74	AW362756.1	EST_HUMAN	PM0-CT0289-271099-001-h07 CT0289 Homo sapiens cDNA
278	5465	10595	0.6	4.00E-74	D87675.1	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
834	5983	11143	1.7	4.00E-74	AB028942.1	NT	Homo sapiens mRNA for KIAA1019 protein, partial cds
1919	7036	12224	0.9	4.00E-74	AB028898.1	NT	ORCTL4 genes, complete cds
1919	7036	12225	0.9	4.00E-74	AB028898.1	NT	ORCTL4 genes, complete cds
2027	7140	12340	1.6	4.00E-74	4506192	NT	ORCTL4 genes, complete cds
2027	7140	12341	1.6	4.00E-74	4506192	NT	ORCTL4 genes, complete cds
2085	7187	12402	1.2	4.00E-74	AB032994.1	NT	Homo sapiens proteasome (prosome, macropain) subunit, beta type, 1 (PSMB1) mRNA
2377	7479	12681	1.0	4.00E-74	AJ006976.1	NT	Homo sapiens PLP gene
3052	8203	13304	4.4	4.00E-74	AJ006976.1	NT	Homo sapiens PLP gene
3483	8624	13736	0.9	4.00E-74	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
3973	9105	14187	1.3	4.00E-74	AL163247.2	NT	Homo sapiens chromosome 21 segment HS21C047
4457	9577	14674	1.6	4.00E-74	7682183	NT	Homo sapiens KIAA0569 gene product (KIAA0569) mRNA
4512	9631	14724	0.8	4.00E-74	Z17227.1	NT	Homo sapiens mRNA for transmembrane receptor protein
5006	10108	15176	3.8	4.00E-74	4504326	NT	Homo sapiens hydroxacyl-Coenzyme A dehydrogenase/3-ketoacyl-Coenzyme A thiolase/enoyl-Coenzyme A hydratase (trifunctional protein), beta subunit (HADHB) mRNA
5006	10108	15177	3.8	4.00E-74	4504326	NT	Homo sapiens hydroxacyl-Coenzyme A dehydrogenase/3-ketoacyl-Coenzyme A thiolase/enoyl-Coenzyme A hydratase (trifunctional protein), beta subunit (HADHB) mRNA
2849	8000	13096	1.1	3.00E-74	AA234789.1	EST_HUMAN	z778b10.r1 Soares_NhhMPu_S1 Homo sapiens cDNA clone IMAGE:669499 5' similar to gb:X04106.cds1 CALCIUM-DEPENDENT PROTEASE, SMALL (HUMAN);
2849	8000	13097	1.1	3.00E-74	AA234789.1	EST_HUMAN	z778b10.r1 Soares_NhhMPu_S1 Homo sapiens cDNA clone IMAGE:669499 5' similar to gb:X04106.cds1 CALCIUM-DEPENDENT PROTEASE, SMALL (HUMAN);
3203	8351		2.2	3.00E-74	AT796960.1	EST_HUMAN	we25c07.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2342124 3' similar to TR:Q13537 Q13537 SIMILAR TO POGO ELEMENT. ;

Table 4

3703	8000	13096	4.8	3.00E-74	AA234789.1	EST_HUMAN	z778b10.1 Soares_NihMPu_S1 Homo sapiens cDNA clone IMAGE:669499 5' similar to gb:XC4106_cds1 CALCIUM-DEPENDENT PROTEASE, SMALL (HUMAN);
3703	8000	13097	4.8	3.00E-74	AA234789.1	EST_HUMAN	z778b10.1 Soares_NihMPu_S1 Homo sapiens cDNA clone IMAGE:669499 5' similar to gb:XC4106_cds1 CALCIUM-DEPENDENT PROTEASE, SMALL (HUMAN);
942	6089	11246	126.2	2.00E-74	7669491	NT	Homo sapiens glyceraldehyde-3-phosphate dehydrogenase (GAPD), mRNA
942	6089	11247	126.2	2.00E-74	7669491	NT	Homo sapiens glyceraldehyde-3-phosphate dehydrogenase (GAPD), mRNA
1158	6293	11448	1.0	2.00E-74	AF020092.1	NT	Human endogenous retrovirus HERV-K.147D
1224	6354	11518	1.2	2.00E-74	AB50528.1	EST_HUMAN	wx51e07.x1 NCI_CGAP_Lu28 Homo sapiens cDNA clone IMAGE:2547204 3' similar to SW:GG55_HUMAN Q08379 GOLGIN-95, contains element MIER22 repetitive element;
1577	6703	11872	1.1	2.00E-74	4885198	NT	Homo sapiens epidermal growth factor receptor (avian erythroblastic leukemia viral (v-erb-b) oncogene homolog) (EGFR) mRNA
1577	6703	11873	1.1	2.00E-74	4885198	NT	Homo sapiens epidermal growth factor receptor (avian erythroblastic leukemia viral (v-erb-b) oncogene homolog) (EGFR) mRNA
2558	7652	12855	1.1	2.00E-74	AI557280.1	EST_HUMAN	PT2.1_15_G11.1.tumor2 Homo sapiens cDNA 3'
4937	10043	15114	2.0	2.00E-74	AL355092.1	NT	Novel human gene mapping to chromosome 22
4937	10043	15115	2.0	2.00E-74	AL355092.1	NT	Novel human gene mapping to chromosome 22
4942	10048	15120	1.9	2.00E-74	J02963.1	NT	Human platelet glycoprotein IIb mRNA, 3' end
47	5257	10373	1.0	1.00E-74	7657334	NT	Homo sapiens Mischapen/NIK-related kinase (MINK), mRNA
334	5515	10640	1.2	1.00E-74	AW816405.1	EST_HUMAN	QVA-ST0234-181199-037-405 ST0234 Homo sapiens cDNA
491	5656	10779	1.2	1.00E-74	8922829	NT	Homo sapiens hypothetical protein FLJ11026 (FLJ11026), mRNA
497	5661	10784	0.9	1.00E-74	X02344.1	NT	Homo sapiens beta 2 gene
588	5748	10863	1.4	1.00E-74	4508020	NT	Homo sapiens zinc finger protein 259 (ZNF259) mRNA
983	6128	11283	0.7	1.00E-74	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
2179	7286	12500	2.2	1.00E-74	AB002059.1	NT	Homo sapiens DNA for Human P2XM, complete cds
3100	8250	13354	6.0	1.00E-74	4758697	NT	Homo sapiens mannosidase, alpha, class 2A, member 1 (MAN2A1), mRNA
3887	9023	14116	4.6	1.00E-74	AL163288.2	NT	Homo sapiens chromosome 21 segment HS21C068
3974	9106	14188	0.9	1.00E-74	BE083080.1	EST_HUMAN	RC2-BT0642-270300-019-108 BT0642 Homo sapiens cDNA
4170	9286	14377	0.9	1.00E-74	BE467769.1	EST_HUMAN	h23n08.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3213663 3' similar to WP:80511.12 CE17351;
5112	10208	15286	1.2	1.00E-74	D83327.1	NT	Homo sapiens DCRR1 mRNA, partial cds
2607	7697		1.5	8.00E-75	AF178228.1	NT	Homo sapiens DNA cytosine-5 methyltransferase 3B (DNMT3B) mRNA, complete cds
2273	7379	12587	0.9	6.00E-75	AI817415.1	EST_HUMAN	Homo sapiens DNA cytosine-5 methyltransferase 3B (DNMT3B) mRNA, complete cds
5128	10223		0.9	6.00E-75	AA789285.1	EST_HUMAN	Homo sapiens DNA cytosine-5 methyltransferase 3B (DNMT3B) mRNA, complete cds
107	5310	10435	1.1	4.00E-75	BE081333.1	EST_HUMAN	Q15377 Y-CHROMOSOME RNA RECOGNITION MOTIF PROTEIN;
451	5617		1.2	4.00E-75	N36757.1	EST_HUMAN	Q15377 Y-CHROMOSOME RNA RECOGNITION MOTIF PROTEIN;
1728	6851	12030	0.5	4.00E-75	AW697230.1	EST_HUMAN	Q15377 Y-CHROMOSOME RNA RECOGNITION MOTIF PROTEIN;
2618	7869	13072	4.7	4.00E-75	BE409464.1	EST_HUMAN	Q15377 Y-CHROMOSOME RNA RECOGNITION MOTIF PROTEIN;
986	6131	11286	1.0	3.00E-75	AF157623.1	NT	Q15377 Y-CHROMOSOME RNA RECOGNITION MOTIF PROTEIN;
987	6131	11286	0.8	3.00E-75	AF157623.1	NT	Q15377 Y-CHROMOSOME RNA RECOGNITION MOTIF PROTEIN;

Table 4

1795	6915	12101	0.7	3.00E-75	AB011153.1	NT	Homo sapiens mRNA for KIAA0581 protein, partial cds
2065	7177	12384	1.1	3.00E-75	4507334	NT	Homo sapiens synaptobrevin 1 (SYN1), mRNA
2373	7475	12676	1.3	3.00E-75	4759153	NT	Homo sapiens synaptosomal-associated protein, 29kD (SNAP29) mRNA
							zks3c07.s1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:486540 3' similar to gb:X65857_cds1 OLFATORY RECEPTOR-LIKE PROTEIN HGMPOYE (HUMAN);
2402	7501	12708	1.0	3.00E-75	AA042813.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C001
2988	8140	13243	1.2	3.00E-75	AL183201.2	NT	Homo sapiens mRNA for KIAA0581 protein, partial cds
3152	8301	13409	1.3	3.00E-75	AB011153.1	NT	Homo sapiens mRNA for KIAA0581 protein, partial cds
3306	8451	13562	1.0	3.00E-75	MT23383.1	NT	Human calcium-dependent phospholipid-binding protein (PLA2) mRNA, complete cds
3308	8451	13563	1.0	3.00E-75	MT23383.1	NT	Human calcium-dependent phospholipid-binding protein (PLA2) mRNA, complete cds
4077	9204	14281	1.4	3.00E-75	D87675.1	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
4336	9459	14547	1.0	3.00E-75	7662421	NT	Homo sapiens KIAA0971 protein (KIAA0971), mRNA
							cg60d02.x1 NCI_CGAP_U14 Homo sapiens cDNA clone IMAGE:2632707 3' similar to contains PTR7.11 PTR7 repetitive element;
2255	7361	12569	1.8	1.00E-75	AW168135.1	EST_HUMAN	H.sapiens ERCC2 gene, exons 1 & 2 (partial)
2916	8067	13176	3.2	1.00E-75	X62221.1	NT	Wb30b10.x1 NCI_CGAP_G06 Homo sapiens cDNA clone IMAGE:2307163 3' similar to TR:O75235 O75235 TRAP1;
38	5248	10357	1.5	9.00E-76	A1652648.1	EST_HUMAN	Wb30b10.x1 NCI_CGAP_G06 Homo sapiens cDNA clone IMAGE:2307163 3' similar to TR:O75235 O75235 TRAP1;
38	5248	10357	1.5	9.00E-76	A1652648.1	EST_HUMAN	Wb30b10.x1 NCI_CGAP_G06 Homo sapiens cDNA clone IMAGE:2307163 3' similar to TR:O75235 O75235 TRAP1;
38	5248	10357	1.5	9.00E-76	A1652648.1	EST_HUMAN	Wb30b10.x1 NCI_CGAP_G06 Homo sapiens cDNA clone IMAGE:2307163 3' similar to TR:O75235 O75235 TRAP1;
214	5407	10530	0.9	9.00E-76	Z45834.1	EST_HUMAN	HSZVC061 normalized infant brain cDNA Homo sapiens cDNA clone c-zvc06
2384	7466		1.2	9.00E-76	AA702415.1	EST_HUMAN	z185b07.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:447541 3'
923	6070	11227	0.6	8.00E-76	4504374	NT	Homo sapiens H factor 1 (complement) (HF1) mRNA
923	6070	11228	0.6	8.00E-76	4504374	NT	Homo sapiens H factor 1 (complement) (HF1) mRNA
2880	8031	13135	1.1	8.00E-76	7706724	NT	Homo sapiens mediator (Sur2), mRNA
							Homo sapiens dihydrodipicolinate dehydrogenase (E3 component of pyruvate dehydrogenase complex, 2-oxo-glutarate complex, branched chain keto acid dehydrogenase complex) (DLD) mRNA
759	5911	11059	1.4	7.00E-76	5016092	NT	Homo sapiens cAMP-specific phosphodiesterase 8A (PDE8A) mRNA, partial cds
3254	8401	13507	2.6	7.00E-76	AF058490.1	NT	Homo sapiens lymphocyte antigen 75 (LY75) mRNA, and translated products
3260	8407	13514	7.1	7.00E-76	4505052	NT	Homo sapiens core-binding factor, runt domain, alpha subunit 2; translocated to, 1; cyclin D-related (CBFA2T1) mRNA
3293	8439	13549	1.1	7.00E-76	4757915	NT	Homo sapiens septaplatin reductase (7,8-dihydrobiopterin:NADP+ oxidoreductase) (SPR) mRNA
4275	9400	14483	4.3	7.00E-76	4507184	NT	Homo sapiens septaplatin reductase (7,8-dihydrobiopterin:NADP+ oxidoreductase) (SPR) mRNA
4275	9400	14484	4.3	7.00E-76	4507184	NT	Homo sapiens septaplatin reductase (7,8-dihydrobiopterin:NADP+ oxidoreductase) (SPR) mRNA
1214	6344		6.7	6.00E-76	BE396253.1	EST_HUMAN	601312019F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3658757 5'
1899	7017	12205	1.3	5.00E-76	DE3874.1	NT	Human mRNA for HMG-1, complete cds
1899	7017	12206	1.3	5.00E-76	DE3874.1	NT	Human mRNA for HMG-1, complete cds
1899	7017	12207	1.3	5.00E-76	DE3874.1	NT	Human mRNA for HMG-1, complete cds
1561	6707	11877	1.0	3.00E-76	4503476	NT	Homo sapiens eukaryotic translation elongation factor 1 beta 2 (EEF1B2) mRNA



Table 4

1581	6707	11876	1.0	3.00E-78	4503476	NT	Homo sapiens eukaryotic translation elongation factor 1 beta 2 (EEF1B2) mRNA
280	5467	10597	1.2	2.00E-76	D84295.1	NT	Human mRNA for possible protein TPRDII, complete cds
339	5520	10644	1.3	2.00E-76	D84295.1	NT	Human mRNA for possible protein TPRDII, complete cds
339	5520	10645	1.3	2.00E-76	D84295.1	NT	Human mRNA for possible protein TPRDII, complete cds
453	5618		0.7	2.00E-76	4557662	NT	Homo sapiens immunoglobulin (CD78a) binding protein 1 (IGBP1) mRNA
575	5735	10852	1.1	2.00E-76	4503944	NT	Homo sapiens glucagon (GCG) mRNA
1014	6154	11310	1.0	2.00E-76	4758053	NT	Homo sapiens cAMP responsive element binding protein 1 (CREB1) mRNA
1518	6645	11813	0.6	2.00E-76	4504028	NT	Homo sapiens GM2 ganglioside activator protein (GM2A) mRNA
1518	6645	11814	0.6	2.00E-76	4504028	NT	Homo sapiens GM2 ganglioside activator protein (GM2A) mRNA
1886	7004	12190	0.5	2.00E-76	AA253954.1	EST_HUMAN	z66011.1 Striatum schizo brain S11 Homo sapiens cDNA clone IMAGE:701925 3'
2811	7962	13068	2.8	2.00E-76	P23266	SWISSPROT	OLFACTORY RECEPTOR-LIKE PROTEIN F5
3257	8404	13511	2.0	2.00E-76	AA445992.1	EST_HUMAN	z66402.1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:780986 3' similar to
3257	8404	13511	2.0	2.00E-76	AA445992.1	EST_HUMAN	SW:ITB5_HUMAN P18084 INTEGRIN BETA-5 SUBUNIT PRECURSOR.
3257	8404	13511	2.0	2.00E-76	AA445992.1	EST_HUMAN	SW:ITB5_HUMAN P18084 INTEGRIN BETA-5 SUBUNIT PRECURSOR.
4043	5467	10597	0.9	2.00E-76	D84295.1	NT	Human mRNA for possible protein TPRDII, complete cds
4600	9714	14806	4.5	2.00E-76	4758981	NT	Human mRNA for possible protein TPRDII, complete cds
4600	9714	14806	4.5	2.00E-76	4758981	NT	Human mRNA for possible protein TPRDII, complete cds
4867	9874	15059	6.3	2.00E-76	AW87618.1	EST_HUMAN	QV3-OT0028-220300-132-b11 OT0028 Homo sapiens cDNA
5068	10166	15242	1.3	2.00E-76	5031660	NT	Homo sapiens EGF-like repeats and discoidin I-like domains 3 (EDIL3), mRNA
4200	9326	14413	2.2	1.00E-76	D63674.1	NT	Human mRNA for HMG-1, complete cds
4200	9326	14414	2.2	1.00E-76	D63674.1	NT	Human mRNA for HMG-1, complete cds
715	5869	11007	0.9	7.00E-77	AW370405.1	EST_HUMAN	RC2-BT0266-241099-011-02 BT0266 Homo sapiens cDNA
1887	7005	12191	1.2	7.00E-77	AA625755.1	EST_HUMAN	z66101.1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:745392 3'
2360	7462	12668	0.8	7.00E-77	4505944	NT	Homo sapiens polymerase (RNA) II (DNA directed) polypeptide E (25KD) (POLR2E) mRNA
2360	7462	12668	0.8	7.00E-77	4505944	NT	Homo sapiens polymerase (RNA) II (DNA directed) polypeptide E (25KD) (POLR2E) mRNA
2360	7462	12669	0.8	7.00E-77	4505944	NT	Homo sapiens polymerase (RNA) II (DNA directed) polypeptide E (25KD) (POLR2E) mRNA
282	5449	10575	1.5	6.00E-77	4504600	NT	Homo sapiens interferon (alpha, beta and omega) receptor 2 (IFNAR2) mRNA
1125	6262	11414	0.9	6.00E-77	AW957753.1	EST_HUMAN	EST369823 MAGE resequences, MAGE Homo sapiens cDNA
1524	6651	11819	17.6	6.00E-77	A1204066.1	EST_HUMAN	qe77h12.x1 Soares_fetal_lung_NbHL19W Homo sapiens cDNA clone IMAGE:1745063 3'
1216	6346	11505	0.6	5.00E-77	AF041015.1	NT	7 Homo sapiens glucokinase (GCK) gene, exon 2
1337	6455	11633	1.2	5.00E-77	4557250	NT	Homo sapiens disintegrin and metalloproteinase domain 10 (ADAM10) mRNA
2736	7820	13024	1.0	5.00E-77	4503160	NT	Homo sapiens cullin 1 (CUL1) mRNA
4605	9719	14812	2.0	5.00E-77	5031660	NT	Homo sapiens EGF-like repeats and discoidin I-like domains 3 (EDIL3), mRNA
4605	9719	14813	2.0	5.00E-77	5031660	NT	Homo sapiens EGF-like repeats and discoidin I-like domains 3 (EDIL3), mRNA
4853	9960	15046	2.1	5.00E-77	AL043953.1	EST_HUMAN	DKFZp334G1728_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp334G1728 5'
1859	6977	12162	0.7	4.00E-77	7706762	NT	Homo sapiens villin-like (VILL) mRNA
1929	7046	12237	1.1	3.00E-77	5730038	NT	Homo sapiens SET domain and mariner transposase fusion gene (SETMAR) mRNA
1929	7046	12238	1.1	3.00E-77	5730038	NT	Homo sapiens SET domain and mariner transposase fusion gene (SETMAR) mRNA

Table 4

3214	8362	13473	6.9	3.00E-77	AI963236.1	EST_HUMAN	w28c03.x1 NCI CGAP_U11 Homo sapiens cDNA clone IMAGE:2508868 3' similar to gb:K00558 TUBULIN ALPHA-1 CHAIN (HUMAN);
1414	6542	11717	0.6	2.00E-77	AW997712.1	EST_HUMAN	RC3-BN0053-170200-011-H01 BN0053 Homo sapiens cDNA
2044	7157	12362	0.8	2.00E-77	L41825.1	NT	Homo sapiens CYP17 gene, 5' end
2056	7168	12374	1.0	2.00E-77	7706315	NT	Homo sapiens CGI-79 protein (LOC51634), mRNA
2549	7946	12844	0.7	2.00E-77	AB037836.1	NT	Homo sapiens mRNA for KIAA1415 protein, partial cds
2549	7946	12845	0.7	2.00E-77	AB037836.1	NT	Homo sapiens mRNA for KIAA1415 protein, partial cds
3305	8450	13560	0.9	2.00E-77	AF016191.1	NT	Rattus norvegicus potassium channel (erg3) mRNA, complete cds
3305	8450	13561	0.9	2.00E-77	AF016191.1	NT	Rattus norvegicus potassium channel (erg3) mRNA, complete cds
3947	9080	14161	1.3	2.00E-77	BE044316.1	EST_HUMAN	h043b05.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:3040113 3' similar to SW:GAG2_HUMAN P10264 RETROVIRUS-RELATED GAG POLYPROTEIN ;
4315	9438	14527	0.9	2.00E-77	AI613519.1	EST_HUMAN	hw22g02.x1 NCI CGAP_Bm52 Homo sapiens cDNA clone IMAGE:2260466 3' similar to TR:O65245 O65245 F21E10.7 PROTEIN. ;
4315	9438	14528	0.9	2.00E-77	AI613519.1	EST_HUMAN	hw22g02.x1 NCI CGAP_Bm52 Homo sapiens cDNA clone IMAGE:2260466 3' similar to TR:O65245 O65245 F21E10.7 PROTEIN. ;
4492	9612		3.5	2.00E-77	4504068	NT	Homo sapiens glutamic-oxaloacetic transaminase 2, mitochondrial (aspartate aminotransferase 2) (GOT2), nuclear gene encoding mitochondrial protein, mRNA
4659	9771	14866	3.6	2.00E-77	AA653025.1	EST_HUMAN	ns68g12.s1 NCI CGAP_P12 Homo sapiens cDNA clone IMAGE:118838 similar to SW:RL29_HUMAN P47914 60S RIBOSOMAL PROTEIN L29. [1] :contains element MSR1 repetitive element ;
37	5246	10353	1.0	1.00E-77	AB033102.1	NT	Homo sapiens mRNA for KIAA1276 protein, partial cds
37	5246	10354	1.0	1.00E-77	AB033102.1	NT	Homo sapiens mRNA for KIAA1276 protein, partial cds
271	5459	10586	0.6	1.00E-77	4502166	NT	Homo sapiens amyloid beta (A4) precursor protein (protease nexin-II, Alzheimer disease) (APP), mRNA
271	5459	10587	0.6	1.00E-77	4502166	NT	Homo sapiens amyloid beta (A4) precursor protein (protease nexin-II, Alzheimer disease) (APP), mRNA
857	7901	11167	1.7	1.00E-77	4502166	NT	Homo sapiens amyloid beta (A4) precursor protein (protease nexin-II, Alzheimer disease) (APP), mRNA
857	7901	11168	1.7	1.00E-77	4502166	NT	Homo sapiens amyloid beta (A4) precursor protein (protease nexin-II, Alzheimer disease) (APP), mRNA
2394	7494	12700	1.2	1.00E-77	AB028024.1	NT	Homo sapiens mRNA for KIAA1101 protein, complete cds
3007	8159	13259	2.8	1.00E-77	4503300	NT	Homo sapiens 2,4-dienoyl CoA reductase 1, mitochondrial (DECRI), mRNA
4256	9381	14462	3.0	1.00E-77	7706299	NT	Homo sapiens CGI-60 protein (LOC51626), mRNA
4423	9543	14635	14.7	1.00E-77	AJ229041.1	NT	Homo sapiens 959 kb contig between AML1 and CBR1 on chromosome 21q22, segment 1/3
4552	9671	14761	2.0	1.00E-77	6552322	NT	Homo sapiens breast cancer 1, early onset (BRCA1), transcript variant BRCA1-exon4, mRNA
5179	10271	15342	2.9	1.00E-77	AW755254.1	EST_HUMAN	CMYAS Human cardiac muscle expression library Homo sapiens cDNA clone 4151935 similar to CMYAS Cardionopathy associated gene 5
2515	7611	12813	1.5	5.00E-78	AW673424.1	EST_HUMAN	ba54h03.y3 NIH MGC_10 Homo sapiens cDNA clone IMAGE:2900405 5' similar to WP:Y48BBA.6 CE22121 ;

Table 4

3339	8483	13598	3.8	5.00E-78	M55586.1	NT	Human collagenase type IV (CLG4) gene, exon 6
4810	9724	14819	1.4	5.00E-78	AB002348.2	NT	Homo sapiens mRNA for KIAA0350 protein, partial cds
1502	6628	11797	0.6	4.00E-78	AL355841.1	NT	Novel human gene mapping to chromosome 22
1629	6755	11925	0.6	4.00E-78	AI995094.1	EST_HUMAN	w97b12.x1 NC1_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2495615 3' similar to SW-WAP_PIG O46565 WHEY ACIDIC PROTEIN PRECURSOR;
2270	7376	12585	0.8	4.00E-78	AF107405.1	NT	Homo sapiens pre-mRNA splicing factor (SFRS3) mRNA, complete cds
4227	9351	14431	1.4	4.00E-78	7656876	NT	Homo sapiens syncytin (LOC30816), mRNA
4664	9776	14872	1.3	4.00E-78	4505806	NT	Homo sapiens phosphatidylinositol 4-kinase, catalytic, alpha polypeptide (PIK4CA) mRNA
4664	9776	14873	1.3	4.00E-78	4505806	NT	Homo sapiens phosphatidylinositol 4-kinase, catalytic, alpha polypeptide (PIK4CA) mRNA
155	5351	10476	0.6	3.00E-78	AF095901.1	NT	Homo sapiens eRF1 gene, complete cds
155	5351	10477	0.6	3.00E-78	AF095901.1	NT	Homo sapiens eRF1 gene, complete cds
3178	8327	13440	0.9	3.00E-78	4507164	NT	Homo sapiens nuclear antigen Sp100 (SP100) mRNA
4015	8882	13971	0.9	3.00E-78	4507334	NT	Homo sapiens synaptotagmin 1 (SYNJ1), mRNA
3083	8234		2.2	2.00E-78	U04489.1	NT	Homo sapiens type IV collagen alpha 5 chain (COL4A5) gene, exon 20
3932	9088		1.7	2.00E-78	AA311872.1	EST_HUMAN	EST182583 Jurkat T-cells VI Homo sapiens cDNA 5' end
1860	6978	12163	1.8	9.00E-79	AA601246.1	EST_HUMAN	not4g08.s1 NC1_CGAP_Phe1 Homo sapiens cDNA clone IMAGE:1100704 3' similar to TRE239140 E239140 SPALT PROTEIN;
4758	8869	14963	2.5	9.00E-79	BE000837.1	EST_HUMAN	RC2-BN0074-090300-014-c12 BN0074 Homo sapiens cDNA
3682	8821	13914	1.2	8.00E-79	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
4391	8513	14601	0.9	8.00E-79	D28476.1	NT	Homo sapiens mRNA for KIAA0045 gene, complete cds
4391	8513	14602	0.9	8.00E-79	D28476.1	NT	Homo sapiens mRNA for KIAA0045 gene, complete cds
4805	9915	15007	1.7	8.00E-79	AF083656.1	NT	Homo sapiens procollagen C-proteinase enhancer protein (PCOLCE) gene, 5' flanking region and complete cds
4805	9915	15008	1.7	8.00E-79	AF083656.1	NT	Homo sapiens procollagen C-proteinase enhancer protein (PCOLCE) gene, 5' flanking region and complete cds
3139	8288		1.1	4.00E-79	8922325	NT	Homo sapiens hypothetical protein FLJ10283 (FLJ10283), mRNA
310	5494	10623	1.4	3.00E-79	AF114488.1	NT	Homo sapiens intersecin short isoform (ITSN) mRNA, complete cds
962	6107	11265	0.9	3.00E-79	AF232708.1	NT	Homo sapiens cell-line tsA201a chloride ion current inducer protein (Cin) gene, complete cds
3060	8211	13310	1.4	3.00E-79	U09410.1	NT	Human zinc finger protein ZNF131 mRNA, partial cds
3727	8864	13957	2.8	3.00E-79	BE265169.1	EST_HUMAN	6011929221F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3536740 5'
4818	9927		5.0	3.00E-79	AF116627.1	NT	Homo sapiens PRO1181 mRNA, complete cds
618	5777	10899	1.1	2.00E-79	BE379926.1	EST_HUMAN	601159415F2 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3511107 5'
912	6058	11217	1.1	2.00E-79	4757841	NT	Homo sapiens BCL2-like 2 (BCL2L2) mRNA
1019	6159		1.4	2.00E-79	AI523747.1	EST_HUMAN	ht8h07.x1 NC1_CGAP_P28 Homo sapiens cDNA clone IMAGE:2118685 3'
2101	7212	12420	5.1	2.00E-79	4585663	NT	Homo sapiens phosphodiesterase 6A, cGMP-specific, rod, alpha (PDE6A), mRNA
2101	7212	12421	5.1	2.00E-79	4585663	NT	Homo sapiens phosphodiesterase 6A, cGMP-specific, rod, alpha (PDE6A), mRNA
2146	7256	12463	1.0	2.00E-79	AJ271408.1	NT	Homo sapiens mRNA for Fas-associated factor, FAF1 (Faf1) gene

Table 4

2265	7371	12581	0.8	2.00E-79	AF244138.1	NT	Homo sapiens hepatocellular carcinoma-associated antigen 88 (HCA88) mRNA, complete cds
3838	8974	14074	0.9	2.00E-79	AF170492.1	NT	Homo sapiens chloride channel CLCA4 (CLCA4) mRNA, complete cds
4074	9201	14287	1.2	2.00E-79	AJ271408.1	NT	Homo sapiens mRNA for Fas-associated factor, FAF1 (Faf1 gene)
4590	9704	14797	1.0	2.00E-79	AL163206.2	NT	Homo sapiens chromosome 21 segment HS21C08
204	5397	10525	1.5	1.00E-79	BE252804.1	EST_HUMAN	601112953F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3353581 5'
3107	8257	13360	3.8	9.00E-80	AA725848.1	EST_HUMAN	ai23e05.s1 Soares testis_NHT Homo sapiens cDNA clone 1343648 3'
3107	8257	13361	3.8	9.00E-80	AA725848.1	EST_HUMAN	ai23e05.s1 Soares testis_NHT Homo sapiens cDNA clone 1343648 3'
3551	8691		1.0	8.00E-80	U94387.1	NT	Homo sapiens Y chromosome spermatogenesis candidate protein (RBM) pseudogene mRNA, partial cds
882	6030	11189	0.8	6.00E-80	AA22197.1	EST_HUMAN	HS6d02.x1 NCI_CGAP_Bn23 Homo sapiens cDNA clone IMAGE:2103459 3' similar to SW:NUEM_HUMAN Q16795 NADH-UBIQUINONE OXIDOREDUCTASE 39 KD SUBUNIT PRECURSOR:
1624	6750	11918	0.7	6.00E-80	U64898.1	NT	Homo sapiens NRD convertase mRNA, complete cds
4188	9314	14397	1.1	6.00E-80	AB032981.1	NT	Homo sapiens mRNA for KIAA1155 protein, partial cds
4188	9314	14398	1.1	6.00E-80	AB032981.1	NT	Homo sapiens mRNA for KIAA1155 protein, partial cds
573	5733	10851	1.1	5.00E-80	4506228	NT	Homo sapiens proteasome (prosome, macropain) 26S subunit, non-ATPase, 3 (PSMD3) mRNA
817	5667	11124	1.3	5.00E-80	AF108830.1	NT	Homo sapiens serine-threonine protein kinase (MNIBH) mRNA, complete cds
817	5667	11125	1.3	5.00E-80	AF108830.1	NT	Homo sapiens serine-threonine protein kinase (MNIBH) mRNA, complete cds
1172	6306		4.8	5.00E-80	X91647.1	NT	H.sapiens nct1 gene (exon 12)
1440	6567		0.8	5.00E-80	AL163283.2	NT	Homo sapiens chromosome 21 segment HS21C063
2311	7414	12623	0.9	5.00E-80	U89358.1	NT	Human (3)hnt protein homolog mRNA, complete cds
2380	7482	12684	1.4	5.00E-80	AB037855.1	NT	Homo sapiens mRNA for KIAA1434 protein, partial cds
2764	7848	13050	1.1	5.00E-80	4504292	NT	Homo sapiens H3 histone family, member J (H3FJ) mRNA
3563	9086	14168	1.1	5.00E-80	AB019038.1	NT	Homo sapiens HMT-1 mRNA for beta-1,4 mannosyltransferase, complete cds
3563	9086	14169	1.1	5.00E-80	AB019038.1	NT	Homo sapiens HMT-1 mRNA for beta-1,4 mannosyltransferase, complete cds
4872	9979	15063	1.7	5.00E-80	AL163288.2	NT	Homo sapiens chromosome 21 segment HS21C068
210	5403		1.6	3.00E-80	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
1308	7912	11604	1.8	2.00E-80	AA215796.1	EST_HUMAN	z58d04.r1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:683719 5'
1308	7912	11605	1.8	2.00E-80	AA215796.1	EST_HUMAN	z58d04.r1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:683719 5'
1757	6878	12059	2.3	2.00E-80	R35321.1	EST_HUMAN	y65a08.r1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:38060 5'
1816	6935	12125	0.7	2.00E-80	AI444821.1	EST_HUMAN	RET487 subtracted retina cDNA library Homo sapiens cDNA clone RET487
2009	7123	12323	2.4	2.00E-80	AL043116.2	EST_HUMAN	DKFZp434D1323_r1 434 (synonym: hhes3) Homo sapiens cDNA clone DKFZp434D1323 5'
337	5518		0.6	1.00E-80	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103
782	5934	11083	1.1	1.00E-80	AF231820.1	NT	Homo sapiens chromosome 21 unknown mRNA
1811	7028		1.1	1.00E-80	AJ732656.1	EST_HUMAN	nm01112.x5 NCI_CGAP_C09 Homo sapiens cDNA clone IMAGE:1076495 3' similar to contains ORF.11 OFR repetitive element:
3515	8656	13763	1.0	1.00E-80	8922391	NT	Homo sapiens hypothetical protein FLJ10379 (FLJ10379) mRNA
4358	9480	14571	1.0	1.00E-80	AF077188.1	NT	Homo sapiens cullin 4A (CUL4A) mRNA, complete cds

Table 4

5192	10283	15351	1.0	1.00E-80	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C078
4280	9414	14503	4.8	6.00E-81	BE256829.1	EST_HUMAN	601111970F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3352840 5'
4280	9414	14504	4.8	6.00E-81	BE256829.1	EST_HUMAN	601111970F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3352840 5'
2170	7279	12492	1.1	5.00E-81	BE268042.1	EST_HUMAN	801125505F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3345480 5'
1779	6900	12088	1.0	4.00E-81	AW779812.1	EST_HUMAN	hm86d02.x1 NCI_CGAP_Co14 Homo sapiens cDNA clone IMAGE:3035807 3' similar to SW:CCPG_BOVIN_P53620 COATOMER GAMMA SUBUNIT
2058	7170	12377	2.1	4.00E-81	8923056	NT	Homo sapiens hypothetical protein FLJ20048 (FLJ20048), mRNA
2058	7170	12378	2.1	4.00E-81	8923056	NT	Homo sapiens mRNA for KIAA1345 protein, partial cds
3134	8283	13390	3.8	4.00E-81	AB037766.1	NT	Homo sapiens mRNA for KIAA1345 protein, partial cds
3576	8715	13812	1.2	4.00E-81	AW004808.1	EST_HUMAN	ws90h03.x1 NCI_CGAP_Co3 Homo sapiens cDNA clone IMAGE:2505269 3' similar to TR:Q43815 O43815 STRIATIN
1246	6375	11532	3.2	3.00E-81	Y18000.1	NT	Homo sapiens NF2 gene
1246	6375	11533	3.2	3.00E-81	Y18000.1	NT	Homo sapiens NF2 gene
2320	7423	12632	0.6	3.00E-81	AF077188.1	NT	Homo sapiens cullin 4A (CUL4A) mRNA, complete cds
2861	8112	13217	5.1	3.00E-81	4506280	NT	Homo sapiens pleiotrophin (heparin binding growth factor 8, neurite growth-promoting factor 1) (PTN) mRNA
2861	8112	13218	5.1	3.00E-81	4506280	NT	Homo sapiens pleiotrophin (heparin binding growth factor 8, neurite growth-promoting factor 1) (PTN) mRNA
2961	8112	13218	5.1	3.00E-81	AL163283.2	NT	Homo sapiens chromosome 21 segment HS21C083
4933	10039	13936	1.0	2.00E-81	AW611542.1	EST_HUMAN	hg55c01.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2952384 3'
4579	9695	14788	0.9	2.00E-81	5453871	NT	homo sapiens platelet-derived growth factor receptor-like (PDGFR) mRNA
1403	6530	11701	1.2	1.00E-81	W26539.1	EST_HUMAN	3333 Human retina cDNA randomly primed sublibrary Homo sapiens cDNA
2144	7254	12462	0.9	1.00E-81	N66951.1	EST_HUMAN	z44812.s1 Soares fetal liver spleen 1N1LS Homo sapiens cDNA clone IMAGE:295823 3'
3602	8741	13836	2.0	1.00E-81	AW960558.1	EST_HUMAN	EST372729 MAGE resequences, MAGF Homo sapiens cDNA
4414	9534	14623	3.1	1.00E-81	AA040370.1	EST_HUMAN	EST372729 MAGE resequences, MAGF Homo sapiens cDNA
4546	9665	14754	7.9	1.00E-81	BE047996.1	EST_HUMAN	EST372729 MAGE resequences, MAGF Homo sapiens cDNA
12	5220	10321	0.6	8.00E-82	AF161406.1	NT	z445h09.r1 Soares pregnant uterus NBHPU Homo sapiens cDNA clone IMAGE:485825 5'
101	5220	10321	1.3	8.00E-82	AF161406.1	NT	z445h09.r1 Soares pregnant uterus NBHPU Homo sapiens cDNA clone IMAGE:485825 5'
263	5450	10576	0.6	8.00E-82	U08988.1	NT	similar to PIR:SS52437 SS52437 CDP-diacylglycerol synthase - fruit fly
797	5948	11098	0.7	8.00E-82	U08988.1	NT	z455c04.y1 NCI_CGAP_Bms2 Homo sapiens cDNA clone IMAGE:2291526 5'
869	6017	11177	1.1	8.00E-82	U08988.1	NT	Human CRFB4 gene, partial cds
1475	6602	11776	1.1	8.00E-82	AB037748.1	NT	Human CRFB4 gene, partial cds
1636	6762	11932	1.2	8.00E-82	6715601	NT	Human CRFB4 gene, partial cds
4150	9276	14357	0.8	8.00E-82	8923432	NT	Human CRFB4 gene, partial cds
4034	9162	14245	0.8	5.00E-82	AA515512.1	EST_HUMAN	transcript variant 2, mRNA
1647	6773	11944	2.4	4.00E-82	AF081484.1	NT	Homo sapiens hypothetical protein FLJ20461 (FLJ20461), mRNA
4638	9752	14845	0.8	4.00E-82	H17755.1	EST_HUMAN	Homo sapiens alpha-tubulin isoform 1 mRNA, complete cds
4638	9752	14845	0.8	4.00E-82	H17755.1	EST_HUMAN	Homo sapiens alpha-tubulin isoform 1 mRNA, complete cds
4638	9752	14846	0.8	4.00E-82	H17755.1	EST_HUMAN	ym40e08.r1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:50499 5'
4638	9752	14846	0.8	4.00E-82	H17755.1	EST_HUMAN	ym40e08.r1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:50499 5'

Table 4

276	5484	10593	4.7	3.00E-82	4502166	NT	Homo sapiens amyloid beta (A $\beta$ ) precursor protein (protease nexin-II, Alzheimer disease) (APP), mRNA
687	5642	10978	0.8	3.00E-82	BE005705.1	EST_HUMAN	RC2-BN0120-010400-013-02 BN0120 Homo sapiens cDNA
703	5658		1.0	3.00E-82	4502506	NT	Homo sapiens complement component 5 (C5) mRNA
770	5622	11071	1.5	3.00E-82	5174702	NT	Homo sapiens transforming growth factor beta-activated kinase-binding protein 1 (TAB1), mRNA
852	6001	11161	1.1	3.00E-82	4502166	NT	Homo sapiens amyloid beta (A $\beta$ ) precursor protein (protease nexin-II, Alzheimer disease) (APP), mRNA
1045	6185		4.7	3.00E-82	AA725848.1	EST_HUMAN	a123605.s1 Soares testis NHT Homo sapiens cDNA clone 1343648 3'
1333	6462	11630	5.5	3.00E-82	AW875073.1	EST_HUMAN	RC6-PT0001-190100-021-B02 PT0001 Homo sapiens cDNA
1450	6577	11751	0.7	3.00E-82	AL163285.2	NT	Homo sapiens chromosome 21 segment HS21C085
1961	7077	12276	0.9	3.00E-82	4501922	NT	Homo sapiens adenylate cyclase activating polypeptide 1 (pituitary) receptor type 1 (ADCYAP1R1) mRNA
3234	8382		2.1	3.00E-82	5453811	NT	Homo sapiens neurotrophic tyrosine kinase, receptor, type 2 (NTRK2) mRNA
4836	8944	15033	0.9	3.00E-82	AA135979.1	EST_HUMAN	zn33b04.r1 Stratagene lung carcinoma 937218 Homo sapiens cDNA clone IMAGE:565711 5' similar to SW:PAGT_BOVIN_Q07537 POLYPEPTIDE N-ACETYLGLACTOSAMINYLTRANSFERASE :
582	5742	10858	0.7	2.00E-82	AB023216.1	NT	Homo sapiens mRNA for KIAA0999 protein, partial cds
582	5742	10859	0.7	2.00E-82	AB023216.1	NT	Homo sapiens mRNA for KIAA0999 protein, partial cds
1660	6784	11960	0.6	2.00E-82	AL046390.1	EST_HUMAN	DKFZp434M117_r1 434 (synonym: hies3) Homo sapiens cDNA clone DKFZp434M117 5'
2176	7285	12496	1.1	2.00E-82	5453855	NT	Homo sapiens pericentriolar material 1 (PCM1) mRNA
3231	8379		1.8	2.00E-82	6997248	NT	Homo sapiens sal (Drosophila)-like 1 (SALL1), mRNA
3772	8909	13998	1.1	2.00E-82	D87675.1	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
4140	9266	14347	1.1	2.00E-82	4504116	NT	Homo sapiens glutamate receptor, ionotropic, kainate 1 (GRIK1) mRNA
4458	9578	14675	1.0	2.00E-82	AB029019.1	NT	Homo sapiens mRNA for KIAA1096 protein, partial cds
4458	9578	14676	1.0	2.00E-82	AB029019.1	NT	Homo sapiens mRNA for KIAA1096 protein, partial cds
4768	9879	14973	3.2	2.00E-82	AF045555.1	NT	Homo sapiens wbscr1 (WBSCR1) and wbscr5 (WBSCR5) genes, complete cds, alternatively spliced and replication factor C subunit 2 (RFC2) gene, complete cds
5013	10115	15185	1.7	2.00E-82	4507580	NT	Homo sapiens tumor necrosis factor receptor superfamily, member 5 (TNFRSF5) mRNA
5013	10115	15186	1.7	2.00E-82	4507580	NT	Homo sapiens tumor necrosis factor receptor superfamily, member 5 (TNFRSF5) mRNA
1284	6393	11552	0.7	1.00E-82	BE084386.1	EST_HUMAN	RC4-BT0310-110300-015-110 BT0310 Homo sapiens cDNA
1285	6394	11553	0.8	1.00E-82	AB011110.2	NT	Homo sapiens mRNA for KIAA0538 protein, partial cds
1392	6519	11687	0.7	8.00E-83	BE383973.1	EST_HUMAN	601273346r1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3614362 5'
1656	7869	11954	0.7	8.00E-83	N66951.1	EST_HUMAN	za48f12.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:295823 3'
2836	7987		1.6	7.00E-83	AA584655.1	EST_HUMAN	no12h01.s1 NCJ_CGAP_Phe1 Homo sapiens cDNA clone IMAGE:1100497 3' similar to contains Alu repetitive element;
4864	9971	15055	8.7	7.00E-83	N27808.1	EST_HUMAN	yx54e09.r1 Soares melanocyte 2NbhM Homo sapiens cDNA clone IMAGE:265576 5'

Table 4

397	5565	10701	1.3	6.00E-83	M33320.1	NT	Human platelet Glycoprotein IIb (GP1Ib) gene, exons 2-29
1747	6869	12047	0.5	6.00E-83	AW573088.1	EST_HUMAN	h31103.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2933525 3' similar to SW/YBEB_HAEIN P44471 HYPOTHETICAL PROTEIN H10034. ;
2984	8136	13241	1.1	6.00E-83	AW616405.1	EST_HUMAN	QV4-ST0234-181189-037-f05 ST0234 Homo sapiens cDNA
3031	8183	13283	0.9	6.00E-83	AA701457.1	EST_HUMAN	z59605.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:435080 3'
931	6078		1.4	5.00E-83	U17883.1	NT	Human succinate dehydrogenase iron-protein subunit (sdhB) gene, exon 5
2004	7871		0.8	5.00E-83	AF006305.1	NT	Homo sapiens 26S proteasome regulatory subunit (SUG2) mRNA, complete cds
3586	8725	13821	0.9	5.00E-83	AL133207.2	NT	Novel human gene mapping to chromosome X
5011	10113	15183	11.0	5.00E-83	4557013	NT	Homo sapiens catalase (CAT) mRNA
5011	10113	15184	11.0	5.00E-83	4557013	NT	Homo sapiens catalase (CAT) mRNA
5094	10192	15271	0.9	5.00E-83	AF083827.1	NT	Homo sapiens catalase (CAT) mRNA
624	5783	10905	1.5	4.00E-83	AF224669.1	NT	Homo sapiens catalase (CAT) mRNA
981	6126		1.5	3.00E-83	AA368311.1	EST_HUMAN	EST79542 Placenta 1 Homo sapiens cDNA similar to similar to endogenous retrovirus ERV9
2750	7834		0.7	3.00E-83	AA632654.1	EST_HUMAN	np87607.s1 NCI_CGAP_Thy1 Homo sapiens cDNA clone IMAGE:1133292 similar to contains THR12 THR repetitive element ;
1759	6880	12061	0.7	2.00E-83	AA933492.1	EST_HUMAN	o68405.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1621592 3' similar to TR:Q92614 Q92614 MYELOBLAST KIAA0216. ;
1759	6880	12062	0.7	2.00E-83	AA933492.1	EST_HUMAN	o68405.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1621592 3' similar to TR:Q92614 Q92614 MYELOBLAST KIAA0216. ;
1883	7001	12186	0.8	2.00E-83	N66951.1	EST_HUMAN	za4812.s1 Soares_fetal_liver_spleen_1NFLS Homo sapiens cDNA clone IMAGE:295823 3'
1983	7098	12301	1.1	2.00E-83	AW247459.1	EST_HUMAN	2819246 5prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2819246 5'
3708	8846		1.0	2.00E-83	AL163202.2	NT	Homo sapiens chromosome 21 segment HS21C002
4241	9366	14447	4.5	2.00E-83	AF202879.1	NT	Homo sapiens hematopoietic progenitor cell antigen CD34 precursor (CD34) mRNA, partial cds
4553	9672	14762	8.1	2.00E-83	7706398	NT	Homo sapiens ankyrin repeat-containing protein ASB-2 (LOC51676), mRNA
4553	9672	14763	8.1	2.00E-83	7706398	NT	Homo sapiens ankyrin repeat-containing protein ASB-2 (LOC51676), mRNA
1273	6402	11560	1.4	1.00E-83	4505492	NT	Homo sapiens oxoglutarate dehydrogenase (lipoamide) (OGDH) mRNA
1273	6402	11561	1.4	1.00E-83	4505492	NT	Homo sapiens oxoglutarate dehydrogenase (lipoamide) (OGDH) mRNA
1390	6517	11684	6.0	1.00E-83	4504326	NT	Homo sapiens hydroxyacyl-Coenzyme A hydratase (trifunctional protein), beta subunit (HADHB) mRNA
1390	6517	11685	6.0	1.00E-83	4504326	NT	Homo sapiens hydroxyacyl-Coenzyme A hydratase (trifunctional protein), beta subunit (HADHB) mRNA
3148	8295	13404	0.8	1.00E-83	7662349	NT	Homo sapiens cell recognition molecule Caspr2 (KIAA0888), mRNA
3793	8930	14023	3.6	1.00E-83	AF053788.1	NT	Rattus norvegicus brain specific contactin-binding protein CBP90 mRNA, partial cds
4151	9277	14356	2.2	1.00E-83	Z25822.1	NT	H.sapiens gene for mitochondrial dodecanoyl-CoA delta-isomerase, exon 3

Table 4

4789	9900	14993	1.4	1.00E-83	4502166	NT	Homo sapiens amyloid beta (A4) precursor protein (protease nexin-II, Alzheimer disease) (APP), mRNA
2348	7450	12657	1.7	6.00E-84	AA77657.4.1	EST_HUMAN	aa86a03.s1 Stratagene schizo brain S11 Homo sapiens cDNA clone IMAGE:971020 3'
697	5852	10988	1.1	5.00E-84	AA3281.1.1	EST_HUMAN	EST96084 Testis 1 Homo sapiens cDNA 5' end
2981	8132		1.0	5.00E-84	AF108718.1	NT	Homo sapiens chromosome 3 subtelomeric region
1354	6482	11648	1.1	4.00E-84	AB037735.1	NT	Homo sapiens mRNA for KIAA1314 protein, partial cds
1389	6516	11683	1.5	4.00E-84	A1685321.1	EST_HUMAN	wa76cd4.x1 Scores_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2302086 3' similar to SW:NRDC_HUMAN 043847 NARDLYSIN PRECURSOR:
4869	9976	15061	1.8	4.00E-84	AF069801.2	NT	Homo sapiens myosin light chain kinase isoform 2 (MLCK) mRNA, complete cds
5080	10158	15233	1.3	4.00E-84	U94982.1	NT	Human 2,4-dienoyl-CoA reductase gene, exons 3 and 4
313	5497	10828	1.4	3.00E-84	AF026200.1	NT	Homo sapiens Bach1 protein homolog mRNA, partial cds
1137	6273	11423	0.9	3.00E-84	4758081	NT	Homo sapiens chondroilin sulfate proteoglycan 2 (versican) (CSPG2) mRNA
1917	7034	12222	1.2	3.00E-84	5453855	NT	Homo sapiens pericentriolar material 1 (PCM1) mRNA
1962	7078	12277	1.1	3.00E-84	AL096880.1	NT	Novel human mRNA containing Zinc finger C2H2 type domains
3542	8683	13783	1.2	3.00E-84	AB026898.1	NT	Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)
3689	8827	13921	4.1	3.00E-84	AF014459.1	NT	Homo sapiens X-linked juvenile retinoschisis precursor protein (XLR51) mRNA, complete cds
2913	8064	13172	9.8	2.00E-84	AF03693.1	NT	Homo sapiens myelin transcription factor 1-like (MYT1-L) mRNA, complete cds
2832	8083	13191	0.9	2.00E-84	X8921.1.1	NT	H.sapiens DNA for endogenous retroviral like element
309	5493	10622	0.5	1.00E-84	AF114488.1	NT	Homo sapiens intersecin short isoform (ITSN) mRNA, complete cds
537	5700	10822	1.8	1.00E-84	4507952	NT	Homo sapiens tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, zeta polypeptide (TYWHAZ) mRNA
1271	8400	11558	0.7	1.00E-84	AA984379.1	EST_HUMAN	am85b1.1.s1 Stratagene schizo brain S11 Homo sapiens cDNA clone IMAGE:162985 3'
2008	7122	12322	1.1	1.00E-84	BE392137.1	EST_HUMAN	601308006F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3626257 5'
3891	8830	13923	2.1	1.00E-84	AA720851.1	EST_HUMAN	mw12e06.s1 NCI CGAP_S51 Homo sapiens cDNA clone IMAGE:1239106 3'
4319	9442	14530	5.6	1.00E-84	AL229041.1	NT	Homo sapiens 959 kb config between AML1 and CBR1 on chromosome 21q22; segment 1/3
4601	9715	14807	3.8	1.00E-84	AL043314.2	EST_HUMAN	DKFZp434N0323_r1 434 (synonym: hies3) Homo sapiens cDNA clone DKFZp434N0323 5'
4601	9715	14808	3.8	1.00E-84	AL043314.2	EST_HUMAN	DKFZp434N0323_r1 434 (synonym: hies3) Homo sapiens cDNA clone DKFZp434N0323 5'
4823	9442	14530	4.3	1.00E-84	AL229041.1	NT	Homo sapiens 959 kb config between AML1 and CBR1 on chromosome 21q22; segment 1/3
951	6097		1.2	9.00E-85	AL169209.2	NT	Homo sapiens chromosome 21 segment HS21C009
1057	6196	11348	0.8	9.00E-85	U51432.1	NT	Homo sapiens nuclear protein Skip mRNA, complete cds
1057	6186	11349	0.8	9.00E-85	U51432.1	NT	Homo sapiens nuclear protein Skip mRNA, complete cds
1560	6687	11854	1.1	9.00E-85	M33282.1	NT	Human plasminogen gene, exon 7
1560	6687	11855	1.1	9.00E-85	M33282.1	NT	Human plasminogen gene, exon 7
1651	6776	11949	1.8	9.00E-85	7657020	NT	Homo sapiens DKFZp434P211 protein (DKFZp434P211), mRNA



Table 4

4158	9284	14364	0.9	9.00E-85	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080
4778	9888	14981	1.1	9.00E-85	5901979	NT	Homo sapiens heat shock transcription factor 2 binding protein (HSF2BP), mRNA
4825	9933	15023	1.0	9.00E-85	AL163286.2	NT	Homo sapiens chromosome 21 segment HS21C068
1120	9257	11409	1.1	7.00E-85	L05094.1	NT	Homo sapiens ribosomal protein L27 mRNA, complete cds
2285	7390	12598	1.2	5.00E-85	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
2530	7628	12827	1.1	5.00E-85	F08331.1	EST_HUMAN	HSC2QH081 normalized infant brain cDNA Homo sapiens cDNA clone c-zq108
2530	7628	12828	1.1	5.00E-85	F08331.1	EST_HUMAN	HSC2QH081 normalized infant brain cDNA Homo sapiens cDNA clone c-zq108
1277	6407	11567	1.2	3.00E-85	AF096157.1	NT	Homo sapiens protein phosphatase 2A BR gamma subunit gene, exon 6
1741	8864	12041	1.2	3.00E-85	T97495.1	EST_HUMAN	ye53g09.t1 Soares fetal liver spleen 1NPLS Homo sapiens cDNA clone IMAGE:121504 5'
4219	9343	14426	0.9	3.00E-85	BE267189.1	EST_HUMAN	601189704F2 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3533616 5'
4883	9991	15072	0.9	3.00E-85	7363442	NT	Homo sapiens olfactory receptor, family 12, subfamily D, member 2 (OR12D2), mRNA
947	6093	11251	0.9	2.00E-85	7657266	NT	Homo sapiens KIAA0929 protein Mx2 interacting nuclear target (MINT) homolog (KIAA0929), mRNA
1024	6164	11318	0.8	2.00E-85	AF248540.1	NT	Homo sapiens intersecin 2 (SH3D1B), mRNA, complete cds
1400	6527	11696	2.6	2.00E-85	5174775	NT	Homo sapiens apolipoprotein C-II (APOC2), mRNA
1400	6527	11697	2.6	2.00E-85	5174775	NT	Homo sapiens apolipoprotein C-II (APOC2), mRNA
2183	7292	12504	0.8	2.00E-85	U10525.1	NT	Human DNA polymerase beta gene, exons 12 and 13
2793	6444		1.4	2.00E-85	7657468	NT	Homo sapiens similar to rat integral membrane glycoprotein POM121 (POM121L1), mRNA
4239	9364	14445	5.4	2.00E-85	4505880	NT	Homo sapiens plasminogen (PLG), mRNA
4822	9931	15021	1.3	2.00E-85	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
2241	7347		0.9	1.00E-85	BE277489.1	EST_HUMAN	601179190F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3546956 5'
1410	6537		2.8	9.00E-86	BE274217.1	EST_HUMAN	601120778F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:2967690 5'
220	5412	10533	1.3	7.00E-86	7662247	NT	Homo sapiens KIAA0680 gene product (KIAA0680), mRNA
921	6067	11223	1.3	7.00E-86	AA860801.1	EST_HUMAN	a168f08.s1 Soares parathyroid_tumor_NbHPA Homo sapiens cDNA clone IMAGE:1403559 3'
921	6067	11224	1.3	7.00E-86	AA860801.1	EST_HUMAN	a168f08.s1 Soares parathyroid_tumor_NbHPA Homo sapiens cDNA clone IMAGE:1403559 3'
1272	6401	11559	3.2	6.00E-86	4505492	NT	Homo sapiens oxoglutarate dehydrogenase (liponamide) (OGDH), mRNA
4380	9502		3.2	6.00E-86	8923209	NT	Homo sapiens hypothalamic protein FLJ20220 (FLJ20220), mRNA
268	5453	10578	1.3	2.00E-86	AA306284.1	EST_HUMAN	EST177232 Jurkat T-cells VI Homo sapiens cDNA 5' end
408	5576		0.6	2.00E-86	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
1173	6307	11461	0.7	2.00E-86	NS6977.1	EST_HUMAN	yz18a08.t1 Soares_multiple_sclerosis_2NbHMSF Homo sapiens cDNA clone IMAGE:283478 5'
2222	7329	12543	1.1	2.00E-86	AB033103.1	NT	Homo sapiens mRNA for KIAA1277 protein, partial cds
3369	8512	13619	1.4	2.00E-86	AW966142.1	EST_HUMAN	EST376215 MAGE resequences, MAGE Homo sapiens cDNA
3686	8824	13917	2.2	2.00E-86	AF156776.1	NT	Homo sapiens lysophosphatidic acid acyltransferase-delta (LPAAT-delta), mRNA, complete cds
3686	8824	13918	2.2	2.00E-86	AF156776.1	NT	Homo sapiens lysophosphatidic acid acyltransferase-delta (LPAAT-delta), mRNA, complete cds

Table 4

3954	9087		2.4	2.00E-86	AW515742.1	EST_HUMAN	hdb7g08.x1 NC1 CGAP_GCC Homo sapiens cDNA clone IMAGE:2916542 3'	
4679	9791	14892	2.8	2.00E-86	AF056490.1	NT	Homo sapiens cAMP-specific phosphodiesterase 8A (PDE8A) mRNA, partial cds	
							Homo sapiens NADH dehydrogenase (ubiquinone) Fe-S protein 1 (75kD) (NADH-coenzyme Q reductase) (NDUFS1) mRNA	
1579	6705	11875	1.1	1.00E-86		4826855	NT	Homo sapiens fibulin 5 (FBLN5) mRNA
3125	8274	13379	2.1	1.00E-86		5453849	NT	Homo sapiens gamma-glutamyl transpeptidase mRNA, complete cds
3197	8346	13459	2.4	1.00E-86	L20492.1		NT	Human gamma-glutamyl transpeptidase mRNA, complete cds
3256	8403	13509	1.3	1.00E-86	AL163209.2		NT	Homo sapiens chromosome 21 segment HS21C009
3256	8403	13510	1.3	1.00E-86	AL163209.2		NT	Homo sapiens chromosome 21 segment HS21C009
3864	9000	14100	11.5	1.00E-86		7706161	NT	Homo sapiens hypothetical protein (LOC51318), mRNA
3864	9000	14101	11.5	1.00E-86		7706161	NT	Homo sapiens hypothetical protein (LOC51318), mRNA
4167	9293	14374	5.8	1.00E-86	AL163300.2		NT	Homo sapiens chromosome 21 segment HS21C100
4832	9840	15029	1.1	1.00E-86	AF100751.1		NT	Homo sapiens FK506-binding protein FKBP23 isoform mRNA, complete cds
471	5636	10765	4.8	8.00E-87	X62245.1		NT	O.cuniculus mRNA for elongation factor 1 alpha
3482	8623	13735	0.9	6.00E-87		7657213	NT	Homo sapiens hormonally upregulated neu tumor-associated kinase (HUNK), mRNA
1142	6278	11430	0.6	5.00E-87	AA38281.1		EST_HUMAN	EST96094 Testis 1 Homo sapiens cDNA 5' end
950	6096	11253	1.3	4.00E-87	AL163210.2		NT	Homo sapiens chromosome 21 segment HS21C010
1155	6280	11444	3.6	4.00E-87	AB037835.1		NT	Homo sapiens mRNA for KIAA1414 protein, partial cds
								y80710.t1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:145579 5' similar to contains Alu repetitive element:
1411	6538	11711	0.9	4.00E-87	R78133.1		EST_HUMAN	Homo sapiens mRNA for KIAA0456 protein, partial cds
1985	7100	12303	0.9	4.00E-87	AB007925.1		NT	Homo sapiens mRNA for KIAA0456 protein, partial cds
2372	7474	12674	1.1	4.00E-87		7706299	NT	Homo sapiens CGI-60 protein (LOC51626), mRNA
2372	7474	12675	1.1	4.00E-87		7706299	NT	Homo sapiens CGI-60 protein (LOC51626), mRNA
								Homo sapiens myeloid/lymphoid or mixed-lineage leukemia (trithorax (Drosophila) homolog); translocated to, 4 (MLLT4) mRNA
3419	8561	13672	2.2	4.00E-87		5174574	NT	Homo sapiens high-mobility group (nonhistone chromosomal) protein 4 (HMG4) mRNA
2749	7833	13034	1.1	2.00E-87		4885420	NT	RC5-HT0580-200300-031-G04 HT0580 Homo sapiens cDNA
4880	9987	15069	0.8	2.00E-87	BE175478.1		EST_HUMAN	RC5-HT0580-200300-031-G04 HT0580 Homo sapiens cDNA
1165	7867		0.8	1.00E-87		7705683	NT	Homo sapiens putative glycolipid transfer protein (LOC51054), mRNA
1413	6540	11713	0.9	1.00E-87	AW361877.1		EST_HUMAN	PM2-CT0265-141099-001-g04 CT0265 Homo sapiens cDNA
1413	6540	11714	0.9	1.00E-87	AW361877.1		EST_HUMAN	PM2-CT0265-141099-001-g04 CT0265 Homo sapiens cDNA
3649	8788	13881	3.2	1.00E-87	Y00052.1		NT	Human mRNA for T-cell cyclophilin
3673	8812	13906	2.5	1.00E-87		4758827	NT	Homo sapiens neurexin III (NRXN3) mRNA
5057	10155	15231	1.0	1.00E-87	U50949.1		NT	Rattus norvegicus taste bud receptor protein TB 641 (TB 641) gene, complete cds
1090	6228	11379	2.5	9.00E-88	AF167465.1		NT	Homo sapiens double stranded RNA activated protein kinase (PKR) gene, exon 12
1327	6456	11622	0.7	9.00E-88	AB037820.1		NT	Homo sapiens mRNA for KIAA1399 protein, partial cds
1327	6456	11623	0.7	9.00E-88	AB037820.1		NT	Homo sapiens mRNA for KIAA1399 protein, partial cds
3574	8713	13811	1.1	9.00E-88	AL163209.2		NT	Homo sapiens chromosome 21 segment HS21C009
4172	9298	14379	2.6	9.00E-88	X91929.1		NT	H.sapiens ECE-1 gene (exon 9)
4172	9298	14380	2.6	9.00E-88	X91929.1		NT	H.sapiens ECE-1 gene (exon 9)
								Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)
4934	10040	15112	1.2	9.00E-88	AB026898.1		NT	ORCTL4 genes, complete cds
1787	6907		1.2	5.00E-88		7681887	NT	Homo sapiens KIAA0063 gene product (KIAA0063), mRNA

Table 4

2602	7692	12898	1.1	5.00E-88	N89399.1	EST_HUMAN	K9719F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA clone K9719 5'
2970	8121	13228	0.9	5.00E-88	AF14488.1	NT	Homo sapiens Intersectin short isoform (ITSN) mRNA, complete cds
2978	8129	13236	0.9	5.00E-88	AF14488.1	NT	Homo sapiens Intersectin short isoform (ITSN) mRNA, complete cds
2978	8129	13237	0.9	5.00E-88	AF14488.1	NT	Homo sapiens Intersectin short isoform (ITSN) mRNA, complete cds
3343	8487		2.3	5.00E-88	AI693217.1	EST_HUMAN	w68108.x1 NCI CGAP Lu24 Homo sapiens cDNA clone IMAGE:2336789 3' similar to contains Alu repetitive element; contains element MER22 MER22 repetitive element ;
3491	8632	13744	0.9	5.00E-88	AF14488.1	NT	Homo sapiens Intersectin short isoform (ITSN) mRNA, complete cds
4631	9745	14842	0.9	5.00E-88	AF14488.1	NT	Homo sapiens Intersectin short isoform (ITSN) mRNA, complete cds
207	5400	10527	1.5	3.00E-88	4826831	NT	Homo sapiens Machado-Joseph disease (spinocerebellar ataxia 3, olivopontocerebellar ataxia 3, autosomal dominant, ataxin 3) (MJD) mRNA
1770	6891		4.8	3.00E-88	4508020	NT	Homo sapiens zinc finger protein 259 (ZNF259) mRNA
2918	8069	13179	4.3	3.00E-88	N69351.1	EST_HUMAN	2248f2.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:295823 3'
4147	9273	14351	1.2	3.00E-88	4501912	NT	Homo sapiens a disintegrin and metalloproteinase domain 23 (ADAM23) mRNA
4147	9273	14352	1.2	3.00E-88	4501912	NT	Homo sapiens a disintegrin and metalloproteinase domain 23 (ADAM23) mRNA
1020	8180	11312	1.4	2.00E-88	7305198	NT	Homo sapiens Calsenilin, presenilin-binding protein, EF hand transcription factor (CSEN), mRNA
1607	6734	11904	0.9	2.00E-88	AF246219.1	NT	Homo sapiens SNARE protein kinase SNAK mRNA, complete cds
1716	6839	12018	1.5	2.00E-88	AF246219.1	NT	Homo sapiens SNARE protein kinase SNAK mRNA, complete cds
4328	9451	14539	1.9	2.00E-88	5031666	NT	Homo sapiens dynein, axonemal, light polypeptide 4 (DNAL4), mRNA
1710	6833	12013	0.8	8.00E-89	4759149	NT	Homo sapiens SMC (mouse) homolog, Y chromosome (SMCY) mRNA
2705	7790	12981	0.5	8.00E-89	BE311557.1	EST_HUMAN	601142409F1 NIH MGC 14 Homo sapiens cDNA clone IMAGE:3508186 5'
426	5593	10726	1.4	7.00E-89	7657213	NT	Homo sapiens homonally upregulated neu tumor-associated kinase (HUNK), mRNA
426	5593	10727	1.4	7.00E-89	7657213	NT	Homo sapiens homonally upregulated neu tumor-associated kinase (HUNK), mRNA
4785	9896	14989	2.9	7.00E-89	4557390	NT	Homo sapiens complement component 8, beta polypeptide (C8B) mRNA
4847	9954	15043	5.1	7.00E-89	AL045748.1	EST_HUMAN	DKFZp434E246.t1 434 (synonym: hhes3) Homo sapiens cDNA clone DKFZp434E246 5'
1006	6146	11300	1.1	6.00E-89	5803114	NT	Homo sapiens inner membrane protein, mitochondrial (IMMT), mRNA
1601	6728	11898	1.9	6.00E-89	4827015	NT	Homo sapiens solute carrier family 4, anion exchanger, member 3 (SLC4A3) mRNA
1601	6728	11899	1.9	6.00E-89	4827015	NT	Homo sapiens solute carrier family 4, anion exchanger, member 3 (SLC4A3) mRNA
2166	7275	12486	1.1	6.00E-89	4506124	NT	Homo sapiens serine/threonine-protein kinase PRP4 homolog (PRP4) mRNA
2383	7485	12686	0.7	6.00E-89	4507788	NT	Homo sapiens ubiquitin-conjugating enzyme E2L 3 (UBE2L3) mRNA
2383	7485	12687	0.7	6.00E-89	4507788	NT	Homo sapiens ubiquitin-conjugating enzyme E2L 3 (UBE2L3) mRNA
3480	8621	13733	0.8	6.00E-89	7661817	NT	Homo sapiens HSPC159 protein (HSPC159), mRNA
4537	9656	14743	3.5	6.00E-89	AB007868.2	NT	Homo sapiens mRNA for KIAA0406 protein, partial cds
4537	9656	14744	3.5	6.00E-89	AB007868.2	NT	Homo sapiens mRNA for KIAA0406 protein, partial cds
5007	10109	15178	2.8	5.00E-89	BE244323.1	EST_HUMAN	TCBAP2E0383 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project=CBA Homo sapiens cDNA clone TCBAP0383
5007	10109	15179	2.8	5.00E-89	BE244323.1	EST_HUMAN	TCBAP2E0383 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project=TCBA Homo sapiens cDNA clone TCBAP0383

Table 4

2847	7996	13095	1.6	3.00E-89	AW976181.1	EST_HUMAN	EST1388290 IMAGE resequences, MAGN Homo sapiens cDNA
121	5570	10707	0.7	2.00E-89	7706670	NT	Homo sapiens PXR2b protein (PXR2b), mRNA
121	5570	10708	0.7	2.00E-89	7706670	NT	Homo sapiens PXR2b protein (PXR2b), mRNA
402	5570	10707	0.9	2.00E-89	7706670	NT	Homo sapiens PXR2b protein (PXR2b), mRNA
402	5570	10708	0.9	2.00E-89	7706670	NT	Homo sapiens PXR2b protein (PXR2b), mRNA
519	5683	10804	0.8	2.00E-89	AB037763.1	NT	Homo sapiens mRNA for KIAA1342 protein, partial cds
1776	6699	12086	1.3	2.00E-89	4503314	NT	Homo sapiens diacylglycerol kinase, gamma (90KD) (DGKG) mRNA
1776	6699	12087	1.3	2.00E-89	4503314	NT	Homo sapiens diacylglycerol kinase, gamma (90KD) (DGKG) mRNA
							to gb:J04131 GAMMA-GLUTAMYLTRANSPEPTIDASE 1 PRECURSOR (HUMAN); contains
							Alu repetitive element;
2852	8003	13101	2.0	2.00E-89	AI222095.1	EST_HUMAN	Homo sapiens topoisomerase-related function protein (TRF42) mRNA, partial cds
4053	9180	14263	1.5	2.00E-89	AF089897.1	NT	H.sapiens HCK gene for tyrosine kinase (PTK), exons 10-11
4061	9188	14272	6.2	2.00E-89	X58742.1	NT	H.sapiens HCK gene for tyrosine kinase (PTK), exons 10-11
4061	9188	14273	6.2	2.00E-89	X58742.1	NT	H.sapiens HCK gene for tyrosine kinase (PTK), exons 10-11
4396	9518	14608	1.1	2.00E-89	AI007378.1	NT	Homo sapiens GGT gene, exon 5
372	5548	10681	1.1	1.00E-89	AI652927.1	EST_HUMAN	wb40h06.x1 NC1_CGAP_GC6 Homo sapiens cDNA clone IMAGE:2308187 3' similar to
1047	6187	11336	0.6	8.00E-90	AL163246.2	NT	SW:BAC1_HUMAN Q14667 TRANSCRIPTION REGULATOR PROTEIN BACH1;
1048	6187	11338	1.0	8.00E-90	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
							Homo sapiens chromosome 21 segment HS21C046
818	5668		0.9	7.00E-90	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-9, and partial
3029	8181	13281	1.1	6.00E-90	X91926.1	NT	cds, alternatively spliced
3029	8181	13282	1.1	6.00E-90	X91926.1	NT	H.sapiens ECE-1 gene (exon 6)
4134	9260	14341	7.3	6.00E-90	8922398	NT	H.sapiens ECE-1 gene (exon 6)
4134	9260	14342	7.3	6.00E-90	8922398	NT	H.sapiens ECE-1 gene (exon 6)
149	5345		3.6	5.00E-90	AB036344.1	NT	Homo sapiens hypothetical protein FLJ10388 (FLJ10388), mRNA
1175	6309	11463	0.5	5.00E-90	U80226.1	NT	Homo sapiens hypothetical protein FLJ10388 (FLJ10388), mRNA
2508	7604	12805	0.8	5.00E-90	AF114487.1	NT	Homo sapiens hypothetical protein FLJ10388 (FLJ10388), mRNA
4440	9560	14656	3.1	5.00E-90	4506354	NT	Homo sapiens hypothetical protein FLJ10388 (FLJ10388), mRNA
4507	9626	14718	1.1	5.00E-90	AA705222.1	EST_HUMAN	Homo sapiens TCE1B gene, exon 1-10b
4507	9626	14719	1.1	5.00E-90	AA705222.1	EST_HUMAN	Homo sapiens TCE1B gene, exon 1-10b
4571	9689	14783	1.0	5.00E-90	AL135549.1	EST_HUMAN	Human gamma-aminobutyric acid transaminase mRNA, partial cds
299	5485	10615	0.6	4.00E-90	AF231820.1	NT	Homo sapiens gamma-aminobutyric acid transaminase mRNA, partial cds
299	5485	10616	0.6	4.00E-90	AF231820.1	NT	Homo sapiens gamma-aminobutyric acid transaminase mRNA, partial cds
587	5747	10864	0.6	4.00E-90	AI805559.1	EST_HUMAN	Homo sapiens intersecin long isoform (ITSN) mRNA, complete cds
1070	6208	11361	1.0	4.00E-90	4505316	NT	Homo sapiens pregnancy-zone protein (PZP) mRNA
1663	6787	11964	3.3	4.00E-90	X99033.1	NT	Homo sapiens pregnancy-zone protein (PZP) mRNA
4557	9675	14767	4.1	4.00E-90	DB7675.1	NT	Homo sapiens pregnancy-zone protein (PZP) mRNA

Table 4

4691	9803	14904	2.0	4.00E-90	AB033070.1	NT	Homo sapiens mRNA for KIAA1244 protein, partial cds
4713	9825	14917	1.9	4.00E-90	M95967.1	NT	Human prolomone converting enzyme (NEC2) gene, exon 8
718	5872		0.6	3.00E-90	W28189.1	EST_HUMAN	43c5 Human retina cDNA randomly primed sublibrary Homo sapiens cDNA
1156	6291	11445	1.2	2.00E-90	5031748	NT	Homo sapiens high-mobility group (nonhistone chromosomal) protein 17 (HMG17), mRNA
1156	6291	11446	1.2	2.00E-90	5031748	NT	Homo sapiens high-mobility group (nonhistone chromosomal) protein 17 (HMG17), mRNA
3771	8908	13997	2.8	2.00E-90	A1138213.1	EST_HUMAN	q64cd2.x1 Soares, placenta, 809weeks_2NbhP8109W Homo sapiens cDNA clone IMAGE:1713410 3' similar to SW.OLF3_MOUSE P23275 OLFACTORY RECEPTOR OR3.
4588	8702	14796	1.1	2.00E-90	AB006627.1	NT	Homo sapiens mRNA for KIAA0289 gene, partial cds
4820	9929	15020	8.3	2.00E-90	5728855	NT	Homo sapiens GRB2-related adaptor protein (GRAP) mRNA
275	5463	10592	1.2	1.00E-90	4502166	NT	Homo sapiens amyloid beta (A4) precursor protein (protease nexin-II, Alzheimer disease) (APP), mRNA
370	7861	10680	1.2	1.00E-90	AF231920.1	NT	Homo sapiens chromosome 21 unknown mRNA
371	7861	10680	1.0	1.00E-90	AF231920.1	NT	Homo sapiens chromosome 21 unknown mRNA
680	5835	10967	0.7	1.00E-90	AJ237589.1	NT	Homo sapiens mRNA for T-box transcription factor (TBX20 gene), partial
680	5835	10988	0.7	1.00E-90	AJ237589.1	NT	Homo sapiens mRNA for T-box transcription factor (TBX20 gene), partial
713	5867	11004	2.6	1.00E-90	AF264750.1	NT	Homo sapiens ALR-like protein mRNA, partial cds
713	5867	11005	2.6	1.00E-90	AF264750.1	NT	Homo sapiens ALR-like protein mRNA, partial cds
1094	6232		0.8	1.00E-90	4507828	NT	Homo sapiens ALR-like protein mRNA, partial cds
1284	6414	11576	1.2	1.00E-90	AF096154.1	NT	Homo sapiens Kruppel-like factor 7 (ubiquitous) (KLF7), mRNA
1284	6414	11577	1.2	1.00E-90	AF096154.1	NT	Homo sapiens protein phosphatase 2A BR gamma subunit gene, exon 3
1644	6770		4.0	1.00E-90	BE379884.1	EST_HUMAN	Homo sapiens protein phosphatase 2A BR gamma subunit gene, exon 3
2823	7974	13077	8.4	1.00E-90	6005720	NT	801195563F2 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:351118 5'
3777	8914	14005	1.2	1.00E-90	AB020710.1	NT	Homo sapiens chromosome 8 open reading frame 2 (C8ORF2), mRNA
3777	8914	14006	1.2	1.00E-90	AB020710.1	NT	Homo sapiens chromosome 8 open reading frame 2 (C8ORF2), mRNA
4326	9449	14537	1.0	1.00E-90	AF167340.1	NT	Homo sapiens mRNA for KIAA0903 protein, partial cds
4101	9227	14312	5.5	8.00E-91	D12234.1	EST_HUMAN	Homo sapiens soluble interleukin 1 receptor accessory protein (IL1RAP) gene, exon 8,
1428	6555	11731	0.9	7.00E-91	AF053768.1	NT	Homo sapiens soluble interleukin 1 receptor accessory protein (IL1RAP) gene, exon 8,
151	5347	10475	0.8	6.00E-91	AW961150.1	EST_HUMAN	alternative exons 9 and complete cds, alternatively spliced
3429	8571	13683	1.5	5.00E-91	AA702794.1	EST_HUMAN	HUMAN0005381 Liver HepG2 cell line, Homo sapiens cDNA clone s381 3'
3601	8740	13834	6.0	5.00E-91	BE074985.1	EST_HUMAN	Rattus norvegicus brain specific cortactin-binding protein CBP90 mRNA, partial cds
3601	8740	13835	6.0	5.00E-91	BE074985.1	EST_HUMAN	EST1373222 MAGe resequences, MAGF Homo sapiens cDNA
4703	9815	14911	0.8	5.00E-91	7110834	NT	EST1373222 MAGe resequences, MAGF Homo sapiens cDNA
4703	9815	14912	0.8	5.00E-91	7110834	NT	EST1373222 MAGe resequences, MAGF Homo sapiens cDNA
1223	6353	11517	2.5	4.00E-91	BE259124.1	EST_HUMAN	290B04.s1 Soares, fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:448015
3166	8315	13427	1.3	4.00E-91	AF156776.1	NT	3'
							PA3-BT0583-170200-001-406 BT0583 Homo sapiens cDNA
							PA3-BT0583-170200-001-406 BT0583 Homo sapiens cDNA
							PA3-BT0583-170200-001-406 BT0583 Homo sapiens cDNA
							Homo sapiens chromosome 22 open reading frame 5 (C22ORF5), mRNA
							Homo sapiens chromosome 22 open reading frame 5 (C22ORF5), mRNA
							Homo sapiens chromosome 22 open reading frame 5 (C22ORF5), mRNA
							601115508F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3356376 5'
							Homo sapiens lysophosphatidic acid acyltransferase-delta (LPAT-delta) mRNA, complete

Table 4

3166	8315	13426	1.3	4.00E-91	AF156776.1	NT	Homo sapiens lysophosphatidic acid acyltransferase-delta (LPAT-delta) mRNA, complete cds
2624	7714	12914	1.0	3.00E-91	7706508	NT	Homo sapiens beta-ureidopropionase (LOC51733), mRNA
2624	7714	12915	1.0	3.00E-91	7706508	NT	Homo sapiens beta-ureidopropionase (LOC51733), mRNA
3297	8443	13552	1.8	3.00E-91	AL163283.2	NT	Homo sapiens chromosome 21 segment HS21C083
3416	8558	13668	3.0	3.00E-91	AB033104.1	NT	Homo sapiens mRNA for KIAA1278 protein, partial cds
3416	8558	13669	3.0	3.00E-91	AB033104.1	NT	Homo sapiens mRNA for KIAA1278 protein, partial cds
3720	8657	13850	0.8	3.00E-91	AF084530.1	NT	Homo sapiens cyclin-D binding Myb-like protein mRNA, complete cds
4487	9607	14700	4.0	3.00E-91	M30938.1	NT	Human Ku (p70/p80) subunit mRNA, complete cds
4805	10012	15092	1.2	3.00E-91	AL163285.2	NT	Homo sapiens chromosome 21 segment HS21C085
4805	10012	15093	1.2	3.00E-91	AL163285.2	NT	Homo sapiens chromosome 21 segment HS21C085
1699	7924	12004	0.9	2.00E-91	AW845499.1	EST_HUMAN	MR1-CT0056-241189-009-b07 CT0056 Homo sapiens cDNA
42	5252	10365	1.0	1.00E-91	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
1225	6355	11519	1.2	1.00E-91	AW449746.1	EST_HUMAN	UI-H-B13-aks-d-01-0-UI-s1 NCJ_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:2735280 3'
435	7888	10733	0.8	9.00E-92	AW858856.1	EST_HUMAN	RC3-CT0347-220300-015-g12 CT0347 Homo sapiens cDNA
435	7888	10734	0.8	9.00E-92	AW858856.1	EST_HUMAN	RC3-CT0347-220300-015-g12 CT0347 Homo sapiens cDNA
1221	6352	11513	2.9	9.00E-92	AJ001689.1	NT	Homo sapiens NKG2D gene, exon 10
1221	6352	11514	2.9	9.00E-92	AJ001689.1	NT	Homo sapiens NKG2D gene, exon 10
87	5293	10419	0.7	8.00E-92	W26367.1	EST_HUMAN	283 Human retina cDNA randomly primed sublibrary Homo sapiens cDNA
283	5470	10600	2.0	8.00E-92	BE386363.1	EST_HUMAN	6012735137 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3614667 5'
2736	7822	13026	0.9	8.00E-92	BE398619.1	EST_HUMAN	601290085F NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3620469 5'
80	5268	10390	0.9	7.00E-92	M60676.1	NT	Human von Willebrand factor pseudogene corresponding to exons 23 through 34
236	7884	10552	0.9	7.00E-92	AB018301.1	NT	Homo sapiens mRNA for KIAA0758 protein, partial cds
236	7884	10553	0.9	7.00E-92	AB018301.1	NT	Homo sapiens mRNA for KIAA0758 protein, partial cds
576	5736		1.3	7.00E-92	AF007822.1	NT	Homo sapiens cytoplasmic Sepsase truncated isoform mRNA, complete cds
1259	6388	11549	0.7	7.00E-92	4502384	NT	Homo sapiens B-cell CLL/lymphoma 7b (BCL7B) mRNA
2139	7249	12455	0.6	7.00E-92	5031570	NT	Homo sapiens ARP2 (actin-related protein 2, yeast) homolog (ACTR2), mRNA
2139	7249	12456	0.6	7.00E-92	5031570	NT	Homo sapiens ARP2 (actin-related protein 2, yeast) homolog (ACTR2), mRNA
2517	7613	12815	0.8	7.00E-92	AF167706.1	NT	Homo sapiens cysteine-rich repeat-containing protein S52 precursor, mRNA, complete cds
2693	7780	12977	1.8	7.00E-92	6005738	NT	Homo sapiens NRAS-related gene (D1S155E), mRNA
2724	7808	13013	1.0	7.00E-92	AB031007.1	NT	Homo sapiens DNA, MHC class I region, 7.1 ancestral haplotype
3301	10286	13555	0.9	7.00E-92	4507500	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA
3301	10286	13556	0.9	7.00E-92	4507500	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA
4484	9604	14697	1.6	7.00E-92	S71824.1	NT	N-CAM=145 kDa neural cell adhesion molecule [human, small cell lung cancer cell line OS2-R, mRNA, 2960 nt]
4484	9604	14698	1.6	7.00E-92	S71824.1	NT	N-CAM=145 kDa neural cell adhesion molecule [human, small cell lung cancer cell line OS2-R, mRNA, 2960 nt]
5110	10206	15284	1.5	7.00E-92	4506118	NT	Homo sapiens prospero-related homeobox 1 (PROX1) mRNA
1569	6895		0.9	5.00E-92	BE390882.1	EST_HUMAN	601283012F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3605018 5'

Table 4

23	5232	10335	0.5	2.00E-92	4501898	NT	Homo sapiens activin A receptor, type IIB (ACVR2B) mRNA
732	5686	11029	1.4	2.00E-92	BE299190.1	EST_HUMAN	601118337F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3028304 5'
732	5686	11030	1.4	2.00E-92	BE299190.1	EST_HUMAN	601118337F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3028304 5'
1686	6610		1.0	2.00E-92	S78653.1	NT	mg-mas-related (human, Genomic, 2416 nt)
1894	7011	12199	0.6	2.00E-92	AI818119.1	EST_HUMAN	wk27d07.x1 NCJ_CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2413549 3' similar to
1894	7011	12200	0.6	2.00E-92	AI818119.1	EST_HUMAN	TR:Q12844 Q12844 BREAKPOINT CLUSTER REGION PROTEIN ;
2002	7117	12318	1.7	2.00E-92	4506860	NT	TR:Q12844 Q12844 BREAKPOINT CLUSTER REGION PROTEIN ;
2623	7713	12913	14.0	2.00E-92	6912457	NT	Homo sapiens syndecan 4 (amphiphylin, ryudocan) (SDC4) mRNA
3562	8701	13797	1.0	2.00E-92	AF231919.1	NT	Homo sapiens calcineurin binding protein 1 (KIAA0330), mRNA
3562	8701	13798	1.0	2.00E-92	AF231919.1	NT	Homo sapiens chromosome 21 unknown mRNA
3631	8770	13864	5.0	2.00E-92	5803180	NT	Homo sapiens stress-induced-phosphoprotein 1 (Hsp70/Hsp90-organizing protein) (STIP-1), mRNA
4191	9317	14401	1.0	2.00E-92	M10976.1	NT	Human endogenous retroviral DNA (4-1), complete retroviral segment
4648	9760	14855	0.8	2.00E-92	AF136523.1	NT	Homo sapiens bile salt export pump (BSEP) mRNA, complete cds
4922	10029		2.5	2.00E-92	AL040437.1	EST_HUMAN	DKFZp434C0414_r1 434 (synonym: hies3) Homo sapiens cDNA clone DKFZp434C0414 5'
1807	6928	12114	1.1	1.00E-92	R78078.1	EST_HUMAN	y806d08.r1 Soares placenta NB2HP Homo sapiens cDNA clone IMAGE:145574 5'
1807	6928	12115	1.1	1.00E-92	R78078.1	EST_HUMAN	y806d08.r1 Soares placenta NB2HP Homo sapiens cDNA clone IMAGE:145574 5'
2028	7141	12342	13.0	1.00E-92	4506668	NT	Homo sapiens ribosomal protein, large, P1 (RPLP1) mRNA
1996	7112		3.3	9.00E-93	AA316723.1	EST_HUMAN	EST188414 HCC cell line (metastasis to liver in mouse) H Homo sapiens cDNA 5' end similar to ribosomal protein L28
2610	7700		0.5	9.00E-93	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
3563	8702	13789	1.0	9.00E-93	BE388571.1	EST_HUMAN	601281867F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3603832 5'
246	5434	10560	2.1	7.00E-93	AF231919.1	NT	Homo sapiens chromosome 21 unknown mRNA
3030	8182		2.4	7.00E-93	AL163247.2	NT	Homo sapiens chromosome 21 segment HS21C047
1359	6487	11653	1.3	5.00E-93	AB014511.1	NT	Homo sapiens mRNA for KIAA0611 protein, partial cds
1385	6512	11677	2.0	5.00E-93	AI674184.1	EST_HUMAN	wc09c08.x1 NCJ_CGAP_P728 Homo sapiens cDNA clone IMAGE:2314670 3'
1385	6512	11678	2.0	5.00E-93	AI674184.1	EST_HUMAN	wc09c08.x1 NCJ_CGAP_P728 Homo sapiens cDNA clone IMAGE:2314670 3'
1459	6586		1.0	5.00E-93	AL163201.2	NT	Homo sapiens chromosome 21 segment HS21C001
3195	8344	13457	2.4	5.00E-93	X04201.1	NT	Human skeletal muscle 1.3 kb mRNA for tropomyosin
82	5288		1.6	4.00E-93	AA458933.1	EST_HUMAN	z506e09.s1 Soares testis NHT Homo sapiens cDNA clone IMAGE:795688 3' similar to
437	5603	10736	0.6	4.00E-93	4557879	NT	SW:CLPA_RAT P37397 CALPONIN, ACIDIC ISOFORM ;
437	5603	10737	0.6	4.00E-93	4557879	NT	Homo sapiens interferon gamma receptor 1 (IFNGR1) mRNA
755	5907	11054	1.3	4.00E-93	7657454	NT	Homo sapiens pascadillo (zebrafish) homolog 1, containing BRCT domain (PES1), mRNA
755	5907	11055	1.3	4.00E-93	7657454	NT	Homo sapiens pascadillo (zebrafish) homolog 1, containing BRCT domain (PES1), mRNA



Table 4

1166	6300	11455	0.7	4.00E-93	8923658	NT	Homo sapiens hypothetical protein FLJ20731 (FLJ20731), mRNA
1834	7051	12244	1.8	4.00E-93	AF047677.1	NT	Homo sapiens dystrophin (DMD) gene, deletion breakpoints 1-3 in intron 5
2349	7451	12658	0.8	4.00E-93	AL163301.2	NT	Homo sapiens chromosome 21 segment HS21C101
2564	7657	12860	0.8	4.00E-93	7656972	NT	Homo sapiens TNF-inducible protein CG12-1 (CG12-1), mRNA
3962	9094	14179	1.4	4.00E-93	4504654	NT	Homo sapiens Interleukin 18 receptor 1 (IL18R1) mRNA
183	5377	10502	2.8	2.00E-93	AB015610.1	NT	Chlorocebus aethiops mRNA for ribosomal protein S4X, complete cds
183	5377	10503	2.8	2.00E-93	AB015610.1	NT	Chlorocebus aethiops mRNA for ribosomal protein S4X, complete cds
320	5504	10632	2.3	2.00E-93	AL163285.2	NT	Homo sapiens chromosome 21 segment HS21C085
321	5504	10632	2.6	2.00E-93	AL163285.2	NT	Homo sapiens chromosome 21 segment HS21C085
2083	7195	12400	1.0	2.00E-93	4758105	NT	Homo sapiens Cdk-associating RS-cyclophilin (CYP), mRNA
2436	7535	12742	0.9	2.00E-93	BE253201.1	EST	Homo sapiens cDNA clone IMAGE:3357243 5'
5086	10186	15264	1.0	2.00E-93	BE253201.1	EST	601116810F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3357243 5'
96	5303	10429	0.6	1.00E-93	AF238997.1	NT	Homo sapiens CTR1 pseudogene
96	5303	10430	0.6	1.00E-93	AF238997.1	NT	Homo sapiens CTR1 pseudogene
507	5671	10794	0.9	1.00E-93	7657016	NT	Homo sapiens hypothetical protein (DJ328E19.C1.1), mRNA
585	5745	10862	1.3	1.00E-93	AI146755.1	EST	oy64b08.x1 NCI_CGAP_CLL1 Homo sapiens cDNA clone IMAGE:1672503 3' similar to
854	6003	11163	1.1	1.00E-93	D87675.1	NT	TR-O62384 Q62384 ZINC FINGER PROTEIN.1
1217	6347	11506	2.2	1.00E-93	8923270	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
1217	6347	11507	2.2	1.00E-93	8923270	NT	Homo sapiens hypothetical protein FLJ20291 (FLJ20291), mRNA
1323	6452	11617	0.6	1.00E-93	AF167706.1	NT	Homo sapiens cysteine-rich repeat-containing protein S52 precursor, mRNA, complete cds
2289	7394	12602	1.0	1.00E-93	AF231981.1	NT	Homo sapiens long chain polyunsaturated fatty acid elongation enzyme (HELO1) mRNA, complete cds
2415	7514	12722	1.5	1.00E-93	AF055066.1	NT	Homo sapiens MHC class 1 region
2459	7558		1.1	1.00E-93	AB037846.1	NT	Homo sapiens mRNA for KIAA1425 protein, partial cds
2792	6403	11562	0.9	1.00E-93	BE297369.1	EST	601177686F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3532965 5'
2792	6403	11563	0.9	1.00E-93	BE297369.1	EST	601177686F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3532965 5'
2903	8054	13159	4.3	1.00E-93	D87675.1	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
4331	9454	14542	1.4	1.00E-93	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
3860	9016	14111	1.7	6.00E-94	AF142482.1	NT	Homo sapiens transcription enhancer factor-5 mRNA, complete cds
1799	8919		1.7	4.00E-94	L05094.1	NT	Homo sapiens ribosomal protein L27 mRNA, complete cds
2621	7711	12911	0.9	4.00E-94	4506008	NT	Homo sapiens protein phosphatase 1, regulatory subunit 10 (PPP1R10) mRNA
4618	9732	14627	3.0	4.00E-94	AI591312.1	EST	hw11f10.x1 NCI_CGAP_Bms2 Homo sapiens cDNA clone IMAGE:2259403 3' similar to
595	5753	10671	1.2	3.00E-94	AB022785.1	NT	TR-Q15265 Q15265 PROTEIN TYROSINE PHOSPHATASE 1
704	5859	10994	1.2	3.00E-94	4502506	NT	Homo sapiens ASH2L gene, complete cds, similar to Drosophila ash2 gene
1706	6829	12009	1.1	3.00E-94	AF167706.1	NT	Homo sapiens complement component 5 (C5) mRNA
1706	6829	12010	1.1	3.00E-94	AF167706.1	NT	Homo sapiens cysteine-rich repeat-containing protein S52 precursor, mRNA, complete cds



Table 4

1735	6858	12036	1.3	3.00E-94	4557556	NT	Homo sapiens E1A binding protein p300 (EP300) mRNA
4095	9221	14304	0.8	3.00E-94	AA464805.1	EST_HUMAN	z663g08.r1 Soares_t0tal_t0tus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:774782 5'
143	5339	10469	0.8	1.00E-94	BE295714.1	EST_HUMAN	601175762F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3531039 5'
616	5774	10895	1.5	1.00E-94	AI394483.1	EST_HUMAN	601175762F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3352559 5'
616	5774	10896	1.5	1.00E-94	AI394483.1	EST_HUMAN	60111696F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3352559 5'
3050	8201	13301	1.9	1.00E-94	BE253433.1	EST_HUMAN	60111696F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3352559 5'
3050	8201	13302	1.9	1.00E-94	BE253433.1	EST_HUMAN	60111696F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3352559 5'
1461	6588	11762	0.6	9.00E-95	AF027302.1	NT	Homo sapiens TNF-alpha stimulated ABC protein (ABC50) mRNA, complete cds
3118	8267	13371	1.1	9.00E-95	7662027	NT	Homo sapiens KIAA0255 gene product (KIAA0255), mRNA
3118	8267	13372	1.1	9.00E-95	7662027	NT	Homo sapiens KIAA0255 gene product (KIAA0255), mRNA
4436	9557	14651	1.6	8.00E-95	AI700998.1	EST_HUMAN	Homo sapiens KIAA0255 gene product (KIAA0255), mRNA
4436	9557	14652	1.6	8.00E-95	AI700998.1	EST_HUMAN	Homo sapiens KIAA0255 gene product (KIAA0255), mRNA
274	5462	10590	3.2	7.00E-95	DB7675.1	NT	we09a04.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2340606 3' similar to
274	5462	10591	3.2	7.00E-95	DB7675.1	NT	we09a04.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2340606 3' similar to
4270	9395	14479	5.9	7.00E-95	M85708.1	NT	we09a04.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2340606 3' similar to
4316	9439	15155	1.4	7.00E-95	AL163246.2	NT	we09a04.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2340606 3' similar to
4882	10085	11226	0.9	2.00E-95	M95929.1	NT	we09a04.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2340606 3' similar to
922	6069	11919	0.6	2.00E-95	7662027	NT	we09a04.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2340606 3' similar to
1625	6751	11920	0.6	2.00E-95	7662027	NT	we09a04.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2340606 3' similar to
1897	7015	12204	2.8	2.00E-95	4507512	NT	we09a04.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2340606 3' similar to
1800	7018	12208	1.2	2.00E-95	BE393873.1	EST_HUMAN	we09a04.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2340606 3' similar to
2376	7478	12679	1.3	2.00E-95	5453665	NT	we09a04.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2340606 3' similar to
2376	7478	12680	1.3	2.00E-95	5453665	NT	we09a04.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2340606 3' similar to
2417	7516	12723	16.6	2.00E-95	7657185	NT	we09a04.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2340606 3' similar to
2468	7564	12767	0.9	2.00E-95	4758423	NT	we09a04.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2340606 3' similar to
2767	6068	11225	0.9	2.00E-95	4504374	NT	we09a04.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2340606 3' similar to
3120	8269	13374	3.5	2.00E-95	AF015452.1	NT	we09a04.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2340606 3' similar to
3517	8658	13764	2.8	2.00E-95	7705900	NT	we09a04.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2340606 3' similar to
3517	8658	13765	2.8	2.00E-95	7705900	NT	we09a04.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2340606 3' similar to
3565	8704	13800	1.0	2.00E-95	AB037807.1	NT	we09a04.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2340606 3' similar to
3690	8829	13922	1.0	2.00E-95	AI280264.1	EST_HUMAN	we09a04.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2340606 3' similar to
4264	9389	14472	2.3	2.00E-95	7657185	NT	we09a04.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2340606 3' similar to
4971	10074	15147	2.6	2.00E-95	7661979	NT	we09a04.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2340606 3' similar to

Table 4

5022	10123	15195	1.0	2.00E-95	AAAA7931.1	EST_HUMAN	Zx11d07.r1 Soares_total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:786157 5'
5022	10123	15196	1.0	2.00E-95	AAAA7931.1	EST_HUMAN	Zx11d07.r1 Soares_total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:786157 5'
1693	6817	11997	0.8	8.00E-96	7657185	NT	Homo sapiens hypothetical protein (HS322B1A), mRNA
1693	6817	11998	0.8	8.00E-96	7657185	NT	Homo sapiens hypothetical protein (HS322B1A), mRNA
3834	8971	14070	1.0	7.00E-96	AF231920.1	NT	Homo sapiens chromosome 21 unknown mRNA
4450	9570	14666	2.0	7.00E-96	AW404800.1	EST_HUMAN	UI-HF-BL0-acm-d-11-0-UI.r1 NIH_MGC_37 Homo sapiens cDNA clone IMAGE:3059397 5'
4450	9570	14669	2.0	7.00E-96	AW404800.1	EST_HUMAN	UI-HF-BL0-acm-d-11-0-UI.r1 NIH_MGC_37 Homo sapiens cDNA clone IMAGE:3059397 5'
2213	7321	12535	0.9	6.00E-96	BE171984.1	EST_HUMAN	MR0-HT0559-250200-002-d07 HT0559 Homo sapiens cDNA
3276	8421	13529	1.0	6.00E-96	AL163201.2	NT	Homo sapiens chromosome 21 segment HS21C001
3437	8579	13691	26.2	6.00E-96	M26873.1	NT	Human glyceraldehyde-3-phosphate dehydrogenase pseudogene 3end
317	5501	10628	0.9	5.00E-96	AB032998.1	NT	Homo sapiens mRNA for KIAA1172 protein, partial cds
824	5973	11131	1.0	5.00E-96	AB032998.1	NT	Homo sapiens mRNA for KIAA1172 protein, partial cds
824	5973	11132	1.0	5.00E-96	AB032998.1	NT	Homo sapiens mRNA for KIAA1172 protein, partial cds
2991	8143	13245	1.0	5.00E-96	6912735	NT	Homo sapiens transient receptor potential channel 5 (TRPC5), mRNA
4810	9920		1.2	5.00E-96	X60812.1	NT	H sapiens DNA for monocamine oxidase type A (7) (partial)
4097	9223		6.2	3.00E-96	H68656.1	EST_HUMAN	y87h12.r1 Soares fetal liver spleen 1nFLS Homo sapiens cDNA clone IMAGE:212327 5'
409	5577		1.2	2.00E-96	4503098	NT	Homo sapiens chondroilin sulfate proteoglycan 4 (melanoma-associated) (CSPG4), mRNA
730	5884	11026	0.5	2.00E-96	AL163248.2	NT	Homo sapiens chromosome 21 segment HS21C048
4651	9763	14856	1.6	2.00E-96	BE148074.1	EST_HUMAN	RC3-HT0230-040500-110-g02 HT0230 Homo sapiens cDNA
655	5812	10940	0.6	1.00E-96	Y18890.1	NT	Human endogenous retrovirus type K (HERV-K), gag, pol and env genes
1742	6865	12042	0.7	1.00E-96	AW955054.1	EST_HUMAN	EST367124 MAGE resequences, MAGEC Homo sapiens cDNA
1742	6865	12043	0.7	1.00E-96	AW955054.1	EST_HUMAN	EST367124 MAGE resequences, MAGEC Homo sapiens cDNA
1806	6925	12112	0.9	1.00E-96	4503756	NT	Homo sapiens flavin containing monooxygenase 2 (FMO2) mRNA
1806	6925	12113	0.9	1.00E-96	4503756	NT	Homo sapiens flavin containing monooxygenase 2 (FMO2) mRNA
2080	7192	12395	0.9	1.00E-96	AF167706.1	NT	Homo sapiens cysteine-rich repeat-containing protein S52 precursor, mRNA, complete cds
2080	7192	12396	0.9	1.00E-96	AF167706.1	NT	Homo sapiens cysteine-rich repeat-containing protein S52 precursor, mRNA, complete cds
2181	7280	12501	1.3	1.00E-96	M75967.1	NT	Human hepatocyte growth factor gene, exon 1
2181	7280	12502	1.3	1.00E-96	M75967.1	NT	Human hepatocyte growth factor gene, exon 1
2219	7872	12541	0.7	1.00E-96	U51472.2	NT	Felis catus superfast myosin heavy chain (slmyHC) mRNA, complete cds
924	8071	11229	1.3	4.00E-97	BE004436.1	EST_HUMAN	CM0-BN0106-170300-283-a06 BN0106 Homo sapiens cDNA
1868	8986	12170	1.1	4.00E-97	5453572	NT	Homo sapiens brefeldin A-inhibited guanine nucleotide-exchange protein 2 (BIG2), mRNA
243	5432	10558	1.2	3.00E-97	AB032998.1	NT	Homo sapiens mRNA for KIAA1172 protein, partial cds

Table 4

520	5684	10805	1.1	3.00E-97	AA042813.1	EST_HUMAN	zh53c07.s1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:486540 3' similar to gb:X65857_cds1 OLFACTORY RECEPTOR-LIKE PROTEIN HGM/POTE (HUMAN);
856	6005	11165	3.7	3.00E-97	4502166	NT	Homo sapiens amyloid beta (A4) precursor protein (protease nexin-II, Alzheimer disease) (APP), mRNA
856	6005	11166	3.7	3.00E-97	4502166	NT	Homo sapiens amyloid beta (A4) precursor protein (protease nexin-II, Alzheimer disease) (APP), mRNA
856	6005	11166	3.7	3.00E-97	4502166	NT	Homo sapiens N-myc (and STAT) interactor (NMI), mRNA
1423	7916	11727	0.6	3.00E-97	4758813	NT	Homo sapiens beta-prime-adaptin (BAM22) gene, exon 7
2389	7874	12893	0.7	3.00E-97	U36255.1	NT	Human beta-prime-adaptin (BAM22) gene, exon 7
3223	8371	13480	1.1	3.00E-97	5174478	NT	Homo sapiens eukaryotic translation elongation factor 1 alpha 1 (EEF1A1) mRNA
4670	9782	14861	12.6	1.00E-97	4503470	NT	PM4-BT0724-010400-008-a12 BT0724 Homo sapiens cDNA
883	6031	11190	2.7	9.00E-98	BE090973.1	EST_HUMAN	Homo sapiens cat eye syndrome critical region gene 1 (CECR1), mRNA
1255	6384	11544	1.3	9.00E-98	8393092	NT	Homo sapiens Testis-specific XK-related protein on Y (XKRY) mRNA
62	5270	10391	0.5	8.00E-98	4758329	NT	Homo sapiens Testis-specific XK-related protein on Y (XKRY) mRNA
62	5270	10392	0.5	8.00E-98	4758329	NT	Homo sapiens Testis-specific XK-related protein on Y (XKRY) mRNA
1350	6478	11644	0.9	8.00E-98	AB033766.1	NT	Homo sapiens hPAD-codony10 mRNA for peptidylarginine deiminase type I, complete cds
1540	6666	11835	1.0	8.00E-98	5031810	NT	Homo sapiens IL2-inducible T-cell kinase (ITK), mRNA
1540	6666	11836	1.0	8.00E-98	5031810	NT	Homo sapiens IL2-inducible T-cell kinase (ITK), mRNA
1695	6819	12000	1.0	8.00E-98	AB017007.1	NT	Homo sapiens PMS2L16 mRNA, partial cds
1695	6819	12001	1.0	8.00E-98	AB017007.1	NT	Homo sapiens PMS2L16 mRNA, partial cds
3728	8863	13956	5.0	8.00E-98	U04469.1	NT	Human mitochondrial creatine kinase (CKMT) gene, complete cds
5049	10149	12861	0.9	8.00E-98	AL163201.2	NT	Homo sapiens chromosome 21 segment HS21C001
2565	7658	12861	0.7	3.00E-98	AB014607.1	NT	Homo sapiens mRNA for KIAA0707 protein, partial cds
2720	7804	12348	0.8	3.00E-98	AA077498.1	EST_HUMAN	7B18H01 Chromosome 7 Fetal Brain cDNA Library Homo sapiens cDNA clone 7B18H01
2033	7146	12348	11.0	2.00E-98	BE294281.1	EST_HUMAN	60172658F NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3528134 5'
2191	7300	12515	0.5	2.00E-98	AL163202.2	NT	Homo sapiens chromosome 21 segment HS21C002
2674	7761	12961	0.7	2.00E-98	7662405	NT	Homo sapiens KIAA0957 protein (KIAA0957), mRNA
4244	9389	14448	4.9	2.00E-98	4758331	NT	Homo sapiens fatty-acid-Coenzyme A ligase, long-chain 4 (FACL4) mRNA
4720	9832	14922	1.5	2.00E-98	AF218902.1	NT	Homo sapiens atracilin precursor (ATRIN) gene, exon 16
4720	9832	14923	1.5	2.00E-98	AF218902.1	NT	Homo sapiens atracilin precursor (ATRIN) gene, exon 16
5069	10167	15243	6.4	2.00E-98	9055269	NT	Homo sapiens low density lipoprotein receptor related protein-deleted in tumor (LRPDI1), mRNA
5069	10167	15244	6.4	2.00E-98	9055269	NT	Homo sapiens low density lipoprotein receptor related protein-deleted in tumor (LRPDI1), mRNA
5163	10257	15327	1.1	2.00E-98	4758975	NT	Homo sapiens protein tyrosine kinase 2 beta (PTK2B) mRNA
399	5567	10704	18.9	1.00E-98	AI862007.1	EST_HUMAN	hw3604.x1 NCI_CGAP_U11 Homo sapiens cDNA clone IMAGE:2261743 3' similar to
447	5613	10744	0.8	1.00E-98	AW998611.1	EST_HUMAN	SW:RL2B_HUMAN P29316 605 RIBOSOMAL PROTEIN L23A.1
1756	6877	12058	6.1	1.00E-98	NA9818.1	EST_HUMAN	PM0-BN0065-100300-001-c06 BN0065 Homo sapiens cDNA yz23f05.t1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:243585 5' similar to PIR:S54204 S54204 ribosomal protein L28 - human

Table 4

1975	7090	12291	0.9	7.00E-99	4759149	NT	Homo sapiens SMC (mouse) homolog, Y chromosome (SMCY) mRNA
1975	7090	12292	0.9	7.00E-99	4759149	NT	Homo sapiens SMC (mouse) homolog, Y chromosome (SMCY) mRNA
3814	8951	14049	1.9	6.00E-99	AW976364.1	EST_HUMAN	EST386473 MAGN resequences, MAGN Homo sapiens cDNA
4842	9756	14850	1.2	6.00E-99	4502660	NT	Homo sapiens CD34 antigen (CD34) mRNA
902	6049	11203	0.9	5.00E-99	U35464.1	NT	Homo sapiens protein C inhibitor (P-CI-B) mRNA, complete cds
902	6049	11204	0.9	5.00E-99	U35464.1	NT	Human protein C inhibitor (P-CI-B) mRNA, complete cds
1922	7039	12228	0.9	5.00E-99	Y11365.1	NT	H. sapiens ILPA gene, exon 8
4463	9583	14680	1.4	5.00E-99	AF009660.1	NT	Homo sapiens T cell receptor beta locus, TCRBV33A2 to TCRBV12S2 region
5066	10164	15241	2.5	5.00E-99	4758697	EST_HUMAN	Homo sapiens mannosidase, alpha, class 2A, member 1 (MAN2A1), mRNA
375	5551	10684	1.0	2.00E-99	AW385237.1	EST_HUMAN	Homo sapiens MYOSIN LIGHT CHAIN ALKALI, NON-MUSCLE ISOFORM (HUMAN);
1219	6350		1.2	2.00E-99	AW274792.1	EST_HUMAN	Human Ku (p70/p80) subunit mRNA, complete cds
3220	8368	13479	1.1	2.00E-99	M30938.1	NT	Human Ku (p70/p80) subunit mRNA, complete cds
4443	9563	14659	3.2	2.00E-99	AF096703.1	NT	Human Ku (p70/p80) subunit mRNA, complete cds
312	5496	10625	0.5	1.00E-99	AF114487.1	NT	Human Ku (p70/p80) subunit mRNA, complete cds
1401	6528	11698	0.8	1.00E-99	M30938.1	NT	Human Ku (p70/p80) subunit mRNA, complete cds
1537	6663	11630	0.5	1.00E-99	AF192523.1	NT	Homo sapiens truncated Niemann-Pick C3 protein (NPC3) mRNA, complete cds
1537	6663	11631	0.5	1.00E-99	AF192523.1	NT	Homo sapiens truncated Niemann-Pick C3 protein (NPC3) mRNA, complete cds
1885	7003	12188	1.1	1.00E-99	4503730	NT	Homo sapiens FK506-binding protein 6 (36kD) (FKBP6) mRNA, and translated products
1885	7003	12189	1.1	1.00E-99	4503730	NT	Homo sapiens FK506-binding protein 6 (36kD) (FKBP6) mRNA, and translated products
3046	8197	13298	0.9	1.00E-99	J03171.1	NT	Human interferon-alpha receptor (HuIFN-alpha-Ree) mRNA, complete cds
4283	9408	14492	2.7	1.00E-99	AF098018.1	NT	Homo sapiens fatty acid amide hydrolase (FAAH) gene, exon 14
4283	9408	14493	2.7	1.00E-99	AF098018.1	NT	Homo sapiens fatty acid amide hydrolase (FAAH) gene, exon 14
5200	10291		1.2	1.00E-99	AL163281.2	NT	Homo sapiens chromosome 21 segment HS21C047
1	5211	10312	1.1	1.00E-100	AL163247.2	NT	Homo sapiens chromosome 21 segment HS21C047
2	5211	10312	0.7	1.00E-100	AL163247.2	NT	Homo sapiens chromosome 21 segment HS21C047
81	5287	10415	0.5	1.00E-100	AW276237.1	EST_HUMAN	Human sapiens chromosome 21 segment HS21C046
162	5367	10482	1.2	1.00E-100	AL163206.2	NT	Homo sapiens chromosome 21 segment HS21C049
314	5498	10627	1.0	1.00E-100	AL163249.2	NT	Homo sapiens chromosome 21 segment HS21C049
340	5521	10646	0.8	1.00E-100	T05087.1	EST_HUMAN	EST02975 Fetal brain, Stratigene (cat#936206) Homo sapiens cDNA clone HFBGR32
430	5597		0.5	1.00E-100	AF003528.1	NT	Homo sapiens X-linked anhidrotic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions
481	5647		2.4	1.00E-100	X89631.1	NT	flanking repeat regions
500	5684	10787	1.4	1.00E-100	BE180609.1	EST_HUMAN	RC3-HT0625-040500-022-B09 HT0625 Homo sapiens cDNA
969	6114	11273	4.3	1.00E-100	7705430	NT	Homo sapiens hypothetical protein (HSPC016), mRNA
1002	6142	11295	0.8	1.00E-100	7661685	NT	Homo sapiens DKFZP586M0122 protein (DKFZP586M0122), mRNA
1002	6142	11296	0.8	1.00E-100	7661685	NT	Homo sapiens DKFZP586M0122 protein (DKFZP586M0122), mRNA
1528	6655		1.3	1.00E-100	AW207555.1	EST_HUMAN	U1-H-B11-alk-c-07-0-U1.s1 NCI_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2722164 3'

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Table 4

604	5762	10882	0.9	1.00E-102	BE252470.1	EST_HUMAN	601108292F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3344326 5'
748	5900	11047	0.7	1.00E-102	D30612.1	NT	Homo sapiens mRNA for repressor protein, partial cds
758	5910	11056	1.5	1.00E-102	4557534	NT	Homo sapiens down-regulated in adenoma (DRA) mRNA
1101	6239	11391	0.7	1.00E-102	M10976.1	NT	Human endogenous retroviral DNA (4-1), complete retroviral segment
1398	6525	11694	33.0	1.00E-102	BE408447.1	EST_HUMAN	60129982F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3629901 5'
2157	7266	12476	0.7	1.00E-102	AF182645.1	NT	Homo sapiens chondrosarcoma-associated protein 2 (CSA2) mRNA, complete cds
2261	7367	12576	1.3	1.00E-102	A1950528.1	EST_HUMAN	wx51e07.x1 NCI_CGAP_Lu28 Homo sapiens cDNA clone IMAGE:2547204 3' similar to SW:GG95_HUMAN Q08379 GOLGIN-95, contains element MER22 repetitive element;
2261	7367	12577	1.3	1.00E-102	A1950528.1	EST_HUMAN	wx51e07.x1 NCI_CGAP_Lu28 Homo sapiens cDNA clone IMAGE:2547204 3' similar to SW:GG95_HUMAN Q08379 GOLGIN-95, contains element MER22 repetitive element;
3026	8178	13279	1.5	1.00E-102	7661979	NT	Homo sapiens KIAA0187 gene product (KIAA0187), mRNA
4139	9265	14346	1.5	1.00E-102	AL163207.2	NT	Homo sapiens chromosome 21 segment HS21C007
4314	9437	14526	2.1	1.00E-102	BE251310.1	EST_HUMAN	601107843F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3343682 5'
5063	10161	15237	1.1	1.00E-102	R66488.1	EST_HUMAN	Y132C04.t1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:140934 5'
93	5300	10426	2.8	1.00E-103	D87078.2	NT	Homo sapiens nuclear protein (KKEID repeat) (NOP56) mRNA
201	5395	10521	0.8	1.00E-103	5453793	NT	Homo sapiens nuclear protein (KKEID repeat) (NOP56) mRNA
1578	6704	11874	0.8	1.00E-103	AF012872.1	NT	Homo sapiens phosphatidylinositol 4-kinase 230 (PI4K230) mRNA, complete cds
1872	6990	12175	1.0	1.00E-103	7657592	NT	Homo sapiens smg GDS-ASSOCIATED PROTEIN (SMAP), mRNA
1932	7049	12240	1.3	1.00E-103	4502428	NT	Homo sapiens bone morphogenetic protein 8 (osteogenic protein 2) (BMP8) mRNA
1932	7049	12241	1.3	1.00E-103	4502428	NT	Homo sapiens bone morphogenetic protein 8 (osteogenic protein 2) (BMP8) mRNA
2257	7363	12572	0.6	1.00E-103	5803184	NT	Homo sapiens synapophysin-like protein (SYPL), mRNA
2401	7500	12707	0.8	1.00E-103	AF060568.1	NT	Homo sapiens promyelocytic leukemia zinc finger protein (PLZF) gene, complete cds
2578	7671	12872	0.9	1.00E-103	N52770.1	EST_HUMAN	YW81d08.s1 Soares_placenta_8u6weeks_2NbHP8109W Homo sapiens cDNA clone IMAGE:259599 3'
3333	8477	13580	3.4	1.00E-103	AW298245.1	EST_HUMAN	UI-H-BWO-q1h-11-Q-UJ.s1 NCI_CGAP_Sub6 Homo sapiens cDNA clone IMAGE:2733165 3'
3383	8535	13640	1.1	1.00E-103	AB040892.1	NT	Homo sapiens mRNA for KIAA1459 protein, partial cds
3592	8731		1.3	1.00E-103	AL048453.2	EST_HUMAN	DKFZp586J1124.t1 586 (synonym: hute1) Homo sapiens cDNA clone DKFZp586J1124
3695	8834		2.4	1.00E-103	AF023861.1	NT	Mecaca mulatta cyclophilin A mRNA, complete cds
3725	8862	13955	1.2	1.00E-103	AA485663.1	EST_HUMAN	ab10d12.s1 Stratagene lung (#937210) Homo sapiens cDNA clone IMAGE:840407 3' similar to contains element LTR10 repetitive element;
3922	9056	14143	3.0	1.00E-103	T23683.1	EST_HUMAN	seq340 b4HBM3A-Co1109+10-Bio Homo sapiens cDNA clone b4HBM3A-Co1109+10-Bio-7 3'
233	5424	10548	0.9	1.00E-104	AL037549.3	EST_HUMAN	DKFZp564H1072.t1 564 (synonym: hbr2) Homo sapiens cDNA clone DKFZp564H1072 5'
233	5424	10549	0.9	1.00E-104	AL037549.3	EST_HUMAN	DKFZp564H1072.t1 564 (synonym: hbr2) Homo sapiens cDNA clone DKFZp564H1072 5'
579	5739	10855	1.1	1.00E-104	AA496139.1	EST_HUMAN	zv51f11.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:757197 3' similar to TR:G487738 G487738 PUTATIVE POTASSIUM CHANNEL SUBUNIT.;
579	5739	10856	1.1	1.00E-104	AA496139.1	EST_HUMAN	zv51f11.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:757197 3' similar to TR:G487738 G487738 PUTATIVE POTASSIUM CHANNEL SUBUNIT.;

Table 4

1845	6963	12149	0.7	1.00E-104	4502428	NT	Homo sapiens bone morphogenetic protein 8 (osteogenic protein 2) (BMP8) mRNA
1898	7016		1.9	1.00E-104	AW054828.1	EST_HUMAN	ws60d04.x1 NCI_CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2501575 3' similar to TR:Q13541 Q13541 4E-BINDING PROTEIN 1.;
2147	7257	12464	2.6	1.00E-104	M34671.1	NT	Human lymphocyte antigen CD58/MEIM43 mRNA, complete cds
2318	7421	12629	1.2	1.00E-104	AF167706.1	NT	Homo sapiens cysteine-rich repeat-containing protein S52 precursor, mRNA, complete cds
2318	7421	12630	1.2	1.00E-104	AF167706.1	NT	Homo sapiens cysteine-rich repeat-containing protein S52 precursor, mRNA, complete cds
2367	7488	12691	0.6	1.00E-104	5031570	NT	Homo sapiens ARP2 (actin-related protein 2, yeast) homolog (ACTR2), mRNA
2842	7993	13091	7.6	1.00E-104	M34671.1	NT	Human lymphocyte antigen CD58/MEIM43 mRNA, complete cds
2886	8037		2.8	1.00E-104	V11151.1	NT	H. sapiens gene encoding phenylpyruvate tautomerase II
3345	8489		1.5	1.00E-104	AA318436.1	EST_HUMAN	EST121658 Adrenal gland tumor Homo sapiens cDNA 5' end
3550	8690	13792	1.0	1.00E-104	AB033102.1	NT	Homo sapiens mRNA for KIAA1276 protein, partial cds
3550	8690	13793	1.0	1.00E-104	AB033102.1	NT	Homo sapiens mRNA for KIAA1276 protein, partial cds
3861	8997	14096	0.9	1.00E-104	AB032998.1	NT	Homo sapiens mRNA for KIAA1172 protein, partial cds
4280	9405	14489	4.3	1.00E-104	X02761.1	NT	Human mRNA for fibronectin (FN precursor)
4504	9623	14714	0.9	1.00E-104	AF231920.1	NT	Homo sapiens chromosome 21 unknown mRNA
4504	9623	14715	0.9	1.00E-104	AF231920.1	NT	Homo sapiens chromosome 21 unknown mRNA
4735	9846		2.8	1.00E-104	AW054828.1	EST_HUMAN	TR:Q13541 Q13541 4E-BINDING PROTEIN 1.;
277	7859	10594	1.0	1.00E-105	4502166	NT	Homo sapiens anyloid beta (A4) precursor protein (protease nexin-II, Alzheimer disease) (APP), mRNA
419	5208	10309	5.7	1.00E-105	4505150	NT	Homo sapiens Meis1 (mouse) homolog (MEIS1) mRNA
1777	6898	12085	1.2	1.00E-105	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080
1894	7002	12187	0.6	1.00E-105	D50918.1	NT	Human mRNA for KIAA0128 gene, partial cds
2142	7252	12460	0.6	1.00E-105	J04977.1	NT	Human Ku autoimmune antigen gene, complete cds
2689	7776		0.9	1.00E-105	AA584808.1	EST_HUMAN	no10005.s1 NCI_CGAP_Phe1 Homo sapiens cDNA clone IMAGE:1100265 3'
2975	8126		2.6	1.00E-105	AJ229041.1	NT	Homo sapiens 959 kb contig between AML1 and CBR1 on chromosome 21q22; segment 1/3
3307	8452	13564	0.9	1.00E-105	7304922	NT	Homo sapiens bromodomain adjacent to zinc finger domain, 28 (BAZ2B), mRNA
3307	8452	13565	0.9	1.00E-105	7304922	NT	Homo sapiens bromodomain adjacent to zinc finger domain, 28 (BAZ2B), mRNA
4008	9139	14221	2.2	1.00E-105	AW961688.1	EST_HUMAN	EST373761 IMAGE resequences, MAGG Homo sapiens cDNA
4856	9862		3.7	1.00E-105	AL163208.2	NT	Homo sapiens chromosome 21 segment HS21C008
5044	10144	15222	1.0	1.00E-105	AB018339.1	NT	Homo sapiens mRNA for KIAA0796 protein, partial cds
5095	10193	15272	2.2	1.00E-105	AB020673.1	NT	Homo sapiens mRNA for KIAA0866 protein, complete cds
5161	10144	15222	1.3	1.00E-105	AB018339.1	NT	Homo sapiens mRNA for KIAA0796 protein, partial cds
145	5341		1.0	1.00E-106	AW503208.1	EST_HUMAN	U1-HF-BND-ak-9-07-0-U1.1 NIH MAGC_50 Homo sapiens cDNA clone IMAGE:3078348 5'
198	5392	10519	0.5	1.00E-106	AI565065.1	EST_HUMAN	tg79601.x1 NCI_CGAP_U1 Homo sapiens cDNA clone IMAGE:2215008 3'
212	5405	10529	0.9	1.00E-106	8922990	NT	Homo sapiens hypothetical protein FLJ11316 (FLJ11316), mRNA
531	5695	10818	0.6	1.00E-108	AW965556.1	EST_HUMAN	EST377629 IMAGE resequences, MAGI Homo sapiens cDNA
589	5749	10866	0.8	1.00E-106	J00146.1	NT	Human dihydrolase reductase pseudogene (psh-hd1)

Table 4

590	5749	10866	1.2	1.00E-106	J00146.1	NT	Human dihydrofolate reductase pseudogene (psl-hd1)
1508	6635	11804	1.0	1.00E-106	AF145712.1	NT	Homo sapiens soluble neuropilin-1 mRNA, complete cds
1674	6798	11976	1.6	1.00E-106	U48724.1	NT	Human epidermal growth factor receptor (EGFR) precursor-mRNA, exon 4, partial cds
1762	6893	12065	1.9	1.00E-106	AA527446.1	EST_HUMAN	ng41cd5.s1 NC1_CGAP_C03 Homo sapiens cDNA clone IMAGE:937352 3' similar to contains element LTR3 repetitive element:
1762	6893	12065	1.9	1.00E-106	AA527446.1	EST_HUMAN	ng41cd5.s1 NC1_CGAP_C03 Homo sapiens cDNA clone IMAGE:937352 3' similar to contains element LTR3 repetitive element:
1762	6893	12066	1.9	1.00E-106	AA527446.1	EST_HUMAN	ng41cd5.s1 NC1_CGAP_C03 Homo sapiens cDNA clone IMAGE:937352 3' similar to contains element LTR3 repetitive element:
2075	7187	12390	1.1	1.00E-106	BE144286.1	EST_HUMAN	MG0-HT0165-140200-008-d10 HT0165 Homo sapiens cDNA
2289	7375	12584	3.0	1.00E-106	4504184	NT	Homo sapiens glutathione S-transferase theta 1 (GSTT1), mRNA
2456	7555	12761	0.6	1.00E-106	AF003528.1	NT	Homo sapiens X-linked anhidrotic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions
2557	7651	12854	1.3	1.00E-106	U64675.2	NT	Homo sapiens sperm membrane protein BS-63 mRNA, complete cds
2559	7653	12856	0.7	1.00E-106	BE313721.1	EST_HUMAN	601149352F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3502117 5'
2728	7813	13019	1.5	1.00E-106	AI276526.1	EST_HUMAN	qf7h10.X1 Soares_NhHMPJ_S1 Homo sapiens cDNA clone IMAGE:1878307 3'
2795	6541	11715	1.1	1.00E-106	4504184	NT	Homo sapiens glutathione S-transferase theta 1 (GSTT1), mRNA
2795	6541	11715	1.1	1.00E-106	4504184	NT	Homo sapiens glutathione S-transferase theta 1 (GSTT1), mRNA
2911	8061	13167	5.0	1.00E-106	AB037747.1	NT	Homo sapiens mRNA for KIAA1326 protein, partial cds
2911	8061	13168	5.0	1.00E-106	AB037747.1	NT	Homo sapiens mRNA for KIAA1326 protein, partial cds
3143	8292	13399	2.4	1.00E-106	8922965	NT	Homo sapiens hypothetical protein FLJ11273 (FLJ11273), mRNA
3143	8292	13400	2.4	1.00E-106	8922965	NT	Homo sapiens hypothetical protein FLJ11273 (FLJ11273), mRNA
3328	8472	13585	0.8	1.00E-106	AB008681.1	NT	Homo sapiens gene for actinin receptor type IIb, complete cds
3350	8494	13605	3.0	1.00E-106	AW503073.1	EST_HUMAN	U1-HF-BP0p-ale-h-06-0-U1.1 NIH_MGC_51 Homo sapiens cDNA clone IMAGE:3074170 5'
3394	8536	13641	1.0	1.00E-106	AB033104.1	NT	Homo sapiens mRNA for KIAA1278 protein, partial cds
3394	8536	13642	1.0	1.00E-106	AB033104.1	NT	Homo sapiens mRNA for KIAA1278 protein, partial cds
3840	8976	14076	1.8	1.00E-106	BE145043.1	EST_HUMAN	PM4-HT0191-281098-002-d06 HT0191 Homo sapiens cDNA
3952	9085	14166	7.2	1.00E-106	AW974650.1	EST_HUMAN	EST386875 MAGC resequences, MAGN Homo sapiens cDNA
3952	9085	14167	7.2	1.00E-106	AW974650.1	EST_HUMAN	EST386875 MAGC resequences, MAGN Homo sapiens cDNA
4497	9617	14708	1.2	1.00E-106	BE144286.1	EST_HUMAN	MR0-HT0165-140200-008-d10 HT0165 Homo sapiens cDNA
5183	10275		1.2	1.00E-106	L41644.1	NT	Homo sapiens dystrophin gene, exon 41
222	5414	10535	0.5	1.00E-107	4506454	NT	Homo sapiens reticulocalbin 1, EF-hand calcium binding domain (RCN1), mRNA
234	5425		1.2	1.00E-107	AJ271735.1	NT	Homo sapiens Xq pseudautosomal region; segment 112
284	5451		1.1	1.00E-107	X60459.1	NT	Human IFNAR gene for interferon alpha/beta receptor
606	5764		1.1	1.00E-107	4826883	NT	Homo sapiens neuronal cell adhesion molecule (NRCAM) mRNA
614	5772	10883	0.6	1.00E-107	AF155103.1	NT	Homo sapiens NY-REN-25 antigen mRNA, partial cds
796	5947	11097	0.9	1.00E-107	X60459.1	NT	Human IFNAR gene for interferon alpha/beta receptor
868	6016	11176	1.2	1.00E-107	X60459.1	NT	Human IFNAR gene for interferon alpha/beta receptor
953	6099	11256	3.6	1.00E-107	AF154121.1	NT	Homo sapiens sodium-dependent high-affinity dicarboxylate transporter (NADCC3) mRNA, complete cds
1257	6386	11547	0.8	1.00E-107	AB032253.1	NT	Homo sapiens BAZ1B mRNA for bromodomain adjacent to zinc finger domain 1B, complete cds



Table 4

1718	6841	12020	0.5	1.00E-107	AF136275.1	NT	Homo sapiens cathepsin Z precursor (CTSZ) gene, exon 3
1797	6917	12103	1.0	1.00E-107	AB007922.2	NT	Homo sapiens mRNA for KIAA0453 protein, partial cds
1797	6917	12104	1.0	1.00E-107	AB007922.2	NT	Homo sapiens mRNA for KIAA0453 protein, partial cds
2161	7270	12481	1.3	1.00E-107	U13729.1	NT	Human dipeptidyl peptidase IV (CD26) gene, exon 20
2487	7584	12789	0.9	1.00E-107	4759153	NT	Homo sapiens synaptosomal-associated protein, 29kD (SNAP29) mRNA
2487	7584	12790	0.9	1.00E-107	4759153	NT	Homo sapiens synaptosomal-associated protein, 29kD (SNAP29) mRNA
2976	8127	13233	1.9	1.00E-107	AW842451.1	EST_HUMAN	PM1-CDN031-190100-001-d03 CDN031 Homo sapiens cDNA
2976	8127	13234	1.9	1.00E-107	AW842451.1	EST_HUMAN	PM1-CDN031-190100-001-d03 CDN031 Homo sapiens cDNA
3061	8212	13311	2.6	1.00E-107	5902097	NT	Homo sapiens SMT3 (suppressor of mit two 3, yeast) homolog 2 (SMT3H2), mRNA
3754	8892	13982	3.9	1.00E-107	AF020671.1	NT	Homo sapiens myotubularin (MTM1) gene, exon 9
939	6086	11243	1.5	1.00E-108	BE298042.1	EST_HUMAN	601177018F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3532348 5'
1244	6373	11531	0.5	1.00E-108	Y18000.1	NT	Homo sapiens NF2 gene
2012	7126		0.7	1.00E-108	A1089548.1	EST_HUMAN	q506102.x1 Soares_pregnant_uterus_NbhPU Homo sapiens cDNA clone IMAGE:1695483 3'
2282	7388	12595	2.7	1.00E-108	AF138303.1	NT	Homo sapiens decorin D mRNA, complete cds, alternatively spliced
2282	7388	12596	2.7	1.00E-108	AF138303.1	NT	Homo sapiens decorin D mRNA, complete cds, alternatively spliced
							b525b10.x1 NIH_MGC_14 Homo sapiens cDNA clone IMAGE:2963899 3' similar to gb:X53777 60S RIBOSOMAL PROTEIN L23 (HUMAN); gb:J05277 Mouse hexokinase mRNA, complete cds (MOUSE);
2378	7480	12682	2.6	1.00E-108	BE206694.1	EST_HUMAN	mRNA, complete cds (MOUSE);
3158	8307	13417	1.9	1.00E-108	4506354	NT	Homo sapiens pregnancy-zone protein (PZP) mRNA
3158	8307	13418	1.9	1.00E-108	4506354	NT	Homo sapiens pregnancy-zone protein (PZP) mRNA
3742	8879	13969	0.9	1.00E-108	5453855	NT	Homo sapiens pericentriolar material 1 (PCM1) mRNA
							h12a11.x1 NCI CGAP_GUT1 Homo sapiens cDNA clone IMAGE:2972060 3' similar to SW-3BP1 MOUSE P55194 SH3-BINDING PROTEIN 3BP-1.1
4065	9192	14276	1.3	1.00E-108	AW664438.1	EST_HUMAN	SV-3BP1 MOUSE P55194 SH3-BINDING PROTEIN 3BP-1.1
4425	9546	14638	2.0	1.00E-108	U72961.1	NT	Human hepatocyte nuclear factor 4-alpha gene, exon 2
4425	9546	14639	2.0	1.00E-108	U72961.1	NT	Human hepatocyte nuclear factor 4-alpha gene, exon 2
							Human hepatocyte nuclear factor 4-alpha gene, exon 2
4555	9673	14764	2.1	1.00E-108	AA186965.1	EST_HUMAN	zpf66101.r1 Stratagene endothelial cell 937223 Homo sapiens cDNA clone IMAGE:625177 5'
4699	9811	14908	2.9	1.00E-108	7661979	NT	Homo sapiens KIAA0187 gene product (KIAA0187), mRNA
4868	9975	15060	2.2	1.00E-108	AJ008005.1	NT	Homo sapiens PSN1 gene, alternative transcript
58	5266	10388	0.9	1.00E-109	D86974.1	NT	Human mRNA for KIAA0220 gene, partial cds
459	5625	10751	1.2	1.00E-109	4507712	NT	Homo sapiens tetrapeptide repeat domain 2 (TTC2) mRNA
583	5743	10860	5.0	1.00E-109	AB023216.1	NT	Homo sapiens mRNA for KIAA0999 protein, partial cds
583	5743	10861	5.0	1.00E-109	AB023216.1	NT	Homo sapiens mRNA for KIAA0999 protein, partial cds
1184	6317	11473	3.3	1.00E-109	M28699.1	NT	Homo sapiens nuclear phosphoprotein B23 (NPM1) mRNA, complete cds
1185	6317	11473	3.3	1.00E-109	M28699.1	NT	Homo sapiens nuclear phosphoprotein B23 (NPM1) mRNA, complete cds
1831	6950	12134	0.5	1.00E-109	D13643.2	NT	Homo sapiens mRNA for KIAA0018 protein, partial cds
2194	7303	12517	0.7	1.00E-109	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
2204	7313	12525	0.7	1.00E-109	Y17123.1	NT	Homo sapiens SNF5/INI1 gene, exon 6
2581	7674	12876	1.4	1.00E-109	A1022328.1	EST_HUMAN	ow55a01.x1 Soares_fetal_liver_spleen_1NFUS_S1 Homo sapiens cDNA clone IMAGE:1654536 3' similar to TR:002197 002197 CIRCULATING CATHODIC ANTIGEN.1

Table 4

2581	7674	12877	1.4	1.00E-109	AN022328.1	EST_HUMAN	ow95a01.x1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1654536 3' similar to TR:O02197 CIRCULATING CATHODIC ANTIGEN.;
2582	7675	12878	1.0	1.00E-109	4504206	NT	Homo sapiens guanylate cyclase activator 1A (retina) (GUCA1A) mRNA
2907	8057	13162	1.3	1.00E-109	BE243666.1	EST_HUMAN	TCBAP-ID1367 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project=TCBA Homo sapiens cDNA clone TCBAP1367
2907	8057	13163	1.3	1.00E-109	BE243668.1	EST_HUMAN	TCBAP-ID1367 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project=TCBA Homo sapiens cDNA clone TCBAP1367
3020	8172	13272	1.9	1.00E-109	N85190.1	EST_HUMAN	J2816F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA clone J2816 5' similar to ZINC FINGER PROTEIN ZNF43
3342	8486	13600	1.5	1.00E-109	AW893192.1	EST_HUMAN	CM3-NN0009-190400-150-410 NN0009 Homo sapiens cDNA
3342	8486	13601	1.5	1.00E-109	AW893192.1	EST_HUMAN	CM3-NN0009-190400-150-410 NN0009 Homo sapiens cDNA
3474	8615	13727	1.2	1.00E-109	AF240698.1	NT	Homo sapiens retinol dehydrogenase homolog isoform-1 (RDH) mRNA, complete cds
3767	8905		1.5	1.00E-109	BE146144.1	EST_HUMAN	MFO-HT0209-110400-108-804 HT0209 Homo sapiens cDNA
3911	9046	14133	1.5	1.00E-109	AB011181.2	NT	Homo sapiens mRNA for KIAA0609 protein, partial cds
3911	9046	14134	1.5	1.00E-109	AB011181.2	NT	Homo sapiens mRNA for KIAA0609 protein, partial cds
4054	9181	14264	3.7	1.00E-109	AI655417.1	EST_HUMAN	ts98a06.x1 NCI_CGAP_G06 Homo sapiens cDNA clone IMAGE:2239330 3' similar to WP:FS3A2.8 CE16100;
4070	9197	14281	1.0	1.00E-109	AA662274.1	EST_HUMAN	nu93c12.s1 NCI_CGAP_P22 Homo sapiens cDNA clone IMAGE:1218262 3' similar to SW:GTT2_HUMAN P30712 GLUTATHIONE S-TRANSFERASE THETA.2;
4070	9197	14282	1.0	1.00E-109	AA662274.1	EST_HUMAN	nu93c12.s1 NCI_CGAP_P22 Homo sapiens cDNA clone IMAGE:1218262 3' similar to SW:GTT2_HUMAN P30712 GLUTATHIONE S-TRANSFERASE THETA.2;
4304	9428	14518	2.3	1.00E-109	4504206	NT	Homo sapiens guanylate cyclase activator 1A (retina) (GUCA1A) mRNA
4496	9616	14707	1.2	1.00E-109	7662083	NT	Homo sapiens KIAA0377 gene product (KIAA0377), mRNA
4639	9946	15035	1.0	1.00E-109	R15400.1	EST_HUMAN	ya48a06.r1 Soares infant brain 11NB Homo sapiens cDNA clone IMAGE:53057 5'
4684	10087	15158	0.9	1.00E-109	BE293673.1	EST_HUMAN	601186822F2 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:2959636 5'
4684	10087	15159	0.9	1.00E-109	BE293673.1	EST_HUMAN	601186822F2 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:2959636 5'
3	5212	10313	0.5	1.00E-110	7549804	NT	Homo sapiens delcidriase, lodothyronine, type II (DIO2), transcript variant 2, mRNA
34	5243	10349	1.3	1.00E-110	5803073	NT	Homo sapiens leucine-zipper-like transcriptional regulator, 1 (LZTR1), mRNA
34	5243	10350	1.3	1.00E-110	5803073	NT	Homo sapiens leucine-zipper-like transcriptional regulator, 1 (LZTR1), mRNA
75	5281	10408	10.0	1.00E-110	CD4498.1	EST_HUMAN	Homo sapiens leucine-zipper-like transcriptional regulator, 1 (LZTR1), mRNA
104	5212	10313	0.6	1.00E-110	7549804	NT	CD4498 Human heart cDNA (Ynakamura) Homo sapiens cDNA clone 3NHG3467
291	5477	10608	0.9	1.00E-110	D87291.1	NT	Homo sapiens delcidriase, lodothyronine, type II (DIO2), transcript variant 2, mRNA
516	5680	10801	1.2	1.00E-110	UB4550.1	NT	Human mRNA for inward rectifier potassium channel, complete cds
1163	6298	11453	1.1	1.00E-110	5031620	NT	Human dystrobrexin (DTN) gene, exon 20
1258	6387	11548	1.0	1.00E-110	AB032253.1	NT	Homo sapiens calcitonin receptor-like (CALCRL) mRNA
1679	6987	12182	0.5	1.00E-110	BE379477.1	EST_HUMAN	Homo sapiens BAZ1B mRNA for bromodomain adjacent to zinc finger domain 1B, complete cds
2810	7961		1.0	1.00E-110	4503098	NT	601237545F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3609683 5'
3048	8199		1.1	1.00E-110	UT8027.1	NT	Homo sapiens chondroitin sulfate proteoglycan 4 (melanoma-associated) (CSPG4), mRNA
							ribosomal protein (L44L) and FTP3 (FTP3) genes, complete cds

Table 4

3966	9098	14182	0.9	1.00E-110	BE018556.1	EST_HUMAN	bb82a05.y1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3048848 5' similar to TR:060312 O60312 KIAA0566 PROTEIN :
4533	9652	14739	2.1	1.00E-110	AI017213.1	EST_HUMAN	ou32b10.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1827963 3' similar to SW:NI21_RAT P52591 NUCLEAR ENVELOPE PORE MEMBRANE PROTEIN POM 121 :
4898	10005		2.3	1.00E-110	7662441	NT	Homo sapiens KIAA1002 protein (KIAA1002), mRNA
168	5362		5.7	1.00E-111	U43701.1	NT	Human ribosomal protein L23a mRNA, complete cds
189	5383	10510	1.0	1.00E-111	4758807	NT	Homo sapiens ras GTPase activating protein-like (NGAP) mRNA
726	5880	11021	1.2	1.00E-111	8393092	NT	Homo sapiens cat eye syndrome critical region gene 1 (CECR1), mRNA
911	6057	11216	25.0	1.00E-111	M25142.1	NT	Human cardiac alpha-myosin heavy chain (MYH6) gene, exons 32 to 34
1564	6691	11860	2.0	1.00E-111	AA213434.1	EST_HUMAN	zq93112.1 Striatogene hNT neuron (#937233) Homo sapiens cDNA clone IMAGE:649583 5'
1564	6691	11861	2.0	1.00E-111	AA213434.1	EST_HUMAN	zq93112.1 Striatogene hNT neuron (#937233) Homo sapiens cDNA clone IMAGE:649583 5'
3642	8781	13874	1.2	1.00E-111	6912641	NT	Homo sapiens sex comb on midleg homolog 1 (SCMH1), mRNA
3642	8781	13875	1.2	1.00E-111	6912641	NT	Homo sapiens sex comb on midleg homolog 1 (SCMH1), mRNA
4080	9207	14292	1.1	1.00E-111	7661569	NT	Homo sapiens DKFZP434D156 protein (DKFZP434D156), mRNA
4235	9359	14441	4.5	1.00E-111	K02268.1	NT	Human encephalin B (enbB) gene, exon 4 and 3' flank and complete cds
582	5790	10867	0.9	1.00E-112	4501854	NT	Homo sapiens acetyl-Coenzyme A carboxylase beta (ACACB), mRNA
594	5752	10869	1.5	1.00E-112	U29103.1	NT	Homo sapiens acetyl-Coenzyme A carboxylase beta (ACACB), mRNA
594	5752	10870	1.5	1.00E-112	U29103.1	NT	Human steroidogenic acute regulatory protein (STAR) gene, exon 5
985	6130	11285	1.0	1.00E-112	AF157623.1	NT	Homo sapiens HTRA serine protease (PRSS11) gene, complete cds
1046	6186	11337	0.6	1.00E-112	P52742	SWISSPROT	Homo sapiens HTRA serine protease (PRSS11) gene, complete cds
1658	6782	11956	2.1	1.00E-112	7662125	NT	ZINC FINGER PROTEIN 135
1658	6782	11957	2.1	1.00E-112	7662125	NT	Homo sapiens KIAA0440 protein (KIAA0440), mRNA
2460	7559	12763	0.9	1.00E-112	AF004713.1	NT	Homo sapiens KIAA0440 protein (KIAA0440), mRNA
3135	8284	13391	1.2	1.00E-112	AF247662.1	NT	Homo sapiens DNA-dependent DNA polymerase (hREV3) mRNA, partial cds
3809	8946	14042	0.8	1.00E-112	BE076073.1	EST_HUMAN	Homo sapiens SR-related protein LD2 mRNA, partial cds
4646	9759	14853	5.1	1.00E-112	AB037832.1	NT	MR2-BT0590-080300-113-09 BT0590 Homo sapiens cDNA
4646	9759	14854	5.1	1.00E-112	AB037832.1	NT	Homo sapiens mRNA for KIAA1411 protein, partial cds
5170	10264	15336	0.9	1.00E-112	9055269	NT	Homo sapiens mRNA for KIAA1411 protein, partial cds
725	5878	11019	1.3	1.00E-113	AI365586.1	EST_HUMAN	Homo sapiens low density lipoprotein receptor related protein-deleted in tumor (LRPDI1), mRNA
725	5878	11020	1.3	1.00E-113	AI365586.1	EST_HUMAN	MR2-BT0590-080300-113-09 BT0590 Homo sapiens cDNA
927	6074	11232	2.2	1.00E-113	MI1965.1	NT	Homo sapiens SR-related protein LD2 mRNA, partial cds
1523	6650	11818	1.1	1.00E-113	AI365586.1	EST_HUMAN	MR2-BT0590-080300-113-09 BT0590 Homo sapiens cDNA
2048	7161	12365	1.2	1.00E-113	6453889	NT	Homo sapiens mRNA for KIAA1411 protein, partial cds
2405	7504	12711	1.0	1.00E-113	AJ006976.1	NT	Homo sapiens low density lipoprotein receptor related protein-deleted in tumor (LRPDI1), mRNA
3091	8242	13345	2.3	1.00E-113	AJ223848.1	NT	Homo sapiens SR-related protein LD2 mRNA, partial cds
5035	10135	15209	1.0	1.00E-113	7657065	NT	Homo sapiens SR-related protein LD2 mRNA, partial cds
5035	10135	15210	1.0	1.00E-113	7657065	NT	Homo sapiens SR-related protein LD2 mRNA, partial cds

Table 4

629	5788	10911	2.6	1.00E-114	TT0551.1	EST_HUMAN	yt15c01.s1 Scores fetal liver spleen 1NF1.S Homo sapiens cDNA clone IMAGE:108288.3' similar to gb:A21187 ALPHA-2-MACROGLOBULIN PRECURSOR (HUMAN); contains Alu repetitive element;
1055	6194	11347	1.3	1.00E-114	8923087	NT	Homo sapiens hypothetical protein FLJ20080 (FLJ20080). mRNA
1281	6420	11585	1.2	1.00E-114	7657529	NT	Homo sapiens ribbed-tumor deletion region protein 1 (RTDR1). mRNA
1848	6774	11945	2.0	1.00E-114	6679073	NT	Homo sapiens nucleoporin-like protein 1 (NLP_1). mRNA
1980	7095	12297	1.2	1.00E-114	BE165972.1	EST_HUMAN	MR3-HT0487-150200-116-d01 HT0487 Homo sapiens cDNA
2773	5247	10355	0.8	1.00E-114	AB033102.1	NT	Homo sapiens mRNA for KIAA1276 protein, partial cds
2773	5247	10356	0.8	1.00E-114	AB033102.1	NT	Homo sapiens mRNA for KIAA1276 protein, partial cds
3092	8243	13346	2.3	1.00E-114	X04086.1	NT	Human gene for catalase (EC 1.11.1.6) exon 2 mapping to chromosome 11, band p13
3934	9068	14153	2.0	1.00E-114	AF149773.1	NT	Homo sapiens NOD1 protein (NOD1) gene, exons 1, 2, and 3
5120	10216	15294	1.2	1.00E-114	AA194468.1	EST_HUMAN	z005605.t1 Striatum muscle 837209 Homo sapiens cDNA clone IMAGE:628632.5' similar to contains MER22.13 MER22 repetitive element;
5121	10217	15295	2.3	1.00E-114	AF004849.1	NT	Homo sapiens PKY protein kinase mRNA, complete cds
21	5230	10333	1.2	1.00E-115	4758111	NT	Homo sapiens HLA-B associated transcript-1 (DBS81E) mRNA
125	5321	10452	1.0	1.00E-115	4505938	NT	Homo sapiens polymerase (RNA) II (DNA directed) polypeptide A (220K) (POLR2A) mRNA
129	5325	10452	0.7	1.00E-115	4557867	NT	Homo sapiens keratin 18 (KRT18). mRNA
289	5475	10605	0.7	1.00E-115	AW804759.1	EST_HUMAN	QV4-UM0094-300300-156-b08 UM0094 Homo sapiens cDNA
374	5550	10863	1.0	1.00E-115	O14867	SWISSPROT	TRANSCRIPTION REGULATOR PROTEIN BACH1 (BTB AND CNC HOMOLOG 1) (HA2303)
525	5689	10810	1.1	1.00E-115	A1339206.1	EST_HUMAN	q0601.x1 NC1_CGAP_G4C Homo sapiens cDNA clone IMAGE:1946809.3' similar to
525	5689	10811	1.1	1.00E-115	A1339206.1	EST_HUMAN	q0601.x1 NC1_CGAP_G4C Homo sapiens cDNA clone IMAGE:1946809.3' similar to
525	5689	10811	1.1	1.00E-115	A1339206.1	EST_HUMAN	TR-O00536 O00536 TTF1-INTERACTING PEPTIDE 5;
769	5921	11069	0.6	1.00E-115	5174702	NT	Homo sapiens transforming growth factor beta-activated kinase-binding protein 1 (TAB1). mRNA
769	5921	11070	0.6	1.00E-115	5174702	NT	Homo sapiens transforming growth factor beta-activated kinase-binding protein 1 (TAB1). mRNA
769	5921	11070	0.6	1.00E-115	5174702	NT	Homo sapiens transforming growth factor beta-activated kinase-binding protein 1 (TAB1). mRNA
771	5923	11072	17.0	1.00E-115	4503794	NT	Homo sapiens ferritin, heavy polypeptide 1 (FTH1) mRNA
1539	6655	11833	0.9	1.00E-115	AF229180.1	NT	Homo sapiens alpha-aminoadipate semialdehyde synthase mRNA, complete cds
1539	6655	11834	0.9	1.00E-115	AF229180.1	NT	Homo sapiens alpha-aminoadipate semialdehyde synthase mRNA, complete cds
1785	6905	12093	1.1	1.00E-115	AJ277892.1	NT	Homo sapiens partial TTN gene for titin
1798	6918	12105	0.5	1.00E-115	U78027.1	NT	Homo sapiens Bruton's tyrosine kinase (BTK), alpha-D-galactosidase A (GLA), L44-like ribosomal protein (L44L) and FTP3 (FTP3) genes, complete cds
2034	7147	12349	0.9	1.00E-115	BE296353.1	EST_HUMAN	601174384F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3529773.5'
2034	7147	12350	0.9	1.00E-115	BE296353.1	EST_HUMAN	601174384F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3529773.5'
2704	7878	12890	0.8	1.00E-115	4758111	NT	Homo sapiens HLA-B associated transcript-1 (DBS81E) mRNA
2820	7971		1.8	1.00E-115	AW804759.1	EST_HUMAN	QV4-UM0094-300300-156-b08 UM0094 Homo sapiens cDNA
3077	8228	13327	2.1	1.00E-115	AJ245922.1	NT	Homo sapiens mRNA for alpha-tubulin 8 (TUBA8 gene)
3077	8228	13328	2.1	1.00E-115	AJ245922.1	NT	Homo sapiens mRNA for alpha-tubulin 8 (TUBA8 gene)

Table 4

3427	8569	13681	4.0	1.00E-115	ALJ277892.1	NT	Homo sapiens partial TTN gene for tilin
3956	9089	14172	4.0	1.00E-115	AB002248.2	NT	Homo sapiens mRNA for KIAA0350 protein, partial cds
4169	9295	14376	1.1	1.00E-115	AL137163.1	NT	Novel human gene mapping to chromosome X
4301	9425	14515	3.4	1.00E-115	6912659	NT	Novel sapiens sir2-like 3 (SIRT3), mRNA
4335	9458	14548	3.8	1.00E-115	4758279	NT	Homo sapiens EphA4 (EPHA4) mRNA
4578	9694	14786	2.6	1.00E-115	AL096857.1	NT	Novel human mRNA from chromosome 1, which has similarities to BAT2 genes
4578	9694	14787	2.6	1.00E-115	AL096857.1	NT	Novel human mRNA from chromosome 1, which has similarities to BAT2 genes
4813	9922	15014	3.0	1.00E-115	AL163268.2	NT	Homo sapiens chromosome 21 segment HS21C068
4813	9922	15015	3.0	1.00E-115	AL163268.2	NT	Homo sapiens chromosome 21 segment HS21C068
560	5722	10838	1.4	1.00E-116	BE275502.1	EST_HUMAN	601121347F1 NIH MGC 20 Homo sapiens cDNA clone IMAGE:2988875 5'
783	5835	11084	1.3	1.00E-116	4507334	NT	Homo sapiens synaptobrevin 1 (SYNU1), mRNA
841	5980		6.9	1.00E-116	4507334	NT	Homo sapiens synaptobrevin 1 (SYNU1), mRNA
1952	7069	12265	0.9	1.00E-116	5174478	NT	Homo sapiens pericentrioh (PCNT) mRNA
1952	7069	12266	0.9	1.00E-116	5174478	NT	Homo sapiens pericentrioh (PCNT) mRNA
2050	7933	12366	1.0	1.00E-116	M19824.1	NT	Human apolipoprotein B-100 (apoB) gene, exons 17 and 18
2050	7933	12367	1.0	1.00E-116	M19824.1	NT	Human apolipoprotein B-100 (apoB) gene, exons 17 and 18
2259	7365	12674	0.7	1.00E-116	5453941	NT	Homo sapiens protein phosphatase, EF hand calcium-binding domain 1 (PPEF1) mRNA
2293	7397		0.5	1.00E-116	U78308.1	NT	Human olfactory receptor olfr17-201-1 (OR17-201-1) gene, olfactory receptor olfr17-32 (OR17-32) gene and olfactory receptor pseudo_olfr17-01 (OR17-01) pseudogene, complete cds
2407	7506	12713	1.6	1.00E-116	AB018333.1	NT	Homo sapiens mRNA for KIAA0790 protein, partial cds
3137	8286	13392	4.7	1.00E-116	L77570.1	NT	Homo sapiens DiGeorge syndrome critical region, centromeric end
3137	8286	13393	4.7	1.00E-116	L77570.1	NT	Homo sapiens DiGeorge syndrome critical region, centromeric end
4281	9406	14490	2.0	1.00E-116	5031954	NT	Homo sapiens sodium phosphate transporter 3 (NPT3) mRNA
4747	9858	14950	2.2	1.00E-116	AB07096.1	EST_HUMAN	PM-BT135-070499-016 BT135 Homo sapiens cDNA
5122	10218	15296	1.2	1.00E-116	AL243213.1	NT	Homo sapiens partial 5-HT4 receptor gene, exons 2 to 5
267	5454	10578	1.4	1.00E-117	4507500	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA
546	5709	10828	1.2	1.00E-117	4826536	NT	Homo sapiens acetyl-Coenzyme A carboxylase alpha (ACACA), mRNA
1061	7806	11353	0.5	1.00E-117	AF124393.1	NT	Mus musculus fragile-X-related protein 1 (Fxr1h) gene, exons 13a through 15
1719	6842	12021	6.3	1.00E-117	AF123320.1	NT	Homo sapiens lymphocyte activation-associated protein mRNA, complete cds
1772	6893	12081	2.1	1.00E-117	H26662.1	EST_HUMAN	Human apolipoprotein B-100 (apoB) gene, exon 10
1790	6910	12096	0.8	1.00E-117	M19816.1	NT	Human apolipoprotein B-100 (apoB) gene, exon 10
2164	7273	12484	1.1	1.00E-117	AW957699.1	EST_HUMAN	EST1369769 MAGE resequences, MAGE Homo sapiens cDNA
3230	8378	13485	1.8	1.00E-117	AA978114.1	EST_HUMAN	op32c11.s1 Soares, NFL T GBC S1 Homo sapiens cDNA clone IMAGE:1578548 3'
3908	9043	14131	3.6	1.00E-117	AA316723.1	EST_HUMAN	EST188414 HCC cell line (metastasis to liver in mouse) II Homo sapiens cDNA 5' end similar to ribosomal protein L29
4247	9372	14452	1.9	1.00E-117	8659564	NT	Homo sapiens collagen, type IV, alpha 5 (Alport syndrome) (COL4A5), mRNA
4475	9595	14690	1.9	1.00E-117	AL042120.1	EST_HUMAN	DKFZp434C120_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434C120 5'
4622	9736	14831	1.4	1.00E-117	X89670.1	NT	H. sapiens mRNA for TFCR16 protein

Table 4

4622	9736	14832	1.4	1.00E-117	X89870.1	NT	H.sapiens mRNA for TPOR16 protein
4705	9817	14914	9.2	1.00E-117	AF134304.2	NT	Homo sapiens Scarl2 (SCAR2) gene, partial cds
4705	9817	14915	9.2	1.00E-117	AF134304.2	NT	Homo sapiens Scarl2 (SCAR2) gene, partial cds
4856	9883	15048	3.4	1.00E-117	AB020673.1	NT	Homo sapiens mRNA for KIAA0866 protein, complete cds
64	5272	10395	3.3	1.00E-118	AF161500.1	NT	Homo sapiens HSPC151 mRNA, complete cds
90	5298	10422	0.9	1.00E-118	AF161500.1	NT	DKFZP341056_r1.434 (synonym: hies3) Homo sapiens cDNA clone DKFZP341056.5
355	5534	10684	0.5	1.00E-118	4507500	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA
806	5870	10793	1.7	1.00E-118	7657016	NT	Homo sapiens hypothetical protein (DJ328E19.C1.1), mRNA
898	7802	11199	1.0	1.00E-118	5174680	NT	Homo sapiens sine oculis homeobox (Drosophila) homolog 1 (SIX1) mRNA
2186	7285	12507	0.9	1.00E-118	BE389705.1	EST_HUMAN	601281947F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3604019.5
2186	7285	12508	0.9	1.00E-118	BE389705.1	EST_HUMAN	601281947F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3604019.5
2186	7295	12509	0.9	1.00E-118	BE389705.1	EST_HUMAN	601281947F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3604019.5
2281	7387		1.4	1.00E-118	AW951729.1	EST_HUMAN	EST363799 MAGE resequences, MAGB Homo sapiens cDNA
2711	7796	12997	0.9	1.00E-118	U07000.1	NT	Human breakpoint cluster region (BCR) gene, complete cds
2711	7796	12998	0.9	1.00E-118	U07000.1	NT	Human breakpoint cluster region (BCR) gene, complete cds
3066	8217		3.7	1.00E-118	Y13932.1	NT	Homo sapiens PRKY exon 7
3159	8308	13419	4.5	1.00E-118	A1347694.1	EST_HUMAN	qp0105.x1 NCI CGAP_Kid5 Homo sapiens cDNA clone IMAGE:1916769.3
3159	8308	13420	4.5	1.00E-118	A1347694.1	EST_HUMAN	qp0105.x1 NCI CGAP_Kid5 Homo sapiens cDNA clone IMAGE:1916769.3
3998	9129	14211	7.7	1.00E-118	D23660.1	NT	Human mRNA for ribosomal protein, complete cds
741	5894	11040	0.8	1.00E-119	AF170492.1	NT	Homo sapiens chloride channel CLCA (CLCA) mRNA, complete cds
1021	7905	11313	0.5	1.00E-119	7705607	NT	Homo sapiens CGI-105 protein (LOC51011), mRNA
1891	7008	12195	0.8	1.00E-119	AB023147.1	NT	Homo sapiens mRNA for KIAA0930 protein, partial cds
3064	8215	13315	1.8	1.00E-119	8922205	NT	Homo sapiens hypothetical protein FL110052 (FL110052), mRNA
							on10b05.s1 NCI CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1556241.3 similar to
							WP-ED4F6.2 CE01214
3202	8350		1.1	1.00E-119	AA916760.1	EST_HUMAN	WP-ED4F6.2 CE01214
3870	9006	14105	1.2	1.00E-119	4504116	NT	Homo sapiens glutamate receptor, ionotropic, kainate 1 (GRIK1) mRNA
5111	10207	15285	1.0	1.00E-119	AA077394.1	EST_HUMAN	7B14F03 Chromosome 7 Fetal Brain cDNA Library Homo sapiens cDNA clone 7B14F03
237	5427	10554	1.4	1.00E-120	AB016301.1	NT	Homo sapiens mRNA for KIAA0758 protein, partial cds
298	5484	10614	1.3	1.00E-120	4507334	NT	Homo sapiens synaptotagmin 1 (SYNJ1), mRNA
1025	6165	11319	0.6	1.00E-120	AF248540.1	NT	Homo sapiens Intersectin 2 (SH3D1B) mRNA, complete cds
1025	6165	11320	0.6	1.00E-120	AF248540.1	NT	Homo sapiens Intersectin 2 (SH3D1B) mRNA, complete cds
1406	6533	11704	1.6	1.00E-120	NA4873.1	EST_HUMAN	yy40g12.r1 Soares melanocyte 2NbHM Homo sapiens cDNA clone IMAGE:273766.5
							yy40g12.r1 Soares melanocyte 2NbHM Homo sapiens cDNA clone IMAGE:273766.5
1583	6709	11880	1.4	1.00E-120	AF167706.1	NT	Homo sapiens cysteine-rich repeat-containing protein S52 precursor, mRNA, complete cds
1684	6808	11990	0.7	1.00E-120	5729777	NT	Homo sapiens collagen, type XII, alpha 1 (COL12A1), mRNA
1684	6808	11991	0.7	1.00E-120	5729777	NT	Homo sapiens collagen, type XII, alpha 1 (COL12A1), mRNA
							Homo sapiens myeloid/lymphoid or mixed-lineage leukemia (trithorax (Drosophila) homolog); translocated to, 4 (MLLT4) mRNA
2060	7172	12379	0.9	1.00E-120	5174574	NT	Homo sapiens myeloid/lymphoid or mixed-lineage leukemia (trithorax (Drosophila) homolog); translocated to, 4 (MLLT4) mRNA
2060	7172	12380	0.9	1.00E-120	5174574	NT	Homo sapiens myeloid/lymphoid or mixed-lineage leukemia (trithorax (Drosophila) homolog); translocated to, 4 (MLLT4) mRNA
2482	7580	12782	0.8	1.00E-120	4755124	NT	Homo sapiens aquaporin 4 (AQP4), splice variant b, mRNA

Table 4

3267	5484	10614	1.1	1.00E-120	4507334	NT	Homo sapiens synaptotaglin 1 (SYN1), mRNA
4260	9385	14468	1.2	1.00E-120	AF058490.1	NT	Homo sapiens cAMP-specific phosphodiesterase 8A (PDE8A) mRNA, partial cds
4260	9385	14469	1.2	1.00E-120	AF058490.1	NT	Homo sapiens cAMP-specific phosphodiesterase 8A (PDE8A) mRNA, partial cds
4543	9662	14752	1.2	1.00E-120	AW378049.1	EST_HUMAN	MRO-HT0209-301189-101-d04 HT0209 Homo sapiens cDNA
4583	9681	14774	2.8	1.00E-120	AF098463.1	NT	Homo sapiens stannocalcin (STC) gene, partial cds
4583	9681	14775	2.8	1.00E-120	AF098463.1	NT	Homo sapiens stannocalcin (STC) gene, partial cds
5168	10262	15333	0.9	1.00E-120	AI190903.1	EST_HUMAN	qcd103.x1 Soares_NHT Homo sapiens cDNA clone IMAGE:1733981.3
67	5274	10398	1.0	1.00E-121	Y18000.1	NT	Homo sapiens NF2 gene
707	7886	10997	1.2	1.00E-121	5032192	NT	Homo sapiens TNF receptor-associated factor 1 (TRAF1) mRNA
1556	8683	11851	1.0	1.00E-121	AB011153.1	NT	Homo sapiens mRNA for KIAA0581 protein, partial cds
1923	7040	12229	0.9	1.00E-121	4755139	NT	Homo sapiens inositol polyphosphate 4-phosphatase, type I, 107KD (INPP4A), splice variant a, mRNA
1923	7040	12230	0.9	1.00E-121	4755139	NT	Homo sapiens inositol polyphosphate 4-phosphatase, type I, 107KD (INPP4A), splice variant a, mRNA
2055	7167	12373	1.2	1.00E-121	6006005	NT	Homo sapiens glutamate receptor, metabotropic 1 (GRM1) mRNA
3042	8193	13295	3.1	1.00E-121	Y19208.1	NT	Homo sapiens h-hb3 gene for hair keratin, exons 1 to 9
3042	8193	13296	3.1	1.00E-121	Y19208.1	NT	Homo sapiens h-hb3 gene for hair keratin, exons 1 to 9
3482	8633	13745	1.1	1.00E-121	AB037758.1	NT	Homo sapiens mRNA for KIAA1337 protein, partial cds
3492	8633	13746	1.1	1.00E-121	AB037758.1	NT	Homo sapiens mRNA for KIAA1337 protein, partial cds
3624	8763	13857	6.6	1.00E-121	AF155156.2	NT	Homo sapiens adaptor-related protein complex AP-4 epsilon subunit mRNA, complete cds
4236	9360	14442	1.2	1.00E-121	AI263294.1	EST_HUMAN	q57b01.x1 NCI CGAP Part1 Homo sapiens cDNA clone IMAGE:2005417.3
4565	9683	14777	5.5	1.00E-121	4506118	NT	Homo sapiens prospero-related homeobox 1 (PROX1) mRNA
4901	10008	15088	2.6	1.00E-121	X91937.1	NT	H. sapiens ECE-1 gene (exon 17)
5050	10160	15227	1.0	1.00E-121	AI904151.1	EST_HUMAN	CM-BT043-080299-075 BT043 Homo sapiens cDNA
333	5514	10639	0.8	1.00E-122	AF114488.1	NT	Homo sapiens intersectin short isoform (ITSN) mRNA, complete cds
864	6012	11173	1.0	1.00E-122	AF114488.1	NT	Homo sapiens intersectin short isoform (ITSN) mRNA, complete cds
1201	6333	11489	1.2	1.00E-122	M20707.1	NT	Human kappa-immunoglobulin germline pseudogene (Ch22.4) variable region (subgroup V kappa II)
1687	6791	11967	1.3	1.00E-122	AF167706.1	NT	Homo sapiens cysteine-rich repeat-containing protein S52 precursor, mRNA, complete cds
2441	7540	12747	3.8	1.00E-122	4506662	NT	Homo sapiens ribosomal protein L8 (RPL8) mRNA
2441	7540	12748	3.8	1.00E-122	4506662	NT	Homo sapiens ribosomal protein L8 (RPL8) mRNA
4738	9849	14941	1.8	1.00E-122	4502166	NT	Homo sapiens amyloid beta (A4) precursor protein (protease nexin-II, Alzheimer disease) (APP), mRNA
4918	10025		1.2	1.00E-122	AW50645.1	EST_HUMAN	UI-HF-8ND-ell-a-03-0-UI.1 NIH MGC 50 Homo sapiens cDNA clone IMAGE:307948.5
181	5375	10500	1.1	1.00E-123	U31519.1	NT	Human phosphoenolpyruvate carboxykinase (PCK1) gene, promoter region and partial cds
996	6138	11292	1.3	1.00E-123	AL163249.2	NT	Homo sapiens chromosome 21 segment HS21C049
1005	6145	11299	1.7	1.00E-123	5803114	NT	Homo sapiens inner membrane protein, mitochondrial (mitofilin) (IMMT), mRNA

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407	5575	10714	0.8	1.00E-129	S37722.1	NT	Insulin-like growth factor binding protein-2 [human, placenta, Genomic, 1019 nt, segment 2 of 4]
1689	6813	11993	1.0	1.00E-129	AL096880.1	NT	Novel human mRNA containing Zinc finger C2H2 type domains
2751	7635	13035	1.2	1.00E-129	4505682	NT	Homo sapiens platelet-derived growth factor receptor, beta polypeptide (PDGFRB) mRNA
2751	7635	13035	1.2	1.00E-129	4505682	NT	Homo sapiens platelet-derived growth factor receptor, beta polypeptide (PDGFRB) mRNA
2751	7635	13036	1.2	1.00E-129	4505682	NT	Homo sapiens platelet-derived growth factor receptor, beta polypeptide (PDGFRB) mRNA
4004	8135	14217	6.1	1.00E-129	4504686	NT	Homo sapiens IMP (inosine monophosphate) dehydrogenase 1 (IMPDH1) mRNA
4073	9200	14286	2.2	1.00E-129	AB040892.1	NT	Homo sapiens mRNA for KIAA1459 protein, partial cds
4183	9309	14386	9.7	1.00E-129	AW755254.1	EST_HUMAN	CMYAS Human cardiac muscle expression library Homo sapiens cDNA clone 4151935 similar to CMYAS Cardiomypathy associated gene 5
4183	9309	14386	9.7	1.00E-129	AW755254.1	EST_HUMAN	CMYAS Human cardiac muscle expression library Homo sapiens cDNA clone 4151935 similar to CMYAS Cardiomypathy associated gene 5
4183	9309	14389	9.7	1.00E-129	AW755254.1	EST_HUMAN	CMYAS Human cardiac muscle expression library Homo sapiens cDNA clone 4151935 similar to CMYAS Cardiomypathy associated gene 5
192	5386	10513	1.0	1.00E-130	AF233453.1	NT	Homo sapiens RACK-like protein PRKCBP1 (PRKCBP1) mRNA, complete cds
192	5386	10514	1.0	1.00E-130	AF233453.1	NT	Homo sapiens RACK-like protein PRKCBP1 (PRKCBP1) mRNA, complete cds
993	6136		0.7	1.00E-130	AJ133269.1	NT	Homo sapiens caveolin-1/2 locus, Contig1, D7S522, genes CAV2 (exons 1, 2a, and 2b), CAV1 (exons 1 and 2)
994	6136		1.2	1.00E-130	AJ133269.1	NT	Homo sapiens caveolin-1/2 locus, Contig1, D7S522, genes CAV2 (exons 1, 2a, and 2b), CAV1 (exons 1 and 2)
1643	6769	11940	2.5	1.00E-130	BE275192.1	EST_HUMAN	601121995F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3346366 5'
1643	6769	11941	2.5	1.00E-130	BE275192.1	EST_HUMAN	601121995F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3346366 5'
1840	7057		0.8	1.00E-130	X04082.1	NT	Human gene for cathepsin (EC 1.11.1.6) exon 9 mapping to chromosome 11, band p13
2253	7359	12566	1.5	1.00E-130	BE280697.1	EST_HUMAN	601155971F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3139408 5'
2253	7359	12567	1.5	1.00E-130	BE280697.1	EST_HUMAN	601155971F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3139408 5'
2743	7827		2.8	1.00E-130	AJ010230.1	NT	Homo sapiens RET finger protein-like 1 antisense transcript, partial
2952	8103	13209	0.8	1.00E-130	4505458	NT	Homo sapiens neuropilin 2 (NRP2) mRNA
2952	8103	13210	0.8	1.00E-130	4505458	NT	Homo sapiens neuropilin 2 (NRP2) mRNA
3530	8671	13775	1.1	1.00E-130	AF240698.1	NT	Homo sapiens retinol dehydrogenase homolog isoform-1 (RDH) mRNA, complete cds
3857	8993	14092	1.1	1.00E-130	AW503580.1	EST_HUMAN	U1-HF-BNU-aky-8-06-0-U1.1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3078731 5'
4438	9559	14654	7.5	1.00E-130	AW843993.1	EST_HUMAN	CM4-CN0045-180200-511-f02 CN0045 Homo sapiens cDNA
5029	10130	15205	1.1	1.00E-130	AW363299.1	EST_HUMAN	RC0-CT0318-201189-031-a11 CT0318 Homo sapiens cDNA
5029	10130	15206	1.1	1.00E-130	AW363299.1	EST_HUMAN	RC0-CT0318-201189-031-a11 CT0318 Homo sapiens cDNA
4	5213	10314	0.9	0	AA228126.1	EST_HUMAN	z58604.r1 Soares_NHMPu_S1 Homo sapiens cDNA clone IMAGE:667590 5' similar to TR:G222811 G222811 ALPHA 1 CHAIN OF TYPE XII COLLAGEN. ;
4	5213	10315	0.9	0	AA228126.1	EST_HUMAN	z58604.r1 Soares_NHMPu_S1 Homo sapiens cDNA clone IMAGE:667590 5' similar to TR:G222811 G222811 ALPHA 1 CHAIN OF TYPE XII COLLAGEN. ;
7	5215	10318	1.4	0	4885136	NT	TR:G222811 G222811 ALPHA 1 CHAIN OF TYPE XII COLLAGEN. ;
15	5223	10324	1.3	0	8923349	NT	Homo sapiens checkpoint suppressor 1 (CHES1) mRNA
15	5223	10325	1.3	0	8923349	NT	Homo sapiens checkpoint suppressor 1 (CHES1) mRNA
20	5229	10331	2.5	0	D83327.1	NT	Homo sapiens hypothetical protein FLJ20371 (FLJ20371) mRNA
20	5229	10331	2.5	0	D83327.1	NT	Homo sapiens DCRR1 mRNA, partial cds

Table 4

20	5229	10332	2.5	0	D83327.1	NT	Homo sapiens DCRR1 mRNA; partial cds
24	5233	10336	1.9	0	AF141349.1	NT	Homo sapiens beta-tubulin mRNA, complete cds
33	5242	10348	1.0	0	M58600.1	NT	Human heparin cofactor II (HCF2) gene, exons 1 through 5
35	5244	10351	0.8	0	6857825	NT	Homo sapiens RNA-binding protein S1, serine-rich domain (RNPS1), mRNA
33	5242	10351	0.8	0	6857825	NT	Homo sapiens RNA-binding protein S1, serine-rich domain (RNPS1), mRNA
51	5260	10377	1.4	0	Y17151.2	NT	Homo sapiens mRNA for multidrug resistance protein 3 (ABCC3)
51	5260	10378	1.4	0	Y17151.2	NT	Homo sapiens mRNA for multidrug resistance protein 3 (ABCC3)
52	5261	10379	1.2	0	D78804.1	EST_HUMAN	HUM516H08B Human placenta polyA+ (TFujiiwara) Homo sapiens cDNA clone GEN-516H08
52	5261	10380	1.2	0	D78804.1	EST_HUMAN	HUM516H08B Human placenta polyA+ (TFujiiwara) Homo sapiens cDNA clone GEN-516H08
53	5262	10381	1.4	0	L16558.1	NT	Human ribosomal protein L7 (RPL7) mRNA, complete cds
55	5264	10384	2.8	0	AW069534.1	EST_HUMAN	Ct48e07.x1 Jla bone marrow stroma Homo sapiens cDNA clone HBMSC, ct48e07 3'
55	5264	10385	2.8	0	AW069534.1	EST_HUMAN	Ct48e07.x1 Jla bone marrow stroma Homo sapiens cDNA clone HBMSC, ct48e07 3'
59	5267	10389	2.0	0	M60676.1	NT	Human von Willebrand factor pseudogene corresponding to exons 23 through 34
61	5269		0.9	0	M60676.1	NT	Human von Willebrand factor pseudogene corresponding to exons 23 through 34
69	5276	10401	0.6	0	4758977	NT	Homo sapiens protein tyrosine phosphatase, non-receptor type substrate 1 (PTPNS1) mRNA
69	5276	10402	0.6	0	4758977	NT	Homo sapiens protein tyrosine phosphatase, non-receptor type substrate 1 (PTPNS1) mRNA
71	5276	10401	0.5	0	4758977	NT	Homo sapiens protein tyrosine phosphatase, non-receptor type substrate 1 (PTPNS1) mRNA
71	5276	10402	0.5	0	4758977	NT	Homo sapiens protein tyrosine phosphatase, non-receptor type substrate 1 (PTPNS1) mRNA
74	5280	10407	14.0	0	AA953770.1	EST_HUMAN	on88e04.s1 Soares, NFL, T, GBC, S1 Homo sapiens cDNA clone IMAGE:1563870 3' similar to SW:1TMOD_HUMAN P28289 TROPOMODULIN, ;
76	5282	10409	1.1	0	4501850	NT	Homo sapiens actin, beta (ACTB) mRNA
77	5283		5.0	0	4504444	NT	Homo sapiens heterogeneous nuclear ribonucleoprotein A1 (HNRPA1) mRNA
86	5292	10418	16.0	0	5016088	NT	Homo sapiens actin, beta (ACTB) mRNA
89	5295	10421	4.6	0	U89277.1	NT	Human polyomelic 1 homolog (HPH1) mRNA, partial cds
94	5301	10427	1.5	0	A114743.1	EST_HUMAN	HA1347 Human fetal liver cDNA library Homo sapiens cDNA
95	5302	10428	1.0	0	AB037784.1	NT	Homo sapiens mRNA for KIAA1363 protein, partial cds
102	5307	10433	2.1	0	X91213.1	NT	H.sapiens next gene (exon 2)
110	5313	10438	1.4	0	AI623701.1	EST_HUMAN	ts38b05.x1 NCI, CGAP, U14 Homo sapiens cDNA clone IMAGE:2230833 3' similar to TR:Q99551 Q99551 MITOCHONDRIAL TRANSCRIPTION TERMINATION FACTOR
111	5313	10438	0.6	0	AI623701.1	EST_HUMAN	ts38b05.x1 NCI, CGAP, U14 Homo sapiens cDNA clone IMAGE:2230833 3' similar to TR:Q99551 Q99551 MITOCHONDRIAL TRANSCRIPTION TERMINATION FACTOR
112	7858	10439	0.6	0	N36040.1	EST_HUMAN	PRECURSOR, ;
112	7858	10440	0.6	0	N36040.1	EST_HUMAN	yy01h09.r1 Soares melanocyte 2NbhM Homo sapiens cDNA clone IMAGE:270017 5'

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Table 4

115	5316	10445	0.9	0	4505458	NT	Homo sapiens neuropilin 2 (NRP2) mRNA
126	5322	10453	1.1	0	4505938	NT	Homo sapiens polymerase (RNA) II (DNA directed) polypeptide A (220KD) (POLR2A) mRNA
126	5322	10454	1.1	0	4505938	NT	Homo sapiens polymerase (RNA) II (DNA directed) polypeptide A (220KD) (POLR2A) mRNA
135	5330	10461	0.5	0	T56945.1	EST_HUMAN	ya83g04.i2 Striatogene fetal spleen (#937205) Homo sapiens cDNA clone IMAGE:58310 5'
135	5330	10462	0.5	0	T56945.1	EST_HUMAN	ya83g04.i2 Striatogene fetal spleen (#937205) Homo sapiens cDNA clone IMAGE:58310 5'
147	5343		3.1	0	4504444	NT	Homo sapiens heterogeneous nuclear ribonucleoprotein A1 (HNRP A1) mRNA
153	5349		5.4	0	4504444	NT	Homo sapiens heterogeneous nuclear ribonucleoprotein A1 (HNRP A1) mRNA
156	5352	10478	1.4	0	AF111168.2	NT	Homo sapiens serine palmitoyl transferase, subunit II gene, complete cds; and unknown genes
156	5354	10479	1.1	0	BE285973.1	EST_HUMAN	601174270F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3529864 5'
159	5354	10479	1.2	0	BE285973.1	EST_HUMAN	601174270F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3529864 5'
160	5355	10480	1.0	0	W73973.1	EST_HUMAN	z66205.i1 Soares fetal heart, NidH19W Homo sapiens cDNA clone IMAGE:345201 5'
161	5356	10481	0.5	0	AF244088.1	NT	similar to gb:X16282_cds1 ZINC FINGER PROTEIN CLONE 647 (HUMAN);
164	5359	10484	6.3	0	AL163202.2	NT	Homo sapiens zinc finger protein mRNA, complete cds
164	5359	10485	6.3	0	AL163202.2	NT	Homo sapiens chromosome 21 segment HS21C002
174	5367	10492	1.5	0	BE018970.1	EST_HUMAN	bp24e12.y1 NIH_MGC_14 Homo sapiens cDNA clone IMAGE:2963854 5' similar to
174	5367	10493	1.5	0	BE018970.1	EST_HUMAN	bp24e12.y1 NIH_MGC_14 Homo sapiens cDNA clone IMAGE:2963854 5' similar to
179	5372	10496	0.7	0	AB018327.1	NT	WP:Y57A10A.Z CE22631 ;
179	5372	10497	0.7	0	AB018327.1	NT	bp24e12.y1 NIH_MGC_14 Homo sapiens cDNA clone IMAGE:2207847 3' similar to
187	5381	10508	44.0	0	D50659.1	NT	WP:Y57A10A.Z CE22631 ;
187	5381	10508	44.0	0	D50659.1	NT	bp24e12.y1 NIH_MGC_14 Homo sapiens cDNA clone IMAGE:2207847 3' similar to
194	5388	10516	1.0	0	AF167174.1	NT	WP:Y57A10A.Z CE22631 ;
194	5388	10517	1.0	0	AF167174.1	NT	bp24e12.y1 NIH_MGC_14 Homo sapiens cDNA clone IMAGE:2207847 3' similar to
203	7883	10523	3.2	0	A1567308.1	EST_HUMAN	gb:J03191 PROFILIN I (HUMAN);
203	7883	10524	3.2	0	A1567308.1	EST_HUMAN	gb:J03191 PROFILIN I (HUMAN);
205	5398	10526	0.7	0	AF195658.1	NT	ig04i08.x1 NCJ CGAP_U13 Homo sapiens cDNA clone IMAGE:2207847 3' similar to
208	5401		5.7	0	4506632	NT	gb:J03191 PROFILIN I (HUMAN);
209	5402		1.2	0	AF132000.1	NT	ig04i08.x1 NCJ CGAP_U13 Homo sapiens cDNA clone IMAGE:2207847 3' similar to
215	5408	10531	0.9	0	AB018264.1	NT	ig04i08.x1 NCJ CGAP_U13 Homo sapiens cDNA clone IMAGE:2207847 3' similar to
216	5408	10531	0.7	0	AB018264.1	NT	ig04i08.x1 NCJ CGAP_U13 Homo sapiens cDNA clone IMAGE:2207847 3' similar to
217	5409	10532	0.6	0	6678444	NT	ig04i08.x1 NCJ CGAP_U13 Homo sapiens cDNA clone IMAGE:2207847 3' similar to
224	5417	10536	1.2	0	BE246780.1	EST_HUMAN	ig04i08.x1 NCJ CGAP_U13 Homo sapiens cDNA clone IMAGE:2207847 3' similar to

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Table 4

324	5507	10633	0.9	0	O14867	SWISSPROT	TRANSCRIPTION REGULATOR PROTEIN BACH1 (BTB AND CNC HOMOLOG 1) (HA2303)
324	5507	10634	0.9	0	O14867	SWISSPROT	TRANSCRIPTION REGULATOR PROTEIN BACH1 (BTB AND CNC HOMOLOG 1) (HA2303)
325	5508	10635	1.4	0	7657213	NT	Homo sapiens homonally upregulated neu tumor-associated kinase (HUNK), mRNA
326	5508	10635	0.8	0	7657213	NT	Homo sapiens homonally upregulated neu tumor-associated kinase (HUNK), mRNA
							Homo sapiens myeloid/lymphoid or mixed-lineage leukemia (trithorax (Drosophila) homolog); translocated to, 4 (MLLT4) mRNA
341	5522	10647	1.3	0	5174574	NT	Homo sapiens moesin (MSN), mRNA
342	5523	10648	0.9	0	4505256	NT	Homo sapiens X-box binding protein 1 (XBP1), mRNA
345	5526	10652	1.3	0	4827057	NT	Homo sapiens X-box binding protein 1 (XBP1), mRNA
348	5529	10657	0.8	0	U71600.1	NT	Human zinc finger protein zfp31 (zfp31), mRNA, partial cds
353	5533	10661	0.7	0	AF231919.1	NT	Homo sapiens chromosome 21 unknown mRNA
353	5533	10662	0.7	0	AF231919.1	NT	Homo sapiens chromosome 21 unknown mRNA
354	7887	10663	1.2	0	AF231919.1	NT	Homo sapiens chromosome 21 unknown mRNA
356	5535	10665	0.9	0	4507500	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1), mRNA
							Homo sapiens GA-binding protein transcription factor, alpha subunit (GABPA), mRNA
358	5537	10668	1.4	0	4503854	NT	Homo sapiens GA-binding protein transcription factor, alpha subunit (GABPA), mRNA
359	5538	10669	1.4	0	D80006.1	NT	Human mRNA for KIAA0184 gene, partial cds
360	5538	10669	0.5	0	D80006.1	NT	Human mRNA for KIAA0184 gene, partial cds
361	5567	10720	1.8	0	AB028942.1	NT	Homo sapiens mRNA for KIAA1019 protein, partial cds
							gb:XS4199 PHOSPHORIBOSYLAMINE--GLYCINE LIGASE (HUMAN);
362	5588	10721	1.0	0	AI363014.1	EST_HUMAN	gb:XS4199 PHOSPHORIBOSYLAMINE--GLYCINE LIGASE (HUMAN);
367	5556	10688	3.4	0	AV754180.1	EST_HUMAN	RC2-CT10320-300100-016-809 CT0320 Homo sapiens CDNA
390	5558	10691	1.4	0	4503680	NT	Homo sapiens IgG Fc binding protein (FC(GAMMA)BP), mRNA
391	5559	10692	0.7	0	4503680	NT	Homo sapiens IgG Fc binding protein (FC(GAMMA)BP), mRNA
391	5559	10693	0.7	0	4503680	NT	Homo sapiens IgG Fc binding protein (FC(GAMMA)BP), mRNA
392	5560	10694	1.2	0	4503680	NT	Homo sapiens IgG Fc binding protein (FC(GAMMA)BP), mRNA
393	5561	10695	0.6	0	4503680	NT	Homo sapiens IgG Fc binding protein (FC(GAMMA)BP), mRNA
393	5561	10696	0.6	0	4503680	NT	Homo sapiens IgG Fc binding protein (FC(GAMMA)BP), mRNA
394	5562	10697	2.4	0	4503680	NT	Homo sapiens IgG Fc binding protein (FC(GAMMA)BP), mRNA
395	5563	10698	0.9	0	4503680	NT	Homo sapiens IgG Fc binding protein (FC(GAMMA)BP), mRNA
396	5564	10699	0.8	0	X74870.1	NT	H. sapiens gene for RNA pol II largest subunit, exons 23-29
396	5564	10700	0.8	0	X74870.1	NT	H. sapiens gene for RNA pol II largest subunit, exons 23-29
400	5568		15.0	0	4506808	NT	H. sapiens gene for RNA pol II largest subunit, exons 23-29
414	5203	10304	1.3	0	R17795.1	EST_HUMAN	Homo sapiens ribosomal protein L19 (RPL19), mRNA
422	5589		0.9	0	4508728	NT	yg09402.1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:31652 5'
423	5590	10722	0.8	0	AB028942.1	NT	Homo sapiens ribosomal protein S5 (RPS5), mRNA
424	5591	10723	1.6	0	4507152	NT	Homo sapiens mRNA for KIAA1019 protein, partial cds
424	5591	10724	1.6	0	4507152	NT	Homo sapiens SON DNA binding protein (SON), mRNA
425	5592	10725	1.2	0	AF193607.1	NT	Homo sapiens SON DNA binding protein (SON), mRNA
438	5504	10738	0.7	0	4557879	NT	Mus musculus truncated SON protein (Son), complete cds
							Homo sapiens interferon gamma receptor 1 (IFNGR1), mRNA

Table 4

443	5609	1.0	0	AA324262.1	EST_HUMAN	EST27054 Cerebellum II Homo sapiens cDNA 5' end
444	5610	0.9	0	BE254447.1	EST_HUMAN	60111520F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3352348 5'
460	5626	1.1	0	4504532	NT	Homo sapiens 5-hydroxytryptamine (serotonin) receptor 1B (HTR1B) mRNA
460	5626	1.1	0	4504532	NT	Homo sapiens 5-hydroxytryptamine (serotonin) receptor 1B (HTR1B) mRNA
465	5630	1.3	0	4557887	NT	Homo sapiens keratin 18 (KRT18) mRNA
465	5630	1.3	0	4557887	NT	Homo sapiens keratin 18 (KRT18) mRNA
475	5641	0.8	0	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
476	5642	2.4	0	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
476	5642	2.4	0	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
485	5650	0.9	0	AB033035.1	NT	Homo sapiens mRNA for KIAA1209 protein, partial cds
485	5660	0.7	0	BE385144.1	EST_HUMAN	60127495F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3615756 5'
486	7890	1.1	0	AW938825.1	EST_HUMAN	PM0-DT0065-130400-002-c06 DT0065 Homo sapiens cDNA
488	5682	1.1	0	AL117233.1	NT	Novel human gene mapping to chromosome 1
499	5663	0.6	0	8923955	NT	Homo sapiens PC326 protein (PC326), mRNA
508	5672	1.3	0	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
516	7891	0.7	0	BE081527.1	EST_HUMAN	QV2-BT0635-160400-142-R05 BT0635 Homo sapiens cDNA
526	5690	1.2	0	AB040809.1	NT	Homo sapiens mRNA for KIAA1476 protein, partial cds
526	5693	3.8	0	6006030	NT	Homo sapiens transcription elongation factor B (SIII), polypeptide 1-like (TCEB1L) mRNA
530	5694	1.4	0	4504036	NT	Homo sapiens guanine nucleotide binding protein (G protein), alpha 11 (Gq class) (GNA11) mRNA
530	5694	1.4	0	4504036	NT	Homo sapiens guanine nucleotide binding protein (G protein), alpha 11 (Gq class) (GNA11) mRNA
536	5699	2.0	0	AF003628.1	NT	Homo sapiens X-linked anhidrotic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions
544	5707	0.6	0	AW135324.1	EST_HUMAN	U1-H-B1-act-h-04-Q-U.s1 NCL_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2713951 3'
554	5717	1.1	0	D10083.1	NT	Homo sapiens RGH1 gene, retrovirus-like element
571	5732	0.9	0	5174742	NT	Homo sapiens ubiquinol-cytochrome c reductase, Rieske iron-sulfur polypeptide 1 (UQCRCF1), nuclear gene encoding mitochondrial protein, mRNA
584	5744	1.8	0	J04066.1	NT	Human apolipoprotein A-I (ApoA-I) gene, exon 1
593	5751	1.5	0	4501854	NT	Homo sapiens acetyl-Coenzyme A carboxylase beta (ACACB), mRNA
598	5756	1.1	0	AF221712.1	NT	Homo sapiens Smad- and Olf-interacting zinc finger protein mRNA, partial cds
598	5756	1.1	0	AF221712.1	NT	Homo sapiens Smad- and Olf-interacting zinc finger protein mRNA, partial cds
607	5765	1.4	0	AF149773.1	NT	Homo sapiens NOD1 protein (NOD1) gene, exons 1, 2, and 3
610	5768	1.0	0	6806918	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
611	5769	0.8	0	6806918	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
611	5769	0.8	0	6806918	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
612	5770	0.9	0	6806918	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
612	5770	0.9	0	6806918	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
619	5778	1.3	0	AA399486.1	EST_HUMAN	Z60007.1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:726732 5'



Table 4

623	5782	10904	2.2	0	D11078.1	NT	Homo sapiens RGH2 gene, retrovirus-like element
627	5786	10907	1.1	0	W78811.1	EST_HUMAN	Zh51b04.1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:415567 5' similar to gb:A21187 ALPHA-2-MACROGLOBULIN PRECURSOR (HUMAN);
627	5786	10908	1.1	0	W78811.1	EST_HUMAN	Zh51b04.1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:415567 5' similar to gb:A21187 ALPHA-2-MACROGLOBULIN PRECURSOR (HUMAN);
630	5789		1.1	0	4885526	NT	Homo sapiens novel SH2-containing protein 3 (NSP3) mRNA
637	5796	10920	1.0	0	6006003	NT	Homo sapiens glutamate receptor, ionotropic, N-methyl D-aspartate 2B (GRIN2B) mRNA
639	5798	10923	1.1	0	5031624	NT	Homo sapiens CCAAT-box-binding transcription factor (CBF2) mRNA
642	5801	10927	1.4	0	U05235.1	NT	Human neutral amino acid transporter (ASCT1) gene, exon 8
646	5805	10930	0.7	0	AF108389.1	NT	Homo sapiens sodium/calcium exchanger isoform NaCa3 (NCX1) mRNA, complete cds
646	5805	10931	0.7	0	AF108389.1	NT	Homo sapiens sodium/calcium exchanger isoform NaCa3 (NCX1) mRNA, complete cds
652	5810	10936	1.4	0	4826947	NT	Homo sapiens protein kinase, X-linked (PRKX) mRNA
652	5810	10937	1.4	0	4826947	NT	Homo sapiens protein kinase, X-linked (PRKX) mRNA
658	7894		1.0	0	X57147.1	NT	Human endogenous retrovirus PHE.1 (ERV9)
667	5823	10951	1.6	0	4504424	NT	Homo sapiens high-mobility group (nonhistone chromosomal) protein 1 (HMGI) mRNA
672	5828	10955	1.5	0	AB029012.1	NT	Homo sapiens mRNA for KIAA1089 protein, partial cds
682	5837	10970	0.7	0	7657468	NT	Homo sapiens similar to rat integral membrane glycoprotein POM121 (POM121L1), mRNA
692	5847	10982	6.6	0	AA614537.1	EST_HUMAN	np48d0.s1 NCL CGAP_Brt.1 Homo sapiens cDNA clone IMAGE:1128633 3' similar to gb:X57352 INTERFERON-INDUCIBLE PROTEIN 1-8U (HUMAN);
696	5851	10986	2.6	0	M60675.1	NT	Human von Willebrand factor gene, exons 23 through 34
696	5851	10987	2.6	0	M60675.1	NT	Human von Willebrand factor gene, exons 23 through 34
706	5861	10996	1.5	0	5032192	NT	Homo sapiens TNF receptor-associated factor 1 (TRAF1) mRNA
712	5865	11002	1.3	0	AF264750.1	NT	Homo sapiens ALR-like protein mRNA, partial cds
712	5865	11003	1.3	0	AF264750.1	NT	Homo sapiens ALR-like protein mRNA, partial cds
719	5873	11013	0.6	0	BE241577.1	EST_HUMAN	TCAP1D0779 Pediatric acute myelogenous leukemia cell (FAB M1) Baylo-HGSC project=TCAP Homo sapiens cDNA clone TCAP0779
739	5892	11037	1.1	0	AF226990.2	NT	Homo sapiens MHC class I antigen (HLA-G) mRNA, HLA-G1 allele, complete cds
739	5892	11038	1.1	0	AF226990.2	NT	Homo sapiens MHC class I antigen (HLA-G) mRNA, HLA-G1 allele, complete cds
740	5893	11039	2.4	0	AF170492.1	NT	Homo sapiens chloride channel CLC4 (CLC4) mRNA, complete cds
743	5898	11042	0.5	0	J03764.1	NT	Human, plasminogen activator inhibitor-1 gene, exons 2 to 9
743	5898	11043	0.5	0	J03764.1	NT	Human, plasminogen activator inhibitor-1 gene, exons 2 to 9
745	5898	11044	0.8	0	AB037760.1	NT	Homo sapiens mRNA for KIAA1339 protein, partial cds
746	5899	11045	1.1	0	6912749	NT	Homo sapiens zinc finger protein 212 (ZNF212), mRNA
747	7898	11046	0.8	0	D30612.1	NT	Homo sapiens mRNA for repressor protein, partial cds
752	5904	11051	1.2	0	R48915.1	EST_HUMAN	Y69g08.t1 Soares breast 2nbH8t Homo sapiens cDNA clone IMAGE:154046 5'
753	5905	11052	0.8	0	5032086	NT	Homo sapiens splicing factor 3a, subunit 1, 120KD (SF3A1), mRNA
762	5914	11061	0.5	0	AB011399.1	NT	Homo sapiens gene for Af-6, complete cds
765	5918	11065	1.0	0	7661965	NT	Homo sapiens KIAA0170 gene product (KIAA0170), mRNA

Table 4

775	5927	11076	1.2	0	D80008.1	NT	Human mRNA for KIAA0184 gene, partial cds
775	5927	11077	1.2	0	D80008.1	NT	Human mRNA for KIAA0184 gene, partial cds
780	5932	11081	0.9	0	X89772.1	NT	H.sapiens mRNA for interferon alpha/beta receptor (long form)
784	5936	11085	0.8	0	AB020717.1	NT	Homo sapiens mRNA for KIAA0910 protein, partial cds
784	5936	11086	0.8	0	AB020717.1	NT	Homo sapiens mRNA for KIAA0910 protein, partial cds
789	5940	11092	2.3	0	5174478	NT	Homo sapiens parcentin (PCNT) mRNA
790	5941	2.4	0	0	4507500	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA
807	5958	11113	0.5	0	7657213	NT	Homo sapiens homonally upregulated neu tumor-associated kinase (HUNK), mRNA
808	5959	11114	1.5	0	7657213	NT	Homo sapiens homonally upregulated neu tumor-associated kinase (HUNK), mRNA
810	5961	11116	1.3	0	4557686	NT	Homo sapiens poliasium voltage-gated channel, Isk-related family, member 1 (KCNE1) mRNA
816	5966	11122	1.2	0	AF108830.1	NT	Homo sapiens serine-threonine protein kinase (MNBH) mRNA, complete cds
816	5966	11123	1.2	0	AF108830.1	NT	Homo sapiens serine-threonine protein kinase (MNBH) mRNA, complete cds
821	5971	11128	1.1	0	4503854	NT	Homo sapiens GA-binding protein transcription factor, alpha subunit (GABPA), mRNA
825	5974	11133	0.5	0	4507500	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA
825	5974	11134	0.5	0	4507500	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA
832	5981	11145	0.5	0	AF027153.1	NT	Homo sapiens sodium/myo-inositol cotransporter (SLC5A3) gene, complete cds
836	5985	11145	1.2	0	AB028942.1	NT	Homo sapiens mRNA for KIAA1019 protein, partial cds
836	5985	11146	1.2	0	AB028942.1	NT	Homo sapiens mRNA for KIAA1019 protein, partial cds
837	5986	11147	2.5	0	4507152	NT	Homo sapiens SON DNA binding protein (SON) mRNA
838	5987	11148	1.0	0	AB028942.1	NT	Homo sapiens SON DNA binding protein (SON) mRNA
839	5988	11149	0.7	0	4506728	NT	Homo sapiens rRNA for KIAA1019 protein, partial cds
843	5992	11152	1.3	0	AB020717.1	NT	Homo sapiens rRNA for KIAA0910 protein, partial cds
843	5992	11153	1.3	0	AB020717.1	NT	Homo sapiens rRNA for KIAA0910 protein, partial cds
844	5993	11154	0.7	0	AA533272.1	EST_HUMAN	Homo sapiens rRNA for KIAA0910 protein, partial cds
844	5993	11155	0.7	0	AA533272.1	EST_HUMAN	Homo sapiens rRNA for KIAA0910 protein, partial cds
849	5998	11156	1.3	0	7657213	NT	Homo sapiens homonally upregulated neu tumor-associated kinase (HUNK), mRNA
849	5998	11157	1.3	0	7657213	NT	Homo sapiens homonally upregulated neu tumor-associated kinase (HUNK), mRNA
850	5999	11158	0.7	0	7657213	NT	Homo sapiens homonally upregulated neu tumor-associated kinase (HUNK), mRNA
850	5999	11159	0.7	0	7657213	NT	Homo sapiens homonally upregulated neu tumor-associated kinase (HUNK), mRNA
873	6021	11182	0.9	0	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
880	6028	11187	0.6	0	BE088592.1	EST_HUMAN	OV0-BT0703-280400-211-g11 BT0703 Homo sapiens cDNA
880	6028	11188	0.6	0	BE088592.1	EST_HUMAN	OV0-BT0703-280400-211-g11 BT0703 Homo sapiens cDNA
890	6038	11197	1.3	0	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
900	6047	2.5	0	0	4504958	NT	Homo sapiens lamelin receptor 1 (67kD, ribosomal protein SA) (LAMR1), mRNA
903	6047	1.1	0	0	4504958	NT	Homo sapiens lamelin receptor 1 (67kD, ribosomal protein SA) (LAMR1), mRNA
904	6050	11205	0.5	0	AF089747.1	NT	Homo sapiens alpha-1-antitrypsin precursor, mRNA, partial cds
905	6051	11206	1.0	0	S69364.1	NT	protein C inhibitor [human, leukocytes, Genomic, 1216 nt, segment 2 of 5]
905	6051	11207	1.0	0	S69364.1	NT	protein C inhibitor [human, leukocytes, Genomic, 1216 nt, segment 2 of 5]
905	6051	11208	1.0	0	S69364.1	NT	protein C inhibitor [human, leukocytes, Genomic, 1216 nt, segment 2 of 5]

Table 4

908	6052	11209	0.7	0	128101.1	NT	Homo sapiens kallistatin (P14) gene, exons 1-4, complete cds
909	6055	11212	36.0	0	Z20856.1	NT	Homo sapiens of cardiac alpha-myosin heavy chain gene
909	6055	11213	36.0	0	Z20656.1	NT	Homo sapiens of cardiac alpha-myosin heavy chain gene
910	6056	11214	57.0	0	Z20656.1	NT	Homo sapiens of cardiac alpha-myosin heavy chain gene
910	6058	11215	57.0	0	Z20656.1	NT	Homo sapiens of cardiac alpha-myosin heavy chain gene
935	6082	11238	12.0	0	M37190.1	NT	Human ras inhibitor mRNA, 3' end
936	6083	11239	4.5	0	M37190.1	NT	Human ras inhibitor mRNA, 3' end
937	6084	11240	18.0	0	M37190.1	NT	Human ras inhibitor mRNA, 3' end
938	6085	11241	0.7	0	4507430	NT	Human ras inhibitor mRNA, 3' end
938	6085	11242	0.7	0	4507430	NT	Human ras inhibitor mRNA, 3' end
938	6085	11242	0.7	0	4507430	NT	Human ras inhibitor mRNA, 3' end
946	7903	11249	0.8	0	A1001948.1	EST_HUMAN	Human ras inhibitor mRNA, 3' end
946	7903	11249	0.8	0	A1001948.1	EST_HUMAN	Human ras inhibitor mRNA, 3' end
946	7903	11250	0.8	0	A1001948.1	EST_HUMAN	Human ras inhibitor mRNA, 3' end
948	6084	11252	2.5	0	7657266	NT	(KIAA0929), mRNA
968	6113	11271	1.3	0	X62207.1	NT	Homo sapiens partial c-fgr gene, exons 2 and 3
968	6113	11272	1.3	0	X62207.1	NT	Homo sapiens partial c-fgr gene, exons 2 and 3
977	6122	11278	1.3	0	4757969	NT	Homo sapiens chromodomain protein, Y chromosome-like (CDYL) mRNA
988	6132	11287	1.1	0	U83688.1	NT	Human beta-tubulin (TUBB4) gene, complete cds
989	6133	11288	2.6	0	U83688.1	NT	Human beta-tubulin (TUBB4) gene, complete cds
989	6133	11288	2.6	0	U83688.1	NT	Human beta-tubulin (TUBB4) gene, complete cds
989	6133	11288	2.3	0	U83688.1	NT	Human beta-tubulin (TUBB4) gene, complete cds
997	6139	11283	0.8	0	AF111170.3	NT	Homo sapiens 14q32 jagged2 gene, complete cds; and unknown gene
998	6139	11283	1.4	0	AF111170.3	NT	Homo sapiens 14q32 jagged2 gene, complete cds; and unknown gene
999	6139	11283	0.6	0	AF111170.3	NT	Homo sapiens 14q32 jagged2 gene, complete cds; and unknown gene
1000	6140	11294	0.8	0	AF111170.3	NT	Homo sapiens 14q32 jagged2 gene, complete cds; and unknown gene
1003	6143	11297	0.8	0	7651685	NT	Homo sapiens inner membrane protein, mitochondrial (mitofilin) (IMMT), mRNA
1007	6147	11301	0.9	0	5803114	NT	Homo sapiens inner membrane protein, mitochondrial (mitofilin) (IMMT), mRNA
1008	6149		0.7	0	AA45680.1	EST_HUMAN	Human ras inhibitor mRNA, 3' end
1012	6152	11306	1.0	0	N43182.1	EST_HUMAN	Human ras inhibitor mRNA, 3' end
1012	6152	11307	1.0	0	N43182.1	EST_HUMAN	Human ras inhibitor mRNA, 3' end
1013	6153	11308	1.0	0	4759249	NT	Human ras inhibitor mRNA, 3' end
1013	6153	11309	1.0	0	4759249	NT	Human ras inhibitor mRNA, 3' end
1017	6157		1.5	0	8922833	NT	Human ras inhibitor mRNA, 3' end
1031	6171	11324	0.8	0	4758669	NT	Human ras inhibitor mRNA, 3' end
1049	6186	11339	0.6	0	4826672	NT	Human ras inhibitor mRNA, 3' end
1049	6186	11340	0.6	0	4826672	NT	Human ras inhibitor mRNA, 3' end
1053	6192	11344	0.9	0	8923624	NT	Human ras inhibitor mRNA, 3' end
1053	6192	11345	0.9	0	8923624	NT	Human ras inhibitor mRNA, 3' end
1054	6193	11346	13.0	0	AJ245922.1	NT	Human ras inhibitor mRNA, 3' end

Table 4

1056	6195	11350	0.9	0	8923087	NT	Homo sapiens hypothetical protein FLJ20080 (FLJ20080), mRNA
1058	6197	11350	1.1	0	5174384	NT	Homo sapiens alkylation repair, alkB homolog (ABH), mRNA
1066	6204	11359	1.2	0	4758117	NT	Homo sapiens Death associated protein 3 (DAP3), mRNA
1080	6218	11369	1.2	0	BE005208.1	EST_HUMAN	MRO-BN0115-200300-003-008 BN0115 Homo sapiens cDNA
1103	6241	11393	1.3	0	7706134	NT	Homo sapiens potassium channel, subfamily K, member 9 (KCCK9), mRNA
1103	6241	11394	1.3	0	7706134	NT	Homo sapiens potassium channel, subfamily K, member 9 (KCCK9), mRNA
1116	6253	11404	1.1	0	4826947	NT	Homo sapiens protein kinase, X-linked (PRKX), mRNA
1116	6253	11405	1.1	0	4826947	NT	Homo sapiens protein kinase, X-linked (PRKX), mRNA
1117	6254	11406	1.9	0	4506712	NT	Homo sapiens ribosomal protein S27a (RPS27A), mRNA
1119	6256	11408	0.9	0	8823290	NT	Homo sapiens hypothetical protein FLJ20309 (FLJ20309), mRNA
1121	6256	11410	3.5	0	AB002059.1	NT	Homo sapiens DNA for Human P2XM, complete cds
1123	6260	11411	4.1	0	AB002059.1	NT	Homo sapiens DNA for Human P2XM, complete cds
1124	6261	11412	0.7	0	7657468	NT	Homo sapiens similar to rat integral membrane glycoprotein POM121 (POM121L1), mRNA
1124	6261	11413	0.7	0	7657468	NT	Homo sapiens similar to rat integral membrane glycoprotein POM121 (POM121L1), mRNA
1128	6284	11416	1.0	0	7706500	NT	Homo sapiens Npw38-binding protein NpwBP (LOC51729), mRNA
1129	6265	11417	1.0	0	A1147650.1	EST_HUMAN	qb22d10.x1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:1697011 3'
1131	6267	11419	1.4	0	AB020710.1	NT	Homo sapiens mRNA for KIAA0903 protein, partial cds
1152	6287	11440	0.8	0	7305076	NT	Homo sapiens glutamate decarboxylase 1 (brain, 67kD) (GAD1), transcript variant GAD25, mRNA
1152	6287	11441	0.8	0	7305076	NT	Homo sapiens glutamate decarboxylase 1 (brain, 67kD) (GAD1), transcript variant GAD25, mRNA
1154	6289	11443	0.5	0	AB037835.1	NT	Homo sapiens mRNA for KIAA1414 protein, partial cds
1161	6286	11452	1.0	0	4557887	NT	Homo sapiens keratin 18 (KRT18), mRNA
1191	6323		1.1	0	7657336	NT	Homo sapiens mult. (E. coli) homolog 3 (MLH3), mRNA
1206	6338	11494	1.1	0	AF264750.1	NT	Homo sapiens ALR-like protein mRNA, partial cds
1206	6338	11495	1.1	0	AF264750.1	NT	Homo sapiens ALR-like protein mRNA, partial cds
1207	6339	11496	1.3	0	AF264750.1	NT	Homo sapiens ALR-like protein mRNA, partial cds
1208	7909	11497	1.0	0	AF264750.1	NT	Homo sapiens ALR-like protein mRNA, partial cds
1226	6356	11520	3.6	0	AF109718.1	NT	Homo sapiens chromosome 3 subtelomeric region
1227	6357	11521	1.3	0	4503098	NT	Homo sapiens chondroilin sulfate proteoglycan 4 (melanoma-associated) (CSPG4), mRNA
1245	6374		1.5	0	Y18000.1	NT	Homo sapiens NF2 gene
1253	6382	11541	16.0	0	4506718	NT	Homo sapiens ribosomal protein S2 (RPS2), mRNA
1260	6389	11550	1.3	0	AF084479.1	NT	Homo sapiens Williams-Beuren syndrome deletion transcript 9 (WBSCR9), mRNA, complete cds
1266	6395	11554	0.6	0	AB040940.1	NT	Homo sapiens mRNA for KIAA1507 protein, partial cds
1266	6395	11555	0.6	0	AB040940.1	NT	Homo sapiens mRNA for KIAA1507 protein, partial cds
1276	6408	11568	2.2	0	5174748	NT	Homo sapiens Wolfraim syndrome (WFS), mRNA

Table 4

1276	6408	11569	2.2	0	5174748	NT	Homo sapiens Wolfram syndrome (WFS) mRNA
1278	6408	11570	2.2	0	5174748	NT	Homo sapiens Wolfram syndrome (WFS) mRNA
1279	6409		0.9	0	AF096156.1	NT	Homo sapiens protein phosphatase 2A B $\gamma$ gamma subunit gene, exon 5
1289	7911	11582	1.1	0	7657529	NT	Homo sapiens ribadoid tumor deletion region protein 1 (RTDR1), mRNA
1289	7911	11583	1.1	0	7657529	NT	Homo sapiens ribadoid tumor deletion region protein 1 (RTDR1), mRNA
1285	6424	11589	0.6	0	5803146	NT	Homo sapiens ring finger protein 9 (RNF9), mRNA
1286	6425	11590	0.8	0	4508004	NT	Homo sapiens zinc finger protein 173 (ZNF173), mRNA
1288	6427	11591	1.1	0	5803146	NT	Homo sapiens ring finger protein 9 (RNF9), mRNA
1300	6429	11593	1.4	0	AB011149.1	NT	Homo sapiens mRNA for KIAA0577 protein, complete cds
1301	6430	11594	1.1	0	7661965	NT	Homo sapiens KIAA0170 gene product (KIAA0170), mRNA
1302	6431	11595	1.6	0	7661965	NT	Homo sapiens KIAA0170 gene product (KIAA0170), mRNA
1303	6432	11596	1.4	0	8567387	NT	Homo sapiens period (Drosophila) homolog 3 (PER3), mRNA
1303	6432	11597	1.4	0	8567387	NT	Homo sapiens period (Drosophila) homolog 3 (PER3), mRNA
1315	6443	11610	1.4	0	M14123.1	NT	Human endogenous retrovirus HERV-K10
1386	6513	11679	0.9	0	AJ250014.1	NT	Homo sapiens mRNA for Familial Cylindromatosis cyd gene
1393	6520	11686	3.3	0	AJ277892.1	NT	Homo sapiens partial TTN gene for titin
1396	6523	11692	1.0	0	AJ208756.1	EST_HUMAN	gg38b06.x1 Soares, testis_NHT Homo sapiens cDNA clone IMAGE:1837427 3' similar to WP:127A1.5 CE14213:
1397	6524	11693	3.0	0	6042206	NT	RAN, member RAS oncogene family/Homo sapiens RAN, member RAS oncogene family (RAN), mRNA
1407	6534	11705	0.5	0	4505646	NT	Homo sapiens proprotein convertase subtilisin/kexin type 2 (PCSK2) mRNA
1407	6534	11706	0.5	0	4505646	NT	Homo sapiens proprotein convertase subtilisin/kexin type 2 (PCSK2) mRNA
1409	6536	11709	0.9	0	7705565	NT	Homo sapiens KIAA1114 protein (KIAA1114), mRNA
1409	6536	11710	0.9	0	7705565	NT	Homo sapiens KIAA1114 protein (KIAA1114), mRNA
1412	6539	11712	1.9	0	AJ238093.1	NT	Homo sapiens partial AF-4 gene, exons 2 to 7 and Alu repeat elements
1421	6549	11724	1.3	0	AF038280.1	NT	Homo sapiens alpha1-6-glucosyltransferase (alpha1-6-GlcT) gene, exon 7
1432	6559	11735	3.5	0	4507720	NT	Homo sapiens titin (TTN) mRNA
1432	6559	11736	3.5	0	4507720	NT	Homo sapiens titin (TTN) mRNA
1437	6564	11740	1.0	0	U35637.1	NT	Human nebulin mRNA, partial cds
1437	6564	11741	1.0	0	U35637.1	NT	Human nebulin mRNA, partial cds
1445	6572	11746	1.1	0	AL132899.1	NT	Novel human gene on chromosome 20
1447	6574	11747	1.0	0	AL137764.1	NT	Novel human gene mapping to chromosome 1
1451	6578	11752	1.2	0	DB7077.1	NT	Human mRNA for KIAA0240 gene, partial cds
1454	6581	11755	1.8	0	6912457	NT	Homo sapiens calcineurin binding protein 1 (KIAA0330), mRNA
1456	6583	11757	0.6	0	7661965	NT	Homo sapiens KIAA0170 gene product (KIAA0170), mRNA
1456	6583	11758	0.6	0	7661965	NT	Homo sapiens KIAA0170 gene product (KIAA0170), mRNA
1457	6584		1.0	0	Y07829.2	NT	Homo sapiens RFB30 gene for RING finger protein
1462	6589	11763	1.3	0	M60676.1	NT	Human von Willebrand factor pseudogene corresponding to exons 23 through 34
1462	6589	11764	1.3	0	M60676.1	NT	Human von Willebrand factor pseudogene corresponding to exons 23 through 34
1495	6621	11791	1.3	0	7706434	NT	Homo sapiens hHDC for homolog of Drosophila headcase (LOC51696), mRNA
1509	6636	11805	1.0	0	AA481172.1	EST_HUMAN	aa34a03.t1 NCJ_GAP_GCB1 Homo sapiens cDNA clone IMAGE:815116 5'

Table 4

1515	6642	11808	4.3	0	AF023860.1	NT	Cercopithecus aethiops cyclophilin A mRNA, complete cds
1515	6642	11809	4.3	0	AF023860.1	NT	Cercopithecus aethiops cyclophilin A mRNA, complete cds
1517	6644	11812	1.0	0	D10884.1	NT	Bovine mRNA for neurocalcin
1519	6646		0.7	0	U78027.1	NT	Homo sapiens Bruton's tyrosine kinase (BTK), alpha-D-galactosidase A (GLA), L44-like ribosomal protein (L44), and F1P3 (F1P3) genes, complete cds
1520	6647	11815	3.9	0	4505404	NT	Homo sapiens transmembrane glycoprotein (GPNMB) mRNA
1520	6647	11816	3.9	0	4505404	NT	Homo sapiens transmembrane glycoprotein (GPNMB) mRNA
1521	6648	11817	1.1	0	7662405	NT	Homo sapiens KIAA0957 protein (KIAA0957), mRNA
1522	6649		3.0	0	7666972	NT	Homo sapiens TNF-inducible protein CG12-1 (CG12-1), mRNA
1527	6654	11821	1.8	0	M88478.1	NT	Human transglutaminase mRNA, complete cds
1530	6657	11823	2.1	0	4507720	NT	Homo sapiens titin (TTN) mRNA
1530	6657	11824	2.1	0	4507720	NT	Homo sapiens titin (TTN) mRNA
1531	7919		10.1	0	4506654	NT	Homo sapiens ribosomal protein L5 (RPL5) mRNA
1532	6658	11825	4.0	0	M14199.1	NT	Human laminin receptor (2H5 epitope) mRNA, 5' end
1541	6668	11836	2.1	0	4507720	NT	Homo sapiens titin (TTN) mRNA
1541	6668	11839	2.1	0	4507720	NT	Homo sapiens titin (TTN) mRNA
1543	6670	11840	4.7	0	4503098	NT	Homo sapiens chondroilin sulfate proteoglycan 4 (melanoma-associated) (CSPG4), mRNA
1562	6689	11857	0.6	0	Z63738.1	NT	H. sapiens hH2Ble gene
1563	6690	11858	1.4	0	5921460	NT	Homo sapiens butyrophilin, subfamily 2, member A1 (BTN2A1), mRNA
1563	6690	11859	1.4	0	5921460	NT	Homo sapiens butyrophilin, subfamily 2, member A1 (BTN2A1), mRNA
1566	7920	11862	0.5	0	AB040005.1	NT	Homo sapiens mRNA for KIAA1472 protein, partial cds
1570	6696	11863	1.0	0	AF157476.1	NT	Homo sapiens DNA polymerase zeta catalytic subunit (REV3) mRNA, complete cds
1572	6698	11866	0.9	0	7662183	NT	Homo sapiens KIAA0569 gene product (KIAA0569), mRNA
1572	6698	11867	0.9	0	7662183	NT	Homo sapiens KIAA0569 gene product (KIAA0569), mRNA
1574	6700	11868	5.1	0	5729876	NT	Homo sapiens heat shock 70KD protein 10 (HSC71) (HSPA10), mRNA
1574	6700	11869	5.1	0	5729876	NT	Homo sapiens heat shock 70KD protein 10 (HSC71) (HSPA10), mRNA
1576	6702	11871	0.9	0	M91803.1	NT	Human sodium channel mRNA
1591	6717	11887	1.7	0	H26973.1	EST_HUMAN	yo76c05.s1 Soares adult brain N2b4HB55Y Homo sapiens cDNA clone IMAGE:183848 3'
1645	6771	11942	1.3	0	A1768104.1	EST_HUMAN	wg81b07.x1 Soares NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2371477 3' similar to TR:Q62788 Q62788 CYS2/HIS2 ZINC FINGER PROTEIN.;
1646	6772	11943	1.2	0	AF057177.1	NT	Homo sapiens T-cell receptor gamma V1 gene region
1650	6775	11947	0.6	0	M29580.1	NT	Human zinc-finger protein 7 (ZFP7) mRNA, complete cds
1650	6775	11948	0.6	0	M29580.1	NT	Human zinc-finger protein 7 (ZFP7) mRNA, complete cds
1652	6777	11950	1.2	0	4557887	NT	Homo sapiens keratin 18 (KRT18) mRNA
1653	6778	11951	0.9	0	7657065	NT	Homo sapiens v-erb avian erythroblastosis virus E26 oncogene related (ERG), mRNA
1657	6781	11955	1.1	0	4557610	NT	Homo sapiens gamma-aminobutyric acid (GABA) A receptor, gamma 2 (GABRG2) mRNA
1659	6783	11958	1.1	0	H30132.1	EST_HUMAN	yo59a08.r1 Soares breast 3NbH8st Homo sapiens cDNA clone IMAGE:182246 5' similar to gb:M64099 GAAMMA-GLUTAMYL TRANSPEPTIDASE 5 PRECURSOR (HUMAN);

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Table 4

1809	6928	12116	0.5	0	AW207280.1	EST_HUMAN	UI-H-B11-afn-1-07-0-UI.s1 NCI_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2722333 3'
1809	6928	12117	0.5	0	AW207280.1	EST_HUMAN	UI-H-B11-afn-1-07-0-UI.s1 NCI_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2722333 3'
1832	6951	12135	0.8	0	BE277465.1	EST_HUMAN	601179164F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3547239 5'
1832	6951	12136	0.8	0	BE277465.1	EST_HUMAN	601179164F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3547239 5'
1852	6970	12155	1.0	0	BE006292.1	EST_HUMAN	RC2-BN0126-200300-012-b04 BN0126 Homo sapiens cDNA
1881	6989	12183	1.3	0	4506384	NT	Homo sapiens RAD1 (S. pombe) homolog (RAD1) mRNA, and translated products
1881	6989	12184	1.3	0	4506384	NT	Homo sapiens RAD1 (S. pombe) homolog (RAD1) mRNA, and translated products
1889	7007	12193	0.6	0	AF157476.1	NT	Homo sapiens DNA polymerase zeta catalytic subunit (REV3) mRNA, complete cds
1890	7929	12193	1.5	0	M98478.1	NT	Human transglutaminase mRNA, complete cds
1890	7929	12194	1.5	0	M98478.1	NT	Human transglutaminase mRNA, complete cds
1895	7012	12201	0.8	0	4507464	NT	Homo sapiens transforming growth factor, beta 3 (TGFB3), mRNA
1895	7012	12202	0.8	0	4507464	NT	Homo sapiens transforming growth factor, beta 3 (TGFB3), mRNA
1903	7021	12210	0.7	0	M55632.1	NT	Human topoisomerase I pseudogene 1
1905	7830	12217	0.9	0	5901905	NT	Homo sapiens butyrophilin, subfamily 3, member A2 (BTN3A2), mRNA
1913	7030	12217	0.7	0	4809282	NT	Homo sapiens histidine ammonia-lyase (HAL) mRNA
1913	7030	12218	0.7	0	4809282	NT	Homo sapiens histidine ammonia-lyase (HAL) mRNA
1924	7041	12232	1.1	0	AL163252.2	NT	Homo sapiens chromosome 21 segment HS21C052
1926	7043	12232	1.2	0	8400716	NT	Homo sapiens nebulin (NEB), mRNA
1926	7043	12233	1.2	0	8400716	NT	Homo sapiens nebulin (NEB), mRNA
1927	7044	12234	2.9	0	4826638	NT	Homo sapiens actinin, alpha 4 (ACTN4) mRNA
1927	7044	12235	2.9	0	4826638	NT	Homo sapiens actinin, alpha 4 (ACTN4) mRNA
1937	7054	12247	1.2	0	AB018333.1	NT	Homo sapiens mRNA for KIAA0790 protein, partial cds
1937	7054	12248	1.2	0	AB018333.1	NT	Homo sapiens mRNA for KIAA0790 protein, partial cds
1943	7060	12252	0.7	0	M33782.1	NT	Human TFEB protein mRNA, partial cds
1943	7060	12253	0.7	0	M33782.1	NT	Human TFEB protein mRNA, partial cds
1945	7062	12254	1.3	0	AW193024.1	EST_HUMAN	X69b01.x1 NCI_CGAP_Pant1 Homo sapiens cDNA clone IMAGE:2679913 3'
1945	7062	12255	1.3	0	AW193024.1	EST_HUMAN	X69b01.x1 NCI_CGAP_Pant1 Homo sapiens cDNA clone IMAGE:2679913 3'
1946	7063	12256	3.0	0	6912457	NT	Homo sapiens calcineurin binding protein 1 (KIAA0330), mRNA
1946	7063	12257	3.0	0	6912457	NT	Homo sapiens calcineurin binding protein 1 (KIAA0330), mRNA
1948	7065	12258	0.9	0	Z47556.1	NT	H. sapiens genes for semenogelin I and semenogelin II
1948	7065	12260	0.9	0	Z47556.1	NT	H. sapiens genes for semenogelin I and semenogelin II
1955	7072	12266	0.8	0	AB040946.1	NT	Homo sapiens mRNA for KIAA1513 protein, partial cds
2011	7125	12325	1.1	0	4557887	NT	Homo sapiens keratin 18 (KRT18) mRNA
2011	7125	12326	1.1	0	4557887	NT	Homo sapiens keratin 18 (KRT18) mRNA
2013	7127	12327	1.0	0	4503648	NT	Homo sapiens coagulation factor IX (plasma thromboplastic component, Christmas disease, hemophilia B) (F9) mRNA
2014	7128	12328	2.0	0	4505606	NT	Homo sapiens pregnancy-associated plasma protein A (PAPPA) mRNA
2015	6536	11709	1.0	0	7705565	NT	Homo sapiens KIAA1114 protein (KIAA1114), mRNA
2015	6536	11710	1.0	0	7705565	NT	Homo sapiens KIAA1114 protein (KIAA1114), mRNA



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2017	7130	12330	0.7	0	AA077589.1	EST_HUMAN	7B22E10 Chromosome 7 Fetal Brain cDNA Library Homo sapiens cDNA clone 7B22E10
2017	7130	12331	0.7	0	AA077589.1	EST_HUMAN	7B22E10 Chromosome 7 Fetal Brain cDNA Library Homo sapiens cDNA clone 7B22E10
2019	7132		0.9	0	7657468	NT	Homo sapiens similar to rat integral membrane glycoprotein POM121 (POM121L1), mRNA
2021	7134		0.6	0	4585663	NT	Homo sapiens phosphodiesterase 6a, cGMP-specific, rod, alpha (PDE6a), mRNA
2022	7135	12334	0.9	0	AF124250.1	NT	Homo sapiens SH2-containing protein Nsp2 mRNA, complete cds
2024	7137		0.7	0	A1244247.1	EST_HUMAN	q98008.x1 NCI_CGAP_U12 Homo sapiens cDNA clone IMAGE:1988871 3 similar to contains Alu repetitive element;
2029	7142	12343	0.9	0	X92841.1	NT	H.sapiens MICA gene
2031	7144	12345	0.5	0	BE326593.1	EST_HUMAN	h62a08.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3133046 3 similar to TR:P97307 P97307 SDF2.1
2031	7144	12346	0.5	0	BE326593.1	EST_HUMAN	h62a08.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3133046 3 similar to TR:P97307 P97307 SDF2.1
2035	7148	12351	0.9	0	7662007	NT	Homo sapiens KIAA0218 gene product (KIAA0218), mRNA
2035	7148	12352	0.9	0	7662007	NT	Homo sapiens KIAA0218 gene product (KIAA0218), mRNA
2040	7153	12359	0.9	0	4757807	NT	Homo sapiens ATPase, Ca++ transporting, plasma membrane 2 (ATP2B2) mRNA
2045	7158	12363	1.3	0	4758489	NT	Homo sapiens GTP binding protein 1 (GTPBP1) mRNA
2067	7179		1.0	0	U90552.1	NT	Human butyrophilin (BTf5) mRNA, complete cds
2068	7180		1.1	0	AF018963.1	NT	Homo sapiens X-linked juvenile retinoschisis protein (XLR1) gene, exon 6 and complete cds
2070	7182	12386	1.1	0	U54777.2	NT	Homo sapiens IMSH6 protein (MSH6) mRNA, complete cds
2071	7183	12387	0.7	0	4503756	NT	Homo sapiens flavin containing monooxygenase 2 (FMO2) mRNA
2074	7186	12389	1.2	0	AW752708.1	EST_HUMAN	IL3-CT0219-271099-022-G10 CT0219 Homo sapiens cDNA
2076	7188	12391	0.7	0	A1904640.1	EST_HUMAN	QV-BT065-020399-092 BT065 Homo sapiens cDNA
2076	7188	12392	0.7	0	A1904640.1	EST_HUMAN	QV-BT065-020399-092 BT065 Homo sapiens cDNA
2112	7223		1.2	0	7657252	NT	Homo sapiens poliovirus large conductance calcium-activated channel, subfamily M, beta member 3-like (KCNCMB3L), mRNA
2132	7242		0.6	0	L14787.1	NT	Human DNA-binding protein mRNA, 3'end
2138	7248	12454	1.0	0	BE274696.1	EST_HUMAN	601122338F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3346888 5'
2140	7250	12457	1.1	0	7662017	NT	Homo sapiens KIAA0244 protein (KIAA0244), mRNA
2141	7251	12458	3.8	0	AB015610.1	NT	Homo sapiens aethiops mRNA for ribosomal protein S4X, complete cds
2141	7251	12459	3.8	0	AB015610.1	NT	Chlorococcus aethiops mRNA for ribosomal protein S4X, complete cds
2143	7253	12461	0.5	0	7661569	NT	Homo sapiens DKFZ434D156 protein (DKFZ434D156), mRNA
2145	7255		0.9	0	M19828.1	NT	Homo sapiens apolipoprotein B-100 (apoB) gene, exons 22 through 29
2148	7258	12465	6.2	0	Y18552.1	NT	Human apolipoprotein B-100 (apoB) gene, exons 22 through 29
2149	7259	12466	4.1	0	4506648	NT	Homo sapiens HLA-B*08:01 gene
2152	7262	12469	0.9	0	U21556.1	NT	Homo sapiens ribosomal protein L3 (RPL3) mRNA
2152	7262	12470	0.9	0	U21556.1	NT	Homo sapiens ribosomal protein L3 (RPL3) mRNA
2156	7936	12475	0.6	0	AF044962.1	NT	Human membrane protein-like protein mRNA, partial cds

Table 4

2159	7268	12478	0.7	0	BE018750.1	EST_HUMAN	bb54e02.y1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3049082 5' similar to TRQ15170 Q15170 TRANSCRIPTION FACTOR S-II-RELATED PROTEIN ;
							zk53c07.s1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:486540 3' similar to gb:X65857_cds1 OLFACTORY RECEPTOR-LIKE PROTEIN HGMPO7E (HUMAN);
2160	7269	12479	0.9	0	AA042813.1	EST_HUMAN	zk53c07.s1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:486540 3' similar to gb:X65857_cds1 OLFACTORY RECEPTOR-LIKE PROTEIN HGMPO7E (HUMAN);
2160	7269	12480	0.9	0	AA042813.1	EST_HUMAN	zk53c07.s1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:486540 3' similar to gb:X65857_cds1 OLFACTORY RECEPTOR-LIKE PROTEIN HGMPO7E (HUMAN);
2168	7277	12488	0.8	0	AL163204.2	NT	Homo sapiens chromosome 21 segment HS21C004
2168	7277	12489	0.8	0	AL163204.2	NT	Homo sapiens chromosome 21 segment HS21C004
2169	7278	12490	1.0	0	7662401	NT	Homo sapiens KIAA0952 protein (KIAA0952), mRNA
2169	7278	12491	1.0	0	7662401	NT	Homo sapiens KIAA0952 protein (KIAA0952), mRNA
2174	7283	12491	1.0	0	U36264.1	NT	Human beta-prime-adaptin (BAM22) gene, exon 16
2183	7302	12516	2.7	0	4557556	NT	Homo sapiens E1A binding protein p300 (EP300) mRNA
2189	7308	12520	0.5	0	7662401	NT	Homo sapiens KIAA0952 protein (KIAA0952), mRNA
2206	7315	12528	1.1	0	AB023195.1	NT	Homo sapiens mRNA for KIAA0978 protein, partial cds
2208	7318	12531	0.9	0	7661965	NT	Homo sapiens KIAA0170 gene product (KIAA0170), mRNA
2209	7318	12532	0.9	0	7661965	NT	Homo sapiens KIAA0170 gene product (KIAA0170), mRNA
2212	7320	12534	1.4	0	AB037784.1	NT	Homo sapiens mRNA for KIAA1363 protein, partial cds
2254	7360	12568	0.9	0	A1076404.1	EST_HUMAN	oz08c07.x1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1674828 3'
2256	7362	12570	0.8	0	AAA29001.1	EST_HUMAN	zy78a11.r1 Soares_total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:759740 5'
2256	7362	12571	0.8	0	AAA29001.1	EST_HUMAN	zy78a11.r1 Soares_total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:759740 5'
2258	7364	12573	0.8	0	AJ010230.1	NT	Homo sapiens RET finger protein-like 1 antisense transcript, partial
2263	7369	12579	1.2	0	4826783	NT	Homo sapiens potassium voltage-gated channel, Shab-related subfamily, member 1 (KCNB1) mRNA
2264	7370	12580	0.7	0	6325466	NT	Homo sapiens flavin containing monooxygenase 3 (FMO3), mRNA
2271	7377	12586	1.0	0	AI347926.1	EST_HUMAN	qp60f09.x1 NCI_CGAP_C08 Homo sapiens cDNA clone IMAGE:1927433 3'
2274	7380	12588	3.7	0	AF044571.1	NT	Homo sapiens phosphotyrosine kinase alpha subunit (PHKA2) gene, exon 32
2275	7381	12589	1.0	0	AI625542.1	EST_HUMAN	ly57c08.x1 NCI_CGAP_U12 Homo sapiens cDNA clone IMAGE:2283182 3'
2280	7386	12593	0.6	0	5803178	NT	Homo sapiens sperm specific antigen 2 (SSFA2), mRNA
2280	7386	12594	0.6	0	5803178	NT	Homo sapiens sperm specific antigen 2 (SSFA2), mRNA
2291	7395	12604	1.5	0	AF058332.1	NT	Homo sapiens titin (TTN) gene, alternative splice products, partial cds
2291	7395	12605	1.5	0	AF058332.1	NT	Homo sapiens titin (TTN) gene, alternative splice products, partial cds
2300	7404	12611	1.0	0	5174678	NT	Homo sapiens signal regulatory protein, beta, 1 (SIRP-BETA-1) mRNA
2304	7407	12615	0.6	0	AF246302.1	NT	Homo sapiens peroxisome proliferative activated receptor delta (PPARD) gene, exons 7 and 8
2305	7408		2.1	0	4506598	NT	Homo sapiens ribosomal protein L12 (RPL12) mRNA
2306	7409	12616	1.0	0	AW867076.1	EST_HUMAN	MR1-SN0033-120400-002-a04 SN0033 Homo sapiens cDNA

Table 4

2307	7410	12617	0.7	0	7662017	NT	Homo sapiens KIAA0244 protein (KIAA0244), mRNA
2308	7411	12618	0.5	0	4758497	NT	Homo sapiens hexose-6-phosphate dehydrogenase (glucose 1-dehydrogenase) (H6PD), mRNA
2308	7411	12619	0.5	0	4758497	NT	Homo sapiens hexose-6-phosphate dehydrogenase (glucose 1-dehydrogenase) (H6PD), mRNA
2310	7413	12620	2.7	0	4505332	NT	Homo sapiens nuclear autoantigenic sperm protein (histone-binding) (NASP) mRNA
2310	7413	12621	2.7	0	4505332	NT	Homo sapiens nuclear autoantigenic sperm protein (histone-binding) (NASP) mRNA
2310	7413	12622	2.7	0	4505332	NT	Homo sapiens nuclear autoantigenic sperm protein (histone-binding) (NASP) mRNA
2327	7430		1.0	0	8922550	NT	Homo sapiens phosphatidylinositol 4-kinase 230 (p4K230) mRNA, complete cds
2366	7468		1.3	0	AF012872.1	NT	Homo sapiens phosphatidylinositol 4-kinase 230 (p4K230) mRNA, complete cds
2369	7471	12673	1.0	0	AW303998.1	EST_HUMAN	ix1507.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2813221 3' similar to TR:054924 EX084.1
2382	7484		0.6	0	AF056332.1	NT	Homo sapiens AK2B processed pseudogene
2386	7487	12690	2.0	0	6006002	NT	Homo sapiens glutamate receptor, ionotropic, N-methyl D-aspartate 2A (GRIN2A) mRNA
2390	7490	12694	0.9	0	D85606.1	NT	Homo sapiens gene for cholesteryl/cholesterol type-A receptor, complete cds
2390	7490	12695	0.9	0	D85606.1	NT	Homo sapiens gene for cholesteryl/cholesterol type-A receptor, complete cds
2398	7488	12704	0.8	0	AF106275.1	NT	Homo sapiens immunoglobulin-like transcript 1c variant 4 (ILT11c) gene, exon 6
2410	7509	12717	1.4	0	5129777	NT	Homo sapiens collagen, type XII, alpha 1 (COL12A1), mRNA
2414	7513	12720	0.9	0	4507280	NT	Homo sapiens serine/threonine kinase 9 (STK9) mRNA
2414	7513	12721	0.9	0	4507280	NT	Homo sapiens serine/threonine kinase 9 (STK9) mRNA
2419	7518	12725	0.8	0	4557887	NT	Homo sapiens keratin 18 (KRT18) mRNA
2428	7527	12733	1.0	0	AW466922.1	EST_HUMAN	Homo sapiens keratin 18 (KRT18) mRNA
2430	7529	12734	1.3	0	AW501010.1	EST_HUMAN	Homo sapiens keratin 18 (KRT18) mRNA
2444	7543	12751	0.8	0	5453965	NT	U1-HF-BF0p-als-c-07-0-U1.r1 NIH_MGC_51 Homo sapiens cDNA clone IMAGE:3072780 5'
2444	7543	12752	0.8	0	5453965	NT	U1-HF-BF0p-als-c-07-0-U1.r1 NIH_MGC_51 Homo sapiens cDNA clone IMAGE:3072780 5'
2457	7556		0.9	0	AW613853.1	EST_HUMAN	Homo sapiens protein kinase, AMP-activated, alpha 2 catalytic subunit (PRKAA2) mRNA
2462	7561	12765	5.8	0	4506744	NT	Homo sapiens protein kinase, AMP-activated, alpha 2 catalytic subunit (PRKAA2) mRNA
2463	7014	12203	1.2	0	7657038	NT	Homo sapiens protein kinase, AMP-activated, alpha 2 catalytic subunit (PRKAA2) mRNA
2467	7565	12768	0.8	0	Z32684.2	NT	Homo sapiens death receptor 6 (DR6), mRNA
2469	7567		2.0	0	5453871	NT	Homo sapiens death receptor 6 (DR6), mRNA
2471	7569	12771	0.7	0	AF058953.1	NT	Homo sapiens mRNA for membrane transport protein (XK gene)
2472	7570	12772	0.7	0	7657468	NT	Homo sapiens platelet-derived growth factor receptor-like (PDGFR) mRNA
2473	7571	12773	20.0	0	4507720	NT	Homo sapiens ATP-specific succinyl-CoA synthetase beta subunit (SCS) mRNA, partial cds
2474	7572	12774	1.1	0	8923340	NT	Homo sapiens similar to rat integral membrane glycoprotein POM121 (POM121L1), mRNA
2475	7573	12775	1.2	0	4507524	NT	Homo sapiens titin (TTN) mRNA
							Homo sapiens hypothetical protein FLJ20366 (FLJ20366), mRNA
							Homo sapiens hypothetical protein FLJ20366 (FLJ20366), mRNA
							Homo sapiens translocation protein 1 (TLOC1) mRNA

Table 4

2481	7579	12781	0.6	0	8051635	NT	Homo sapiens exportin, tRNA (nuclear export receptor for tRNAs) (XPOT), mRNA
2486	7583	12787	1.6	0	AI804747.1	EST_HUMAN	luc2c11.x1 NCI_CGAP_P128 Homo sapiens cDNA clone IMAGE:2253716 3' similar to contains element MSR1 repetitive element:
2486	7583	12788	1.6	0	AI804747.1	EST_HUMAN	luc2c11.x1 NCI_CGAP_P128 Homo sapiens cDNA clone IMAGE:2253716 3' similar to contains element MSR1 repetitive element:
2488	7585	12791	1.0	0	AW888221.1	EST_HUMAN	MXRA5 Human matrix remodeling associated gene 5 similar to MXRA5 Matrix remodeling associated gene 5
2509	7605	12806	1.4	0	4557336	NT	Homo sapiens argininosuccinate synthetase (ASS), mRNA
2509	7605	12807	1.4	0	4557338	NT	Homo sapiens argininosuccinate synthetase (ASS), mRNA
2510	7606	12808	1.2	0	4506402	NT	Homo sapiens retinoic acid induced 3 (RAI3) mRNA
2510	7606	12809	1.2	0	4506402	NT	Homo sapiens retinoic acid induced 3 (RAI3) mRNA
2511	7607	12810	1.0	0	AW589700.1	EST_HUMAN	Hg19e07.x1 NCI_CGAP_G08 Homo sapiens cDNA clone IMAGE:2946084 3' similar to TR:O00246 O00246 HYPOTHETICAL 9.3 KD PROTEIN:
2514	7610	12812	2.8	0	AW937782.1	EST_HUMAN	QV3-DT0045-140200-082-e11 DT0045 Homo sapiens cDNA
2540	7636	12836	1.1	0	BE296613.1	EST_HUMAN	601173631F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3529159 5'
2553	7876	12850	0.9	0	AB037836.1	NT	Homo sapiens mRNA for KIAA1415 protein, partial cds
2553	7876	12851	0.9	0	AB037836.1	NT	Homo sapiens mRNA for KIAA1415 protein, partial cds
2554	7876	12851	1.4	0	BE084725.1	EST_HUMAN	MR0-BT0659-280200-003-c06 BT0659 Homo sapiens cDNA
2560	7654	12857	1.0	0	8923955	NT	Homo sapiens PC326 protein (PC326), mRNA
2562	7656	12857	1.2	0	4504866	NT	Homo sapiens ring finger protein (C3HC4 type) 8 (RNF8), mRNA
2569	7662	12864	1.3	0	AB037742.1	NT	Homo sapiens mRNA for KIAA1321 protein, partial cds
2570	7663	12865	1.0	0	AI571737.1	EST_HUMAN	Homo sapiens mRNA for KIAA1321 protein, partial cds
2571	7664	12866	0.8	0	5032150	NT	(TAF2) mRNA
2573	7666	12868	2.1	0	AB037859.1	NT	Homo sapiens MSH5 gene, partial cds; and CLIC1, DDAD, G6b, G6c, G6d, G6e, G6f, BAT5, G5b, CSK2B, BAT4, G4, Apo M, BAT3, BAT2, AIF-1, 1C7, LST-1, LTB, TNF, and LTA genes, complete cds
2574	7667	12869	1.0	0	AF129756.1	NT	Homo sapiens MSH5 gene, partial cds; and CLIC1, DDAD, G6b, G6c, G6d, G6e, G6f, BAT5, G5b, CSK2B, BAT4, G4, Apo M, BAT3, BAT2, AIF-1, 1C7, LST-1, LTB, TNF, and LTA genes, complete cds
2574	7667	12870	1.0	0	AF129756.1	NT	Homo sapiens MSH5 gene, partial cds; and CLIC1, DDAD, G6b, G6c, G6d, G6e, G6f, BAT5, G5b, CSK2B, BAT4, G4, Apo M, BAT3, BAT2, AIF-1, 1C7, LST-1, LTB, TNF, and LTA genes, complete cds
2577	7670	12871	1.1	0	BE293328.1	EST_HUMAN	601143722F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:3051389 5'
2585	7678	12890	3.8	0	L19185.1	NT	Human natural killer cell enhancing factor (NKEFB) mRNA, complete cds
2595	7687	12890	0.9	0	4504686	NT	Homo sapiens IMP (inosine monophosphate) dehydrogenase 1 (IMPDH1) mRNA
2601	7949	12897	2.5	0	4507720	NT	Homo sapiens tlin (TTN) mRNA
2606	7698	12901	1.1	0	U78027.1	NT	Homo sapiens Bruton's tyrosine kinase (BTK), alpha-D-galactosidase A (GLA), L44-like ribosomal protein (L44L) and F1P3 (F1P3) genes, complete cds
2609	7699	12901	1.9	0	AF173227.1	NT	Homo sapiens guanylate cyclase-activating protein 2 (GUCA1B) gene, exon 1
2613	7703	12902	1.2	0	AB011108.1	NT	Homo sapiens mRNA for KIAA0536 protein, partial cds

Table 4

2616	7706	12905	1.0	0	AB002289.1	NT	Human mRNA for KIAA0301 gene, partial cds
2617	7707	12906	0.5	0	45022442	NT	Homo sapiens bullous pemphigoid antigen 1 (230/240K) (BPAG1) mRNA
2619	7709	12908	1.2	0	U22377.1	NT	Homo sapiens related zinc finger protein (rf) mRNA, complete cds
2619	7709	12909	1.2	0	U22377.1	NT	Human Zn-15 related zinc finger protein (rf) mRNA, complete cds
2622	7712	12912	1.3	0	AA987015.1	EST_HUMAN	RC1-OT0086-220300-011-d07 OT0086 Homo sapiens cDNA
2626	7716	12917	1.0	0	AA994842.1	EST_HUMAN	ous8e08.s1 NCI CGAP B2 Homo sapiens cDNA clone IMAGE:1632038 3'
2627	7717	12918	1.2	0	AF265208.1	NT	Homo sapiens SWI-SNF complex protein p270 mRNA, partial cds
2628	7718	12918	1.0	0	7662223	NT	Homo sapiens KIAA0649 gene product (KIAA0649) mRNA
2656	7745	12945	0.6	0	8922843	NT	Homo sapiens hypothetical protein FLJ11052 (FLJ11052) mRNA
2690	7777		3.2	0	AA316723.1	EST_HUMAN	EST188414 HCC cell line (metastasis to liver in mouse) II Homo sapiens cDNA 5' end similar to ribosomal protein L29
2691	7778	12975	0.9	0	J03537.1	NT	Human ribosomal protein S6 mRNA, complete cds
2698	7784	12984	1.3	0	U36253.1	NT	Human beta-prime-adaptin (BAP22) gene, exon 5
2700	7786	12986	1.1	0	7669517	NT	Homo sapiens neuregulin 1 (NRG1) transcript variant SMDF, mRNA
2701	7787	12987	3.7	0	AF110763.1	NT	Homo sapiens skeletal muscle LIM-protein 1 (FHL1) gene, complete cds
2708	7793	12994	10.4	0	Y00052.1	NT	Human mRNA for T-cell cyclophilin
2709	7794	12995	3.2	0	T07303.1	EST_HUMAN	EST05192 Fetal brain, Striatogene (cat#836206) Homo sapiens cDNA clone HFBEG84 similar to Ring canal protein
2712	7853	12999	13.5	0	4506696	NT	Homo sapiens ribosomal protein S20 (RPS20) mRNA
2713	7797		1.3	0	AI065139.1	EST_HUMAN	HA0977 Human fetal liver cDNA library Homo sapiens cDNA
2715	7799	13002	0.8	0	5174486	NT	Homo sapiens spermatogenesis associated PD1 (KIAA0757) mRNA
2715	7799	13003	0.8	0	5174486	NT	Homo sapiens spermatogenesis associated PD1 (KIAA0757) mRNA
2716	7800	13004	0.9	0	8923441	NT	Homo sapiens hypothetical protein FLJ20477 (FLJ20477) mRNA
2716	7800	13005	0.9	0	8923441	NT	Homo sapiens hypothetical protein FLJ20477 (FLJ20477) mRNA
2717	7801	13006	0.8	0	7661839	NT	Homo sapiens HT002 protein (HT002) mRNA
2718	7802		5.7	0	M11147.1	NT	Human fertilin L chain mRNA, complete cds
2719	7803	13007	0.6	0	U21556.1	NT	Human membrane protein-like protein mRNA, partial cds
2719	7803	13008	0.6	0	U21556.1	NT	Human membrane protein-like protein mRNA, partial cds
2723	7807	13011	1.2	0	4757863	NT	Homo sapiens cerebellar degeneration-related protein (34KD) (CDR1) mRNA
2723	7807	13012	1.2	0	4757863	NT	Homo sapiens cerebellar degeneration-related protein (34KD) (CDR1) mRNA
2727	7811	13017	0.8	0	4504918	NT	Homo sapiens keratin 8 (KRT8) mRNA
2730	7814	13020	1.0	0	BE176836.1	EST_HUMAN	RC4-HT0587-170300-012-d11 HT0587 Homo sapiens cDNA
2741	7825		1.3	0	AL163201.2	NT	Homo sapiens chromosome 21 segment HS21C001
2742	7826	13030	1.3	0	DG3879.1	NT	Human mRNA for KIAA0156 gene, complete cds
2748	7832		1.1	0	4503098	NT	Homo sapiens chondroitin sulfate proteoglycan 4 (melanoma-associated) (CSPG4) mRNA
2758	7842	13045	0.6	0	7427522	NT	Homo sapiens protein tyrosine phosphatase, receptor type, T (PTPRT) mRNA
2761	7845	13047	3.5	0	AA90647.1	EST_HUMAN	aa01g04.t1 Soares_NihMPu.S1 Homo sapiens cDNA clone IMAGE:812022 5' similar to SW:ZN22_HUMAN P17026 ZINC FINGER PROTEIN 22 : contains element LTR6 repetitive element :

Table 4

2761	7845	13048	3.5	0	AA490647.1	EST_HUMAN	aa01g04.t1 Scores_NIHMPu_S1 Homo sapiens cDNA clone IMAGE:812022 5' similar to SW:ZN22_HUMAN P-17026 ZINC FINGER PROTEIN 22 :contains element LTR6 repetitive element;
2763	7847		4.0	0	6912633	NT	Homo sapiens ribosomal protein L13a (RPL13A) mRNA
2766	7850	13053	0.7	0	AF036943.1	NT	Homo sapiens myelin transcription factor 1-like (MTF1-L) mRNA, complete cds
2767	7851	13054	1.1	0	4504918	NT	Homo sapiens keratin 8 (KRT8) mRNA
2769	7853	13055	1.1	0	AW505486.1	EST_HUMAN	U1-HF-8N0-amb-d-02-0-U1.t1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3081626 5'
2769	7853	13056	1.1	0	AW505486.1	EST_HUMAN	U1-HF-8N0-amb-d-02-0-U1.t1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3081626 5'
2770	7854	13057	3.7	0	4506648	NT	Homo sapiens ribosomal protein L3 (RPL3) mRNA
2770	7854	13058	3.7	0	4506648	NT	Homo sapiens ribosomal protein L3 (RPL3) mRNA
2775	5373	10498	1.6	0	576830.1	NT	glycoprotein D-Duffy group antigen [human, blood, Genomic DNA, 3068 nt]
2778	7860		0.7	0	AB033281.1	NT	Homo sapiens BTBRCP2 mRNA for F-box and WD-repeats protein isoform C, complete cds
2784	5871	11011	1.4	0	AF264750.1	NT	Homo sapiens ALR-like protein mRNA, partial cds
2784	5871	11012	1.4	0	AF264750.1	NT	Homo sapiens ALR-like protein mRNA, partial cds
2789	6163	11316	1.2	0	4503202	NT	Homo sapiens cytochrome P450, subfamily 1 (dioxin-inducible), polypeptide 1 (glaucoma 3, primary infantile) (CYP1B1) mRNA
2789	6163	11317	1.2	0	4503202	NT	Homo sapiens cytochrome P450, subfamily 1 (dioxin-inducible), polypeptide 1 (glaucoma 3, primary infantile) (CYP1B1) mRNA
2805	7857	13066	2.4	0	X85980.1	NT	H. sapiens serine hydroxymethyltransferase pseudogene
2806	7956		1.3	0	AF068624.1	NT	Homo sapiens 5-aminolevulinic synthase 2 (ALAS2) gene, complete cds
2808	7960		1.1	0	AB040960.1	NT	Homo sapiens mRNA for KIAA1527 protein, partial cds
2814	7965		1.1	0	AJ238852.1	NT	Homo sapiens partial rp13 gene for ribosomal protein L3, U82 snoRNA, U83a snoRNA and U83b snoRNA genes
2815	7966	13070	2.2	0	AL163201.2	NT	Homo sapiens chromosome 21 segment HS21C001
2819	7970	13073	5.9	0	M80802.1	NT	Human AHNK nucleoprotein mRNA, 5' end
2822	7973	13075	1.6	0	BE154504.1	EST_HUMAN	PMO-HT0343-281299-003-e02 HT0343 Homo sapiens cDNA
2822	7973	13076	1.6	0	BE154504.1	EST_HUMAN	PMO-HT0343-281299-003-e02 HT0343 Homo sapiens cDNA
2824	7975		1.4	0	X73426.1	NT	H. sapiens lcl3 gene for HLH type transcription factor
2826	7977		2.8	0	AL163268.2	NT	Homo sapiens chromosome 21 segment HS21C068
2826	7979	13079	2.6	0	M98478.1	NT	Human transglutininase mRNA, complete cds
2833	7984	13083	4.5	0	D50657.1	NT	Homo sapiens gamma-cytoplasmic actin (ACTGP3) pseudogene
2833	7984	13084	4.5	0	D50657.1	NT	Homo sapiens gamma-cytoplasmic actin (ACTGP3) pseudogene
2837	7988	13087	1.3	0	AL08657.1	NT	Novel human mRNA from chromosome 1, which has similarities to BAT2 genes
2838	7989		4.6	0	Y10658.1	NT	H. sapiens mRNA for nuclear DNA helicase II
2838	7990		1.0	0	AF152303.1	NT	Homo sapiens protocadherin alpha C1 (PCDH-alpha-C1) mRNA, complete cds
2840	7991	13088	25.1	0	4503470	NT	Homo sapiens eukaryotic translation elongation factor 1 alpha 1 (EEF1A1) mRNA
2840	7991	13089	25.1	0	4503470	NT	Homo sapiens eukaryotic translation elongation factor 1 alpha 1 (EEF1A1) mRNA
2851	8002	13100	2.4	0	4507280	NT	Homo sapiens serine/threonine kinase 9 (STK9) mRNA

Table 4

2854	8005	13104	1.4	0	AL047589.1	EST_HUMAN	DKFZ586G0621_r1 586 (synonym: hute1) Homo sapiens cDNA clone DKFZ586G0621
2855	8006	13105	1.3	0	7681883	NT	Homo sapiens KIAA0054 gene product; Helicase (KIAA0054). mRNA
2855	8006	13106	1.3	0	7661883	NT	Homo sapiens KIAA0054 gene product; Helicase (KIAA0054). mRNA
2856	8007		3.4	0	4503098	NT	Homo sapiens chondroitin sulfate proteoglycan 4 (melanoma-associated) (CSPG4). mRNA
2856	8009	13108	5.0	0	BE081896.1	EST_HUMAN	QV2-BT0636-130400-136403 BT0636 Homo sapiens cDNA
2858	8009	13109	5.0	0	BE081896.1	EST_HUMAN	QV2-BT0636-130400-136403 BT0636 Homo sapiens cDNA
2866	8017	13120	1.6	0	AL163206.2	NT	Homo sapiens chromosome 21 segment HS21C006
2866	8017	13121	1.6	0	AL163206.2	NT	Homo sapiens chromosome 21 segment HS21C006
2867	8018	13122	1.1	0	AA215579.1	EST_HUMAN	z66b11.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:683517 3' similar to contains Alu repetitive element;
2874	8025		3.1	0	Y19210.1	NT	Homo sapiens hrb5 gene for hair keratin, exons 1 to 9
2877	8028	13131	1.2	0	4758279	NT	Homo sapiens EphA4 (EPHA4) mRNA
2878	8029	13132	18.7	0	4503470	NT	Homo sapiens eukaryotic translation elongation factor 1 alpha 1 (EEF1A1) mRNA
2879	8030	13133	1.3	0	AI561002.1	EST_HUMAN	tr18d07.x1 NCI_CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2167981 3' similar to tr18d07.x1 NCI_CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2167981 3' similar to
2879	8030	13134	1.3	0	AI561002.1	EST_HUMAN	tr18d07.x1 NCI_CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2167981 3' similar to
2881	8032	13136	1.9	0	P52740	SWISSPROT	TR-O16247 O16247_F44E7.2 PROTEIN. ;
2882	8033	13137	1.5	0	AF152338.1	NT	ZINC FINGER PROTEIN 132
2887	8048	13149	1.3	0	AB033093.1	NT	Homo sapiens protocadherin gamma C4 (PCDH-gamma-C4) mRNA, complete cds
2887	8048	13150	1.3	0	AB033093.1	NT	Homo sapiens mRNA for KIAA1267 protein, partial cds
2888	8049	13151	5.0	0	AB040841.1	NT	Homo sapiens mRNA for KIAA1508 protein, partial cds
2888	8049	13152	5.0	0	AB040841.1	NT	Homo sapiens mRNA for KIAA1508 protein, partial cds
2901	8052	13155	2.7	0	7661903	NT	Homo sapiens KIAA0100 gene product (KIAA0100). mRNA
2901	8052	13156	2.7	0	7661903	NT	Homo sapiens KIAA0100 gene product (KIAA0100). mRNA
2902	8053	13157	3.2	0	5174574	NT	Homo sapiens myeloid/lymphoid or mixed-lineage leukemia (t(11;16)(p13;p11) homology); translocated to, 4 (MLLT4) mRNA
2902	8053	13158	3.2	0	5174574	NT	Homo sapiens myeloid/lymphoid or mixed-lineage leukemia (t(11;16)(p13;p11) homology); translocated to, 4 (MLLT4) mRNA
2915	8066	13174	2.0	0	4505084	NT	Homo sapiens melanoma antigen, family B, 4 (MAGEB4). mRNA
2915	8066	13175	2.0	0	4505084	NT	Homo sapiens melanoma antigen, family B, 4 (MAGEB4). mRNA
2917	8068	13177	0.9	0	4885214	NT	Homo sapiens v-erb-a avian erythroblastic leukemia viral oncogene homolog-like 4 (ERBB4) mRNA
2917	8068	13178	0.9	0	4885214	NT	Homo sapiens v-erb-a avian erythroblastic leukemia viral oncogene homolog-like 4 (ERBB4) mRNA
2924	8075	13183	1.6	0	4758827	NT	Homo sapiens neuroligin III (NRLN3) mRNA
2927	8078	13186	1.3	0	X15309.1	NT	H.sapiens NF-H gene, exon 4
2927	8078	13187	1.3	0	X15309.1	NT	H.sapiens NF-H gene, exon 4
2929	8080	13189	7.9	0	AF108275.1	NT	Homo sapiens immunoglobulin-like transcript 1c variant 4 (ILT1c) gene, exon 6

Table 4

2843	8094	1.1	0	AI149880.1	EST_HUMAN	q14309.x1 Soares testis NIH Homo sapiens cDNA clone IMAGE:1752809.3'
2853	8104	1.0	0	4506118	NT	Homo sapiens prospero-related homeobox 1 (PROX1) mRNA
2854	8105	2.2	0	AB004884.1	NT	Homo sapiens mRNA for PKU-alpha, partial cds
2864	8115	1.3	0	7662223	NT	Homo sapiens KIAA0737 gene product (KIAA0737), mRNA
2865	8116	1.6	0	5729755	NT	Homo sapiens calcium channel, voltage-dependent, gamma subunit 3 (CACNG3), mRNA
2865	8116	1.6	0	5729755	NT	Homo sapiens calcium channel, voltage-dependent, gamma subunit 3 (CACNG3), mRNA
2890	8142	0.9	0	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
2892	8144	1.0	0	M74099.1	NT	Human displacement protein (CCAT) mRNA
3001	8153	0.8	0	4506882	NT	Homo sapiens semangelin I (SEMG1) mRNA
3009	8161	7.9	0	5579469	NT	Homo sapiens heat shock 70KD protein 1 (HSPA1A), mRNA
3009	8161	7.9	0	5579469	NT	Homo sapiens heat shock 70KD protein 1 (HSPA1A), mRNA
3011	8163	5.1	0	AL359403.1	NT	isoform 2 of a novel human mRNA from chromosome 22
3014	8166	2.0	0	AF017433.1	NT	Homo sapiens putative transcription factor CR53 (CR53) mRNA, partial cds
3017	8169	1.7	0	AF196779.1	NT	Homo sapiens transcription factor IGHM enhancer 3, JM11 protein, JM4 protein, T54 protein, JM10 protein, A4 differentiation-dependent protein, triple LIM domain protein 6, and synapophysin genes, complete cds; and L-type calcium channel a2
3019	8171	1.0	0	4504664	NT	Homo sapiens Interleukin 2 receptor, beta (IL2RB) mRNA
3038	8190	2.8	0	X03529.1	NT	Human germiline gene 16.1 for Ig lambda L-chain C region (Ig-LC16.1)
3043	8194	1.9	0	AF199355.1	NT	Homo sapiens F-box protein FBL5 (FBL5) mRNA, complete cds
3047	8198	1.9	0	AF064589.1	NT	Homo sapiens melanoma-associated antigen (MAGE-C1) gene, complete cds
3068	8219	2.9	0	AF265208.1	NT	Homo sapiens SWI-SNF complex protein p270 mRNA, partial cds
3069	8220	4.0	0	AF149773.1	NT	Homo sapiens NOD1 protein (NOD1) gene, exons 1, 2, and 3
3074	8225	4.2	0	7662139	NT	Homo sapiens KIAA0469 gene product (KIAA0469), mRNA
3075	8226	1.6	0	AF042075.1	NT	Homo sapiens olfactory receptor-like protein (OLFR 42B) gene, OLFR 42B-9110 allele, partial cds
3102	8252	3.5	0	4826763	NT	Homo sapiens potassium voltage-gated channel, Shab-related subfamily, member 1 (KCNB1) mRNA
3111	8260	19.6	0	L20941.1	NT	Human ferritin heavy chain mRNA, complete cds
3115	8264	1.8	0	AB011121.1	NT	Homo sapiens mRNA for KIAA0549 protein, partial cds
3115	8264	1.8	0	AB011121.1	NT	Homo sapiens mRNA for KIAA0549 protein, partial cds
3123	8272	9.4	0	T94870.1	EST_HUMAN	yo32f03.s1 Striatogene lung (8937210) Homo sapiens cDNA clone IMAGE:119453.3 similar to SP-S29539 S29539 BASIC PROTEIN, 23K -
3140	8289	1.0	0	A1968086.1	EST_HUMAN	wu12h10x1 NCI CGAP GC6 Homo sapiens cDNA clone IMAGE:2516803.3'
3145	8284	4.0	0	X98922.1	NT	H.sapiens mRNA for gamma-glutamyltransferase
3145	8284	4.0	0	X98922.1	NT	H.sapiens mRNA for gamma-glutamyltransferase
3156	8305	1.5	0	4758827	NT	Homo sapiens neurexin III (NRXN3) mRNA
3156	8305	1.5	0	4758827	NT	Homo sapiens neurexin III (NRXN3) mRNA
3163	8312	7.7	0	4504659	NT	Homo sapiens interleukin 1 receptor, type I (IL1R1) mRNA



Table 4

3184	8313	13425	3.3	0	4507720	NT	Homo sapiens titin (TTN) mRNA
3184	8313	13426	3.3	0	4507720	NT	Homo sapiens titin (TTN) mRNA
3180	8329	13442	2.4	0	M28699.1	NT	Homo sapiens nucleolar phosphoprotein B23 (NPM1) mRNA, complete cds
							Homo sapiens solute carrier family 25 (mitochondrial carrier, adenine nucleotide translocator), member 5 (SLC25A5), nuclear gene encoding mitochondrial protein, mRNA
3183	8332	13444	2.2	0	4502098	NT	
3188	8337	13450	0.8	0	4756055	NT	Homo sapiens CREB binding protein (Rubinstein-Taybi syndrome) (CREBBP) mRNA
3188	8337	13451	0.8	0	4756055	NT	Homo sapiens CREB binding protein (Rubinstein-Taybi syndrome) (CREBBP) mRNA
3190	8339	13452	26.3	0	AA774783.1	EST_HUMAN	ae87b11.s1 Striatogene schizo brain S11 Homo sapiens cDNA clone IMAGE:971133 3'
3210	8358	13467	1.6	0	4557590	NT	Homo sapiens fibrillin 1 (Marfan syndrome) (FBN1) mRNA
3215	8363	13474	3.4	0	4507720	NT	Homo sapiens titin (TTN) mRNA
3224	8372		4.4	0	M65189.1	NT	Homo sapiens 43 processed pseudogene
							Human connexin 43 processed pseudogene
3225	8373	13481	1.2	0	AF019413.1	NT	Homo sapiens FLA class III region containing tenascin X (tenascin-X) gene, partial cds; cytochrome P450 21-hydroxylase (CYP21B), complement component C4 (C4B) G11, helicase (SKI2W), RD, complement factor B (Bf), and complement component C2 (C2) genes>
3227	8375	13483	4.2	0	AF055084.1	NT	Homo sapiens very large G-protein coupled receptor-1 (VLGR1) mRNA, complete cds
3237	10264	13491	3.5	0	4502014	NT	Homo sapiens A kinase (PRKA) anchor protein 1 (AKAP1), mRNA
3237	10264	13492	3.5	0	4502014	NT	Homo sapiens A kinase (PRKA) anchor protein 1 (AKAP1), mRNA
3252	8399	13505	2.0	0	AF266208.1	NT	Homo sapiens SWI-SNF complex protein p270 mRNA, partial cds
3253	8400	13506	0.9	0	8923624	NT	Homo sapiens hypothetical protein FLJ20695 (FLJ20695), mRNA
							Homo sapiens hypothetical protein FLJ20695 (FLJ20695), mRNA
3282	8427	13535	4.9	0	A1589294.1	EST_HUMAN	ts5808.x2 NCL CGAP_Pant1 Homo sapiens cDNA clone IMAGE:222535 3' similar to SW:RL11_RAT P25121 60S RIBOSOMAL PROTEIN L11, contains Alu repetitive element;
3289	8435	13543	3.0	0	AF128893.1	NT	Homo sapiens telomerase reverse transcriptase (TERT) gene, exons 1-6
3289	8435	13544	3.0	0	AF128893.1	NT	Homo sapiens telomerase reverse transcriptase (TERT) gene, exons 1-6
3289	8435	13544	3.0	0	AF128893.1	NT	Homo sapiens telomerase reverse transcriptase (TERT) gene, exons 1-6
3289	8436	13545	1.0	0	7657213	NT	Homo sapiens hormonally upregulated neu tumor-associated kinase (HUNK), mRNA
3289	8436	13546	1.0	0	7657213	NT	Homo sapiens hormonally upregulated neu tumor-associated kinase (HUNK), mRNA
3292	8436	13547	1.0	0	4502582	NT	Homo sapiens caspase 8, apoptosis-related cysteine protease (CASP8) mRNA
3292	8436	13548	1.0	0	4502582	NT	Homo sapiens caspase 8, apoptosis-related cysteine protease (CASP8) mRNA
3296	8442	13551	11.1	0	AF111163.1	NT	Homo sapiens p70 (MEFV) gene, complete cds
3298	8444	13553	1.0	0	AB040940.1	NT	Homo sapiens mRNA for KIAA1507 protein, partial cds
3357	8500	13608	1.7	0	7363436	NT	Homo sapiens olfactory receptor, family 10, subfamily C, member 1 (OR10C1), mRNA
3357	8500	13609	1.7	0	7363436	NT	Homo sapiens olfactory receptor, family 10, subfamily C, member 1 (OR10C1), mRNA
3360	8503	13611	1.4	0	7706239	NT	Homo sapiens neuroblastoma-amplified protein (LOC51594), mRNA
							Homo sapiens T-type calcium channel alpha1 subunit Alpha1-a isoform (CACNA1a) mRNA, complete cds
3361	8504	13612	1.0	0	AF211189.1	NT	Homo sapiens KIAA0952 protein (KIAA0952), mRNA
3377	8520	13626	1.4	0	7662401	NT	Homo sapiens KIAA0952 protein (KIAA0952), mRNA
3377	8520	13627	1.4	0	7662401	NT	Homo sapiens KIAA0952 protein (KIAA0952), mRNA
3378	8521	13628	1.0	0	4502398	NT	Homo sapiens beaded filament structural protein 1, filensin (BFSP1) mRNA

Table 4

3381	8524	13630	1.7	0	5803067	NT	Homo sapiens leukocyte immunoglobulin-like receptor, subfamily A (with TM domain), member 2 (IL1RAP2), mRNA
3390	7787	12987	6.0	0	AF110763.1	NT	Homo sapiens skeletal muscle LIM-protein 1 (FHL1) gene, complete cds
3395	8537	13643	2.1	0	7657038	NT	Homo sapiens death receptor 6 (DR6), mRNA
3398	8540	13647	1.5	0	AJ272726.1	NT	Homo sapiens mRNA for rapa-2 (rapa gene)
3398	8540	13648	1.5	0	AJ272726.1	NT	Homo sapiens mRNA for rapa-2 (rapa gene)
3400	8542	13650	5.5	0	K02380.1	NT	Bacteriophage P1 replication region including repA, parA, and parB genes and IncA, IncB, and IncC incompatibility determinants
3402	8544	13652	1.2	0	7427522	NT	Homo sapiens protein tyrosine phosphatase, receptor type, T (PTPRT), mRNA
3409	8551	13658	3.7	0	AJ935159.1	EST_HUMAN	wp14d10.x1 NC1_CGAP_Lu19 Homo sapiens cDNA clone IMAGE:2464819 3' similar to TR:073634 073634 NEURAL CELL ADHESION MOLECULE. ;
3409	8551	13658	3.7	0	AJ935159.1	EST_HUMAN	wp14d10.x1 NC1_CGAP_Lu19 Homo sapiens cDNA clone IMAGE:2464819 3' similar to TR:073634 073634 NEURAL CELL ADHESION MOLECULE. ;
3409	8551	13659	3.7	0	AJ935159.1	EST_HUMAN	wp14d10.x1 NC1_CGAP_Lu19 Homo sapiens cDNA clone IMAGE:2464819 3' similar to TR:073634 073634 NEURAL CELL ADHESION MOLECULE. ;
3413	8555	13684	2.7	0	AJ278120.1	NT	Homo sapiens mRNA for putative ankyrin-repeat containing protein (ORF1)
3420	8562	13673	2.9	0	6552332	NT	Homo sapiens v-fos FBJ murine osteosarcoma viral oncogene homolog (FOS), mRNA
3420	8562	13674	2.9	0	6552332	NT	Homo sapiens v-fos FBJ murine osteosarcoma viral oncogene homolog (FOS), mRNA
3426	8568	13680	1.1	0	M14123.1	NT	Human endogenous retrovirus HERV-K10
3431	8573	13685	6.2	0	U43293.1	NT	Human MDS1A (AML1/MDST fusion) mRNA, partial cds
3440	8582	13695	2.1	0	AF045452.1	NT	Homo sapiens cell-line KG1 transcriptional regulatory protein p54 mRNA, complete cds
3440	8582	13696	2.1	0	AF045452.1	NT	Homo sapiens cell-line KG1 transcriptional regulatory protein p54 mRNA, complete cds
3446	8590	13704	1.2	0	AF231922.1	NT	Homo sapiens chromosome 21 unknown mRNA
3455	8596	13707	0.9	0	AA626677.1	EST_HUMAN	ab51f12.r1 Striatogene lung carcinoma 937218 Homo sapiens cDNA clone IMAGE:844367 5'
3455	8596	13708	0.9	0	AA626677.1	EST_HUMAN	ab51f12.r1 Striatogene lung carcinoma 937218 Homo sapiens cDNA clone IMAGE:844367 5'
3455	8596	13709	0.9	0	AA626677.1	EST_HUMAN	ab51f12.r1 Striatogene lung carcinoma 937218 Homo sapiens cDNA clone IMAGE:844367 5'
3458	8599	13712	1.1	0	4508028	NT	Homo sapiens zinc finger protein 45 (a Kruppel-associated box (KRAB) domain polypeptide) (ZNF45) mRNA
3461	8602	13714	2.2	0	BE304791.1	EST_HUMAN	601143853F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:3051373 5'
3461	8602	13715	2.2	0	BE304791.1	EST_HUMAN	601143853F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:3051373 5'
3463	8604	13717	1.4	0	4826795	NT	Homo sapiens potassium voltage-gated channel, Isk-related family, member 2 (KCNE2) mRNA
3470	8611	13723	0.9	0	AJ384007.1	EST_HUMAN	te3sg12.x1 Soares_NHMPu_S1 Homo sapiens cDNA clone IMAGE:2088742 3' similar to TR:000498 000498 MYASTHENIA GRAVIS AUTOANTIGEN GRAVIN ;
3473	8614	13726	1.0	0	M10976.1	NT	Human endogenous retroviral DNA (4-1), complete retroviral segment
3495	8637	13749	0.8	0	4506884	NT	Homo sapiens semangolin II (SEMG2) mRNA
3497	8639	13757	1.3	0	AF078868.1	NT	Homo sapiens homologous yeast-44.2 protein mRNA, complete cds
3505	8647	13757	1.4	0	AL133204.1	NT	Novel human gene mapping to chromosome X
3507	8648	13758	1.0	0	AB040909.1	NT	Homo sapiens mRNA for KIAA1476 protein, partial cds

Table 4

3527	8668	1.0	0	AI081907.1	EST_HUMAN	ox77c11.x1 Soares. NihHMPu_S1 Homo sapiens cDNA clone IMAGE:1662356 3' similar to WP:119B4.4 CE13742.
3528	8670	1.3	0	6325463	NT	Homo sapiens butyrophilin, subfamily 3, member A3 (BTN3A3), mRNA
3533	8674	4.5	0	AW652217.1	EST_HUMAN	CUO-CT0225-230300-169-401 CT0225 Homo sapiens cDNA
3540	8681	1.0	0	AF116846.1	NT	Homo sapiens gamma-glutamylcysteine synthetase (GLCLC) gene, partial cds
3564	8703	1.1	0	4826967	NT	Homo sapiens retinoblastoma-binding protein 2 (RBBP2) mRNA
3566	8705	1.0	0	AW664693.1	EST_HUMAN	h184g01.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2979024 3'
3569	8708	1.1	0	4826763	NT	h184g01.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2979024 3'
3571	8710	1.0	0	7662319	NT	Homo sapiens heparan sulfate (glucosamine) 3-O-sulfotransferase 1 (HS3ST1) mRNA
3578	8717	0.8	0	4557752	NT	Homo sapiens KIAA0806 gene product (KIAA0806), mRNA
3578	8717	0.8	0	4557752	NT	Homo sapiens midline 1 (Opitz/BBB syndrome) (MID1) mRNA
3596	8735	1.5	0	D87327.1	NT	Homo sapiens mRNA for G protein-coupled inward rectifier potassium channel, complete cds
3600	8739	28.7	0	7669491	NT	Homo sapiens glyceraldehyde-3-phosphate dehydrogenase (GAPD), mRNA
3616	8755	4.3	0	AB026542.1	NT	Homo sapiens WAVE2 mRNA for WASP-family protein, complete cds
3619	8758	3.3	0	AF124250.1	NT	Homo sapiens SH2-containing protein Nsp2 mRNA, complete cds
3619	8758	3.3	0	AF124250.1	NT	Homo sapiens SH2-containing protein Nsp2 mRNA, complete cds
3623	8762	1.5	0	AA852743.1	EST_HUMAN	NHTBCae15g09f Normal Human Trabecular Bone Cells Homo sapiens cDNA clone
3623	8762	1.5	0	AA852743.1	EST_HUMAN	NHTBCae15g09f Normal Human Trabecular Bone Cells Homo sapiens cDNA clone
3623	8762	1.5	0	AA852743.1	EST_HUMAN	NHTBCae15g09f Normal Human Trabecular Bone Cells Homo sapiens cDNA clone
3626	8765	2.2	0	AL163204.2	NT	NHTBCae15g09f Normal Human Trabecular Bone Cells Homo sapiens cDNA clone
3626	8765	2.2	0	AL163204.2	NT	NHTBCae15g09f Normal Human Trabecular Bone Cells Homo sapiens cDNA clone
3630	8769	1.8	0	5729928	NT	NHTBCae15g09f Normal Human Trabecular Bone Cells Homo sapiens cDNA clone
3632	8771	1.3	0	AB018339.1	NT	NHTBCae15g09f Normal Human Trabecular Bone Cells Homo sapiens cDNA clone
3645	8784	3.5	0	AW298134.1	EST_HUMAN	U1-H-BWO-als-e-12-0-U1.s1 NCI_CGAP_Sub6 Homo sapiens cDNA clone IMAGE:2733022 3'
3645	8784	3.5	0	AW298134.1	EST_HUMAN	U1-H-BWO-als-e-12-0-U1.s1 NCI_CGAP_Sub6 Homo sapiens cDNA clone IMAGE:2733022 3'
3645	8784	3.5	0	AW298134.1	EST_HUMAN	U1-H-BWO-als-e-12-0-U1.s1 NCI_CGAP_Sub6 Homo sapiens cDNA clone IMAGE:2733022 3'
3645	8784	3.5	0	AW298134.1	EST_HUMAN	U1-H-BWO-als-e-12-0-U1.s1 NCI_CGAP_Sub6 Homo sapiens cDNA clone IMAGE:2733022 3'
3668	8807	1.0	0	AB004630.1	NT	Human gene for Type XIX collagen a1 chain, exon 6
3669	8808	1.0	0	AA463659.1	EST_HUMAN	Human gene for Type XIX collagen a1 chain, exon 6
3677	8816	3.4	0	7657468	NT	Human gene for Type XIX collagen a1 chain, exon 6
3687	8825	0.9	0	AB037836.1	NT	Human gene for Type XIX collagen a1 chain, exon 6
3689	8838	3.9	0	7662183	NT	Human gene for Type XIX collagen a1 chain, exon 6
3701	8840	7.9	0	4506718	NT	Human gene for Type XIX collagen a1 chain, exon 6
3705	8843	1.0	0	7657065	NT	Human gene for Type XIX collagen a1 chain, exon 6
3705	8843	1.0	0	7657065	NT	Human gene for Type XIX collagen a1 chain, exon 6
3746	8884	1.1	0	AF145712.1	NT	Human gene for Type XIX collagen a1 chain, exon 6

Table 4

3747	8885	1.0	0	AF195658.1	NT	Homo sapiens DNA mismatch repair protein (MLH3) gene, complete cds	
3748	8886	13974	2.3	0	AF179733.1	NT	Pan troglodytes olfactory receptor (PTR208) gene, partial cds
3751	8889	13978	1.7	0	7657468	NT	Homo sapiens similar to rat integral membrane glycoprotein POM121 (POM121L1), mRNA
3751	8889	13979	1.7	0	7657468	NT	Homo sapiens similar to rat integral membrane glycoprotein POM121 (POM121L1), mRNA
3752	8890	13980	1.5	0	AF020091.1	NT	Homo sapiens smooth muscle myosin heavy chain SM1 mRNA, alternatively spliced, partial cds
3758	8896	13987	1.1	0	AI377689.1	EST_HUMAN	h62f10.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2091307.3'
3759	8897	1.7	0	AF152496.1	NT	Homo sapiens proteodherin beta 3 (PCDH-beta3) mRNA, complete cds	
3760	8898	13988	4.5	0	4758199	NT	Homo sapiens desmoplakin (DPL, DPLI) (DSP) mRNA
3763	8901	13990	11.7	0	S78685.1	NT	Homo sapiens ATP-sensitive inwardly rectifying K-channel subunit (KCNJ6/IR1) gene, complete cds
3764	8902	13991	2.0	0	7710148	NT	Homo sapiens methyl CpG binding protein 2 (MECP2), mRNA
3765	8903	13992	2.4	0	7662183	NT	Homo sapiens KIAA0569 gene product (KIAA0569), mRNA
3768	8906	13994	1.3	0	AF069601.2	NT	Homo sapiens myosin light chain kinase isoform 2 (MLCK) mRNA, complete cds
3768	8906	13995	1.3	0	AF069601.2	NT	Homo sapiens myosin light chain kinase isoform 2 (MLCK) mRNA, complete cds
3769	8907	13996	2.0	0	4504534	NT	Homo sapiens 5-hydroxytryptamine (serotonin) receptor 1D (HTR1D) mRNA
3773	8910	13999	1.6	0	AL163279.2	NT	Homo sapiens chromosome 21 segment HS21C079
3775	8912	14002	1.1	0	6912735	NT	Homo sapiens transient receptor potential channel 5 (TRPC5), mRNA
3780	8917	14010	5.7	0	4503178	NT	Homo sapiens chromosome X open reading frame 5 (CXORF5) mRNA
3780	8917	14011	5.7	0	4503178	NT	Homo sapiens chromosome X open reading frame 5 (CXORF5) mRNA
3782	8919	14014	3.9	0	U09412.1	NT	Human zinc finger protein ZNF134 mRNA, complete cds
3784	8921	14015	1.6	0	4826783	NT	Homo sapiens potassium voltage-gated channel, Shab-related subfamily, member 1 (KCNB1) mRNA
3787	8924	14018	1.0	0	AF012615.1	NT	Homo sapiens familial mental retardation protein 2 (FMR2) gene, exon 11
3788	8925	14019	1.9	0	4759171	NT	Homo sapiens SC35-interacting protein 1 (SRRP129), mRNA
3790	8927	14021	0.8	0	AF099177.1	NT	Homo sapiens amphiphysin gene, partial cds
3799	8936	14030	2.5	0	AI884727.1	EST_HUMAN	wk01f01.x1 NCI_CGAP_Lym12 Homo sapiens cDNA clone IMAGE:2411065.3' similar to TRC043340 O43340 R28830.2; contains element PTR7 repetitive element;
3802	8939	14034	6.1	0	4506742	NT	Homo sapiens ribosomal protein S8 (RPS8), mRNA
3807	8944	14040	1.4	0	AL040338.1	EST_HUMAN	DKFZp434N0413.1 t1 434 (synonym: hhes3) Homo sapiens cDNA clone DKFZp434N0413.5'
3813	8950	14047	1.0	0	6005887	NT	Homo sapiens AP1 gamma subunit binding protein 1 (AP1GBP1), mRNA
3813	8950	14048	1.0	0	6005887	NT	Homo sapiens AP1 gamma subunit binding protein 1 (AP1GBP1), mRNA
3815	8952	14050	2.5	0	4504138	NT	Homo sapiens glutamate receptor, metabotropic 3 (GRM3) mRNA
3816	8953	1.8	0	0	4505078	NT	Homo sapiens melanoma antigen, family B, 1 (MAGEB1) mRNA
3820	8957	14053	0.9	0	AF149412.1	NT	Homo sapiens HBP1 heparin-binding and FGF-binding protein gene, complete cds
3830	8967	14066	1.3	0	4506758	NT	Homo sapiens ryanodine receptor 3 (RYR3) mRNA
3833	8970	14069	1.6	0	4585642	NT	Homo sapiens zinc finger protein (KIAA0412) mRNA

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Table 4

4032	9160	14243	1.1	0	8922391	NT	Homo sapiens hypothetical protein FLJ10379 (FLJ10379). mRNA
4032	9160	14244	1.1	0	8922391	NT	Homo sapiens hypothetical protein FLJ10379 (FLJ10379). mRNA
4041	9169	14254	4.6	0	AI982597.1	EST_HUMAN	wu0404.x1 NCJ CGAP GC6 Homo sapiens cDNA clone IMAGE:2515975.3'
4041	9169	14255	4.6	0	AI982597.1	EST_HUMAN	wu0404.x1 NCJ CGAP GC6 Homo sapiens cDNA clone IMAGE:2515975.3'
4044	9171	14257	0.9	0	BE184856.1	EST_HUMAN	MR1-HT0707-100500-001-802 HT0707 Homo sapiens cDNA
4044	9171	14258	0.9	0	BE184856.1	EST_HUMAN	MR1-HT0707-100500-001-802 HT0707 Homo sapiens cDNA
4048	9175		2.0	0	BE274217.1	EST_HUMAN	6011207786.1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:2967690.5'
4055	9182	14265	1.0	0	4507476	NT	Homo sapiens transglutaminase 3 (E polypeptide, protein-glutamine-gamma-glutamyltransferase) (TGMS3) mRNA
4056	9183	14266	2.0	0	5729725	NT	Homo sapiens nuclear receptor coactivator 3 (NCOA3). mRNA
4064	9191		6.2	0	AW675599.1	EST_HUMAN	ba5104.x1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:2900095.3' similar to SW:TH12_BOVIN Q95108 MITOCHONDRIAL THIOREDOXIN PRECURSOR ;
4069	9196	14280	1.5	0	AW408788.1	EST_HUMAN	UI-HF-BM0-adx-c-02-0-UI.1 NIH_MGC_38 Homo sapiens cDNA clone IMAGE:3063147.5'
4071	9198	14283	1.3	0	8922466	NT	Homo sapiens hypothetical protein FLJ10498 (FLJ10498). mRNA
4071	9198	14284	1.3	0	8922466	NT	Homo sapiens hypothetical protein FLJ10498 (FLJ10498). mRNA
4081	9208		2.0	0	5174632	NT	Homo sapiens polycystic kidney disease (polycystin) and REJ (sperm receptor for egg jelly, sea urchin homolog)-like (PKDREJ) mRNA
4098	9224	14307	7.8	0	AA401438.1	EST_HUMAN	zu68h07.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:743197.3' similar to contains Alu repetitive element;contains element MER35 repetitive element ;
4098	9224	14308	7.8	0	AA401438.1	EST_HUMAN	zu68h07.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:743197.3' similar to contains Alu repetitive element;contains element MER35 repetitive element ;
4113	9239	14323	3.8	0	4507720	NT	Homo sapiens titin (TTN) mRNA
4113	9239	14324	3.8	0	4507720	NT	Homo sapiens titin (TTN) mRNA
4126	9252	14333	0.9	0	4508882	NT	Homo sapiens semenogelin 1 (SEMG1) mRNA
4130	9256	14335	8.2	0	4758199	NT	Homo sapiens desmoplakin (DPI, DPL) (DSP) mRNA
4130	9256	14336	8.2	0	4758199	NT	Homo sapiens desmoplakin (DPI, DPL) (DSP) mRNA
4137	9263		0.9	0	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103
4163	9289	14369	1.1	0	AJ003145.1	NT	Homo sapiens mRNA for olfactory receptor protein, pseudogene
4176	9302	14383	7.8	0	J02610.1	NT	Homo sapiens B-100 mRNA, complete cds
4180	9316	14400	1.0	0	AW936689.1	EST_HUMAN	Human apolipoprotein B-100 mRNA, complete cds
4196	9322	14408	0.9	0	4826827	NT	PM2-DT0023-080300-004-808 DT0023 Homo sapiens cDNA
4196	9322	14409	0.9	0	4826827	NT	Homo sapiens myelodysplasia syndrome 1 (MDS1) mRNA
4198	9324	14411	5.7	0	AF174590.1	NT	Homo sapiens myelodysplasia syndrome 1 (MDS1) mRNA
4206	9331		1.9	0	AI189844.1	EST_HUMAN	q423f06.x1 Soares_placenta_8w6weeks_2NBHP8109V Homo sapiens cDNA clone IMAGE:1724579.3 similar to contains MER20.b2 MER20 repetitive element ;
4210	9334		4.1	0	U14520.1	NT	Human CBFA3 (Cbfa3) gene, partial cds
4224	9348	14429	1.0	0	4505646	NT	Homo sapiens propionin convertase subtilisin/kexin type 2 (PCSK2) mRNA
4230	9354	14436	0.9	0	6563384	NT	Homo sapiens protein kinase C, nu (PRKCN). mRNA
4230	9354	14437	0.9	0	6563384	NT	Homo sapiens protein kinase C, nu (PRKCN). mRNA
4237	9361	14443	1.2	0	U10991.1	NT	Human G2 protein mRNA, partial cds

Table 4

4237	9361	14444	1.2	0	U10991.1	NT	Human G2 protein mRNA, partial cds
4245	9370	14449	10.2	0	6912281	NT	Homo sapiens COMPLEMENT C1q RECEPTOR (C1QR) mRNA
4263	9388		1.2	0	AF153047.2	NT	Homo sapiens gap junction protein connexin-36 (CX36) gene, complete cds
4268	9393	14475	1.6	0	U03901.1	NT	Human Ig light chain V L 1 region germline (humiv1c2c) gene, partial cds
							Homo sapiens plasma membrane calcium ATPase isoform 1 (ATP2B1) gene, alternative splice products, partial cds
4274	9399	14482	5.2	0	L14561.1	NT	H. sapiens H2B/h gene
4278	9403	14487	2.8	0	Z80780.1	NT	H. sapiens H2B/h gene
4278	9403	14488	2.8	0	Z80780.1	NT	H. sapiens H4/d gene for H4 histone
4284	9409	14494	1.6	0	X60483.1	NT	H. sapiens H4/d gene for H4 histone
4284	9409	14495	1.6	0	X60483.1	NT	H. sapiens H4/d gene for H4 histone
4289	9413	14501	9.0	0	7662091	NT	Homo sapiens KIAA0390 gene product (KIAA0390), mRNA
4289	9413	14502	9.0	0	7662091	NT	Homo sapiens KIAA0390 gene product (KIAA0390), mRNA
4299	9423	14514	10.8	0	4885126	NT	Homo sapiens caudal type homeo box transcription factor 4 (CDX4), mRNA
4302	9426	14516	1.0	0	AB037781.1	NT	Homo sapiens myosin regulatory light chain interacting protein (MIR), mRNA
4333	9456	14544	1.1	0	7019456	NT	Homo sapiens ACTN2 gene for alpha-Actinin 2, exon 10
4346	9469	14557	8.1	0	AJ249765.1	NT	Homo sapiens ACTN2 gene for alpha-Actinin 2, exon 10
4346	9469	14558	8.1	0	AJ249765.1	NT	Homo sapiens ACTN2 gene for alpha-Actinin 2, exon 10
4368	9490		1.9	0	AF200629.1	NT	Homo sapiens HPS1 gene, intron 5
							xc68608.x1 NCJ_CGAP_Es02 Homo sapiens cDNA clone IMAGE:2589446 3' similar to SW:AHNK_HUMAN Q09688 NEUROBLAST DIFFERENTIATION ASSOCIATED PROTEIN
4401	9522	14612	40.2	0	AW084964.1	EST_HUMAN	AHNK:
4403	10301		1.9	0	8051619	NT	Homo sapiens LIM domain kinase 2 (LIMK2), transcript variant 2a, mRNA
							Homo sapiens vascular endothelial cell growth factor 165 receptor/neuropilin (VEGF165) mRNA, complete cds
4405	9525	14615	1.4	0	AF016050.1	NT	Homo sapiens chromosome 21 segment HS21C007
4408	9528		7.5	0	AL163207.2	NT	Homo sapiens chromosome 21 segment HS21C007
4410	9530	14619	1.3	0	AW381570.1	EST_HUMAN	PM1-HT0305-10199-002-003 HT0305 Homo sapiens cDNA
4416	9536	14626	1.8	0	AJ278120.1	NT	Homo sapiens mRNA for putative ankyrin-repeat containing protein (ORF1)
4416	9536	14627	1.8	0	AJ278120.1	NT	Homo sapiens mRNA for putative ankyrin-repeat containing protein (ORF1)
4418	9538	14629	3.9	0	4758467	NT	Homo sapiens G protein-coupled receptor 50 (GPR50) mRNA
4419	9539	14630	2.3	0	AF108830.1	NT	Homo sapiens serine-threonine protein kinase (MNBH) mRNA, complete cds
4424	9544	14636	1.5	0	Z66526.1	NT	H. sapiens pancreatic polypeptide receptor PP1 gene
							Homo sapiens ATP-sensitive inwardly rectifying K-channel subunit (KCNJ6/BIR1) gene, exon
4429	9550	14643	1.1	0	S78684.1	NT	Homo sapiens pyrin (MEFV) gene, complete cds
4430	9551	14644	2.0	0	AF111163.1	NT	Homo sapiens pyrin (MEFV) gene, complete cds
4430	9551	14645	2.0	0	AF111163.1	NT	Homo sapiens pyrin (MEFV) gene, complete cds
4438	10302	14655	3.1	0	6005973	NT	Homo sapiens zinc finger protein 195 (ZNF195), mRNA
4444	9584	14660	5.4	0	AF208161.1	NT	Homo sapiens syntenin precursor, mRNA, complete cds
4446	9589	14667	1.9	0	AF152337.1	NT	Homo sapiens syntenin gamma C3 (PCDH-gamma-C3) mRNA, complete cds
4452	9572	14671	1.4	0	5454175	NT	Homo sapiens zinc finger protein 211 (ZNF211), mRNA
4462	9582	14679	15.2	0	4503470	NT	Homo sapiens eukaryotic translation elongation factor 1 alpha 1 (EEF1A1) mRNA

Table 4

4473	9593	14688	1.5	0	4503098	NT	Homo sapiens chondroitin sulfate proteoglycan 4 (melanoma-associated) (CSPG4), mRNA
4477	9597	14693	1.6	0	4502556	NT	Homo sapiens calcium/calmodulin-dependent protein kinase IV (CAMK4), mRNA
4481	9601		2.8	0	L35485.1	NT	Homo sapiens iduronate sulphate sulphasylase (IDS), gene, complete cds
4483	9603	14695	9.8	0	7662091	NT	Homo sapiens KIAA0390 gene product (KIAA0390), mRNA
4483	9603	14696	9.8	0	7662091	NT	Homo sapiens KIAA0390 gene product (KIAA0390), mRNA
4498	9618	14709	2.0	0	AF143314.1	NT	Homo sapiens PTEN (PTEN) gene, exons 3 through 5
4500	9620	14711	8.7	0	AJ245418.1	NT	Homo sapiens mRNA for G7c protein (G7c gene located in the class III region of the major histocompatibility complex)
4500	9620	14712	8.7	0	AJ245418.1	NT	Homo sapiens mRNA for G7c protein (G7c gene located in the class III region of the major histocompatibility complex)
4511	9630		0.8	0	D87675.1	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
4523	9642		1.5	0	AA174072.1	EST_HUMAN	zp18g08.s1 Strata gene fetal retina 937202 Homo sapiens cDNA clone IMAGE:609854 3'
4526	9645		1.6	0	7657410	NT	Homo sapiens cdz (odd Oz/ten-m, Drosophila) homolog 1 (ODZ1), mRNA
4528	9647		1.2	0	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
4529	9648	14737	1.7	0	AF184110.1	NT	Homo sapiens cyclophilin-related protein (NKTR), gene, complete cds
4530	9649	14738	4.4	0	AL163300.2	NT	Homo sapiens chromosome 21 segment HS21C100
4531	9650		1.9	0	AB037521.1	NT	Homo sapiens gene for natriuretic protein, partial cds
4541	9660	14748	1.9	0	4557867	NT	Homo sapiens keratin 18 (KRT18), mRNA
4541	9660	14749	1.9	0	4557867	NT	Homo sapiens keratin 18 (KRT18), mRNA
4542	9661	14750	1.3	0	AF153819.1	NT	Homo sapiens inwardly-rectifying potassium channel Kir2.1 (KCNJ2), gene, exon 2 and complete cds
4542	9661	14751	1.3	0	AF153819.1	NT	Homo sapiens inwardly-rectifying potassium channel Kir2.1 (KCNJ2), gene, exon 2 and complete cds
4554	9239	14323	7.4	0	4507720	NT	Homo sapiens titin (TTN), mRNA
4554	9239	14324	7.4	0	4507720	NT	Homo sapiens titin (TTN), mRNA
4560	9678	14770	22.0	0	Y18890.1	NT	Human endogenous retrovirus type K (HERV-K), gag, pol and env genes
4566	9684	14778	2.3	0	BE081527.1	EST_HUMAN	OV2-BT0635-160400-142-h05 BT0635 Homo sapiens cDNA
4574	9691		2.0	0	AF086641.1	NT	Homo sapiens truncated tenascin XB (TNXB), gene, partial cds and TNXA gene recombination breakpoint region
4580	9696	14789	2.7	0	AB037820.1	NT	Homo sapiens mRNA for KIAA1399 protein, partial cds
4580	9696	14790	2.7	0	AB037820.1	NT	Homo sapiens mRNA for KIAA1399 protein, partial cds
4581	9697	14791	2.6	0	M74099.1	NT	Human displacement protein (CCAT), mRNA
4585	9700	14794	1.8	0	6453812	NT	Homo sapiens butyrophilin, subfamily 2, member A2 (BTN2A2), mRNA
4585	9700	14795	1.8	0	6453812	NT	Homo sapiens butyrophilin, subfamily 2, member A2 (BTN2A2), mRNA
4586	5330	10461	1.0	0	T56945.1	EST_HUMAN	ya83g04.12 Strata gene fetal spleen (#937205) Homo sapiens cDNA clone IMAGE:68310 5'
4586	5330	10462	1.0	0	T56945.1	EST_HUMAN	ya83g04.12 Strata gene fetal spleen (#937205) Homo sapiens cDNA clone IMAGE:68310 5'
4587	9701		1.0	0	BE278730.1	EST_HUMAN	601158935F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:350521 5'



Table 4

4593	9707	14799	1.1	0	BE390050.1	EST_HUMAN	601285246f1 NIH MGC 44 Homo sapiens cDNA clone IMAGE:3607067 5'
4614	9728	14822	37.4	0	IM80902.1	NT	Human AHNK nucleoprotein mRNA, 5' end
4617	9731	14825	3.1	0	IM69197.1	NT	Human haptoglobin and haptoglobin-related protein (HP and HPR) genes, complete cds
4617	9731	14826	3.1	0	IM69197.1	NT	Human haptoglobin and haptoglobin-related protein (HP and HPR) genes, complete cds
4620	9734	14829	1.1	0	AF184110.1	NT	Homo sapiens cyclophilin-related protein (NKTR) gene, complete cds
4621	9735	14830	1.3	0	7662181	NT	Homo sapiens KIAA0563 gene product (KIAA0563), mRNA
4636	9750		1.5	0	X58467.1	NT	Human CYP2D7A pseudogene for cytochrome P450 2D6
4644	9756	14851	1.0	0	7304922	NT	Homo sapiens bromodomain adjacent to zinc finger domain, 2B (BAZ2B), mRNA
4644	9756	14852	1.0	0	7304922	NT	Homo sapiens bromodomain adjacent to zinc finger domain, 2B (BAZ2B), mRNA
4652	9764	14859	1.1	0	AF028601.1	NT	Homo sapiens alpha-3 type IX collagen (COL9A3) gene, promoter region, and exons 1-26
4655	9767	14862	0.9	0	7019320	NT	Homo sapiens protein0008 (AD013), mRNA
4655	9767	14863	0.9	0	7019320	NT	Homo sapiens protein0008 (AD013), mRNA
4676	9786	14887	1.8	0	AW444637.1	EST_HUMAN	UI-H-B13-q1w-c-04-U1.s1 NC1_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:2733294 3'
4686	9798		1.8	0	AF083242.1	NT	Homo sapiens HSPC024-iso mRNA, complete cds
4697	9809		2.0	0	M65189.1	NT	Human connexin 43 processed pseudogene
4737	9848	14940	2.8	0	X87205.1	NT	M.fascicularis mRNA for metalloproteinase-like, disintegrin-like protein, IVa
4739	9850	14942	1.3	0	AF084479.1	NT	Homo sapiens Williams-Beuren syndrome deletion transcript 9 (WBSCR9) mRNA, complete cds
4740	9851	14943	1.5	0	AF097416.1	NT	Mus musculus zinc finger transcription factor Kaiso mRNA, complete cds
4741	9852	14944	3.5	0	4503766	NT	Homo sapiens fragile X mental retardation 2 (FMR2) mRNA
4743	9854	14946	61.8	0	4885048	NT	Homo sapiens actin, alpha, cardiac muscle (ACTC), mRNA
4744	9855	14947	1.4	0	P52740	SWISSPROT	ZINC FINGER PROTEIN 132
4746	9857	14949	1.0	0	8922180	NT	Homo sapiens hypothetical protein DKFZp762E1312 (DKFZp762E1312), mRNA
4748	9859	14951	0.8	0	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
4752	9863	14956	7.8	0	8923080	NT	Homo sapiens hypothetical protein FLJ20073 (FLJ20073), mRNA
4756	9867	14960	1.0	0	7661979	NT	Homo sapiens KIAA0187 gene product (KIAA0187), mRNA
4757	9868	14961	1.7	0	M94081.1	NT	Human Tcr-C-delta gene, exons 1-4; Tcr-V-delta gene, exons 1-2; T-cell receptor alpha (Tcr-alpha) gene, J1-J61 segments; and Tcr-C-alpha gene, exons 1-4
4757	9868	14962	1.7	0	M94081.1	NT	Human Tcr-C-delta gene, exons 1-4; Tcr-V-delta gene, exons 1-2; T-cell receptor alpha (Tcr-alpha) gene, J1-J61 segments; and Tcr-C-alpha gene, exons 1-4
4759	9870	14984	1.7	0	X94628.1	NT	H.sapiens MeCP-2 gene
4759	9870	14985	1.7	0	X94628.1	NT	H.sapiens MeCP-2 gene
4762	9873	14988	1.1	0	M55582.1	NT	Human collagenase type IV (CLG4) gene, exon 2
4763	9874	14989	3.2	0	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080
4776	9886	14979	1.0	0	5032150	NT	Homo sapiens TATA box binding protein (TBP)-associated factor, RNA polymerase II, l, 28kD (TAF2) mRNA
4786	9897	14990	0.8	0	6806918	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
4788	9899	14992	1.4	0	X92841.1	NT	H.sapiens MICA gene
4791	9902	14995	2.0	0	4565642	NT	Homo sapiens zinc finger protein (KIAA0412) mRNA

Table 4

4792	9903	14996	1.2	0	AB014533.1	NT	Homo sapiens mRNA for KIAA0633 protein, partial cds
4794	9905	14996	2.3	0	6677648	NT	Mus musculus zinc finger protein interacting with K protein 1 (ZIK1), mRNA
4795	9906	14999	1.1	0	5174560	NT	Homo sapiens meningoangioma expressed antigen 6 (coiled-coil proline-rich) (MGEA6), mRNA
4797	9908	15001	8.6	0	4756199	NT	Homo sapiens desmoplakin (DPI, DP11) (DSP) mRNA
4799	9910	15003	1.2	0	Y16723.1	NT	Homo sapiens gene encoding filensin, exon 8
4800	9911	15004	1.6	0	7705546	NT	Homo sapiens zinc-finger DNA-binding protein (HUM-HOXY1), mRNA
4801	9912	15009	1.3	0	AJ010442.1	NT	Homo sapiens mRNA for immunoglobulin kappa light chain, anti-RHD, Iherad 7
4806	9916	15009	24.9	0	AF055066.1	NT	Homo sapiens MHC class 1 region
4808	9918	15012	2.4	0	4505508	NT	Homo sapiens oploid receptor, delta 1 (OPROD1) mRNA
4809	9919	15012	2.5	0	AF091711.1	NT	Homo sapiens splice variant AKAP350 mRNA, partial cds
4812	9239	14323	5.5	0	4507720	NT	Homo sapiens titin (TTN) mRNA
4812	9239	14324	5.5	0	4507720	NT	Homo sapiens titin (TTN) mRNA
4814	9923	15016	0.9	0	AJ277892.1	NT	Homo sapiens partial TTN gene for titin
4824	9932	15022	12.0	0	4507720	NT	Homo sapiens COL4A6 gene for $\alpha 6(IV)$ collagen, exon 44 and partial cds
4827	9935	15025	1.0	0	D63562.1	NT	Homo sapiens farnesyl diphosphate synthase (farnesyl pyrophosphate synthetase, dimethylallyltransferase, geranyltransferase) (FDPs) mRNA
4831	9939	15028	1.5	0	4503684	NT	Homo sapiens sialyltransferase 8 (alpha-N-acetylneuraminase: alpha-2,8-sialyltransferase, GD3 synthase) (SIAT8) mRNA
4837	9545	14637	1.1	0	4506952	NT	Human mRNA for transcription factor AREB8, complete cds
4845	9852	15040	1.3	0	D15050.1	NT	Human mRNA for transcription factor AREB8, complete cds
4845	9852	15041	1.3	0	D15050.1	NT	Human mRNA for transcription factor AREB8, complete cds
4854	9861	15047	0.9	0	AB026898.1	NT	Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)
4871	9978	15062	1.3	0	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
4879	9986	15068	1.5	0	AW452728.1	EST_HUMAN	U1-H-B13-a1v-t-02-0-U1-s1 NC1_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:3068691 3'
4885	9993	15074	1.2	0	8922928	NT	Homo sapiens hypothetical protein FLJ111190 (FLJ11190), mRNA
4886	9932	15022	8.0	0	4507720	NT	Homo sapiens titin (TTN) mRNA
4886	9932	15022	8.0	0	4507720	NT	Homo sapiens titin (TTN) gene, alternative splice products, partial cds
4888	9995	15076	2.8	0	AF058332.1	NT	Homo sapiens titin (TTN) gene, alternative splice products, partial cds
4888	9995	15077	2.8	0	AF058332.1	NT	Homo sapiens titin (TTN) gene, alternative splice products, partial cds
4894	10001	15084	3.0	0	4507720	NT	Homo sapiens titin (TTN) mRNA
4897	10004	15084	4.3	0	U14967.1	NT	Human ribosomal protein L21 mRNA, complete cds
4910	10017	15101	2.6	0	BE408663.1	EST_HUMAN	Human ribosomal protein L21 mRNA, complete cds
4915	10022	15101	5.4	0	4758199	NT	6013037299-1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3638118 5'
4925	10032	15106	1.0	0	AB028866.1	NT	Homo sapiens desmoplakin (DPI, DP11) (DSP) mRNA
4939	10045	15116	1.7	0	8923441	NT	Homo sapiens mRNA for KIAA1043 protein, partial cds
4939	10045	15116	1.7	0	8923441	NT	Homo sapiens hypothetical protein FLJ20477 (FLJ20477), mRNA
4939	10045	15117	1.7	0	8923441	NT	Homo sapiens hypothetical protein FLJ20477 (FLJ20477), mRNA

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Table 4

4953	10058	15128	1.1	0	U82671.2	NT	Homo sapiens chromosome Xq28 melanoma antigen family A2a (MAGEA2A), melanoma antigen family A12 (MAGEA12), melanoma antigen family A2b (MAGEA2B), melanoma antigen family A3 (MAGEA3), caltactin (CALT), NAD(P)H dehydrogenase-like protein (NSDHL), and L1>
4953	10058	15129	1.1	0	U82671.2	NT	Homo sapiens chromosome Xq28 melanoma antigen family A2a (MAGEA2A), melanoma antigen family A12 (MAGEA12), melanoma antigen family A2b (MAGEA2B), melanoma antigen family A3 (MAGEA3), caltactin (CALT), NAD(P)H dehydrogenase-like protein (NSDHL), and L1>
4957	9239	14323	5.8	0	4507720	NT	Homo sapiens titin (TTN) mRNA
4957	9239	14324	5.8	0	4507720	NT	Homo sapiens titin (TTN) mRNA
4959	10062	15134	3.5	0	4507720	NT	Homo sapiens titin (TTN) mRNA
4960	10063	15135	7.8	0	4507720	NT	Homo sapiens titin (TTN) mRNA
4968	10071		1.2	0	4758225	NT	Homo sapiens E2F transcription factor 2 (E2F2) mRNA
4978	10081	15151	1.4	0	AF016705.1	NT	Homo sapiens E6-AP ubiquitin-protein ligase (UBE3A) gene, exon 3
4987	10080		1.3	0	AL163209.2	NT	Homo sapiens chromosome 21 segment HS21C009
4990	10093		37.8	0	D50657.1	NT	Homo sapiens gamma-cytoplasmic actin (ACTGP3) pseudogene
5000	10103	15171	2.3	0	AL277892.1	NT	Homo sapiens partial TTN gene for titin
5001	10104	15172	3.0	0	4507720	NT	Homo sapiens titin (TTN) mRNA
5003	10106	15174	4.2	0	4507720	NT	Homo sapiens titin (TTN) mRNA
5005	9239	14323	2.9	0	4507720	NT	Homo sapiens titin (TTN) mRNA
5005	9239	14324	2.9	0	4507720	NT	Homo sapiens titin (TTN) mRNA
5016	10120	15192	2.4	0	X52988.1	NT	Bacillus amyloquelicifaciens sacB gene for levansucrase (EC 2.4.1.10)
5037	10137	15213	1.8	0	AF240635.1	NT	Homo sapiens vascular endothelial cadherin 2 mRNA, complete cds
5037	10137	15214	1.8	0	AF240635.1	NT	Homo sapiens vascular endothelial cadherin 2 mRNA, complete cds
5040	10140	15218	1.0	0	5454153	NT	Homo sapiens cyclophilin (USA-CYP) mRNA
5054	10154	15230	1.2	0	6677700	NT	Homo sapiens G-protein coupled receptor (RE2), mRNA
5055	9239	14323	11.2	0	4507720	NT	Homo sapiens titin (TTN) mRNA
5055	9239	14324	11.2	0	4507720	NT	Homo sapiens titin (TTN) mRNA
5058	9239	14323	14.9	0	4507720	NT	Homo sapiens titin (TTN) mRNA
5058	9239	14324	14.9	0	4507720	NT	Homo sapiens titin (TTN) mRNA
5065	10163	15240	1.3	0	4557362	NT	Homo sapiens PR domain containing 1, with ZNF domain (PRDM1) mRNA
5070	10168	15245	1.0	0	M10905.1	NT	Human cellular fibronectin mRNA
5070	10168	15246	1.0	0	M10905.1	NT	Human cellular fibronectin mRNA
5071	10169	15247	1.1	0	U91328.1	NT	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, RoRet gene, and sodium phosphate transporter (NPT3) gene, complete cds
5080	10178	15258	3.0	0	4507720	NT	Homo sapiens titin (TTN) mRNA
5096	9239	14323	6.3	0	4507720	NT	Homo sapiens titin (TTN) mRNA
5098	9239	14324	6.3	0	4507720	NT	Homo sapiens titin (TTN) mRNA
5098	10195	15275	1.3	0	L35475.1	NT	Human olfactory receptor-like gene, complete cds
5098	10195	15276	1.3	0	L35475.1	NT	Human olfactory receptor-like gene, complete cds

Table 4

5099	9239	14323	9.4	0	4507720	NT	Homo sapiens tlin (TTN) mRNA
5099	9239	14324	9.4	0	4507720	NT	Homo sapiens tlin (TTN) mRNA
5124	10220	15297	0.9	0	AF195658.1	NT	Homo sapiens DNA mismatch repair protein (MLH3) gene, complete cds
5126	10221	15298	1.4	0	5360213	NT	Homo sapiens glypican 3 (GPC3) mRNA
5130	10225	15300	0.8	0	AE000327.1	NT	Escherichia coli K-12 MG1655 section 217 of 400 of the complete genome
5140	10235	15310	1.1	0	4885474	NT	Homo sapiens melanoma antigen, family C, 1 (MAGEC1), mRNA
5159	10254	15325	1.0	0	4885474	NT	Homo sapiens melanoma antigen, family C, 1 (MAGEC1), mRNA
5162	10256	15326	1.6	0	4758697	NT	Homo sapiens mannosidase, alpha, class 2A, member 1 (MAN2A1), mRNA
5165	10259	15329	1.1	0	AF245703.1	NT	Homo sapiens toll-like receptor 8 (TLR8) mRNA, complete cds
5165	10259	15330	1.1	0	AF245703.1	NT	Homo sapiens toll-like receptor 8 (TLR8) mRNA, complete cds
5186	10278	15346	1.7	0	AF006061.1	NT	Homo sapiens placental growth hormone isoform hGH-V3 (hGH-V) mRNA, complete cds
5187	9239	14323	10.4	0	4507720	NT	Homo sapiens tlin (TTN) mRNA
5187	9239	14324	10.4	0	4507720	NT	Homo sapiens tlin (TTN) mRNA
5189	10280	15348	6.8	0	4507720	NT	Homo sapiens tlin (TTN) mRNA
5193	10284		1.4	0	AL163285.2	NT	Homo sapiens chromosome 21 segment HS21C085
5195	10286	15354	4.0	0	4507720	NT	Homo sapiens tlin (TTN) mRNA
5195	10286	15355	4.0	0	4507720	NT	Homo sapiens tlin (TTN) mRNA
5196	10287	15356	1.0	0	4502398	NT	Homo sapiens beaded filament structural protein 1, filensin (BFSP1) mRNA

## CLAIMS

1. A spatially-addressable set of single exon nucleic acid probes for measuring gene expression in a sample derived  
5 from human heart comprising a plurality single exon nucleic probes, said probes comprising any one of the nucleotide sequences set out in SEQ ID NOS: 1 - 5,202 or a complementary sequence, or a portion of such a sequence.
- 10 2. A spatially-addressable set of single exon nucleic acid probes as claimed in claim 1 wherein each of said plurality of probes is separately and addressably amplifiable.
3. A spatially-addressable set of single exon nucleic acid  
15 probes as claimed in claim 1 wherein each of said plurality of probes is separately and addressably isolatable from said plurality.
4. A spatially-addressable set of single exon nucleic acid  
20 probes as claimed in any of claims 1 to 3 wherein said probes comprise any one of the nucleotide sequences set out in SEQ ID NOS.: 5,203 - 10,283.
5. A spatially-addressable set of single exon nucleic acid  
25 probes as claimed in any of claims 1 to 4, wherein each of said plurality of probes is amplifiable using at least one common primer.
6. A spatially-addressable set of single exon nucleic acid  
30 probes as claimed in any of claims 1 to 5 wherein the set comprises between 50 - 20,000 single exon nucleic acid probes.
7. A spatially-addressable set of single exon nucleic acid  
35 probes as claimed in any of claims 1 to 6, wherein the

average length of the single exon nucleic acid probes is between 200 and 500 bp.

8. A spatially-addressable set of single exon nucleic acid  
5 probes as claimed in any of claims 1 to 7, wherein at least 50% of said single exon nucleic acid probes lack prokaryotic and bacteriophage vector sequence.

9. A spatially-addressable set of single exon nucleic acid  
10 probes as claimed in any of claims 1 to 8, wherein at least 50% of said single exon nucleic acid probes lack homopolymeric stretches of A or T.

10. A spatially-addressable set of single exon nucleic acid  
15 probes as claimed in any of claims 1 - 9 characterised in that said set of probes is addressably disposed upon a substrate.

11. A spatially-addressable set of single exon nucleic acid  
20 probes as claimed in claim 10 wherein said substrate is selected from glass, amorphous silicon, crystalline silicon and plastic.

12. A microarray comprising a spatially addressable set of  
25 single exon nucleic acid probes as claimed in any of claims 1 - 11.

13. A single exon nucleic acid probe for measuring human  
gene expression in a sample derived from human heart  
30 comprising a nucleotide sequence as set out in any of SEQ ID NOs.: 1 - 5,202 or a complementary sequence or a fragment thereof wherein said probe hybridizes at high stringency to a nucleic acid molecule expressed in the human heart.

14. A single exon nucleic acid probe as claimed in claim 13 comprising a nucleotide sequence as set out in any of SEQ ID NOs.: 5,203 - 10,283 or a complementary sequence or a fragment thereof.

5

15. A single exon nucleic acid probe for measuring human gene expression in a sample derived from human heart which is a nucleic acid molecule having a sequence encoding a peptide comprising a peptide sequence as set out in any of  
10 SEQ ID NOs.: 10,284 - 15,322, or a complementary sequence or a fragment thereof wherein said probe hybridizes at high stringency to a nucleic acid expressed in the human heart.

16. A single exon nucleic acid probe as claimed in any one  
15 of claims 13 to 15 wherein said single exon nucleic acid probe comprises between 15 and 25 contiguous nucleotides of said SEQ ID NO.

17. A single exon nucleic acid probe as claimed in any one  
20 of claims 13 to 15, wherein said probe is between 3 - 25 kb in length.

18. A single exon nucleic acid probe as claimed in any one  
of claims 13 - 17, wherein said probe is DNA, RNA or PNA.  
25

19. A single exon nucleic acid probe as claimed in any one of claims 13 - 18, wherein said probe is detectably labeled.

30 20. A single exon nucleic acid probe as claimed in any one of claims 13 - 19, wherein said probe lacks prokaryotic and bacteriophage vector sequence.

21. A single exon nucleic acid probe as claimed in any one

of claims 13 - 20, wherein said probe lacks homopolymeric stretches of A or T.

22. A method of measuring gene expression in a sample  
5 derived from human heart, comprising:  
    contacting the microarray of claim 12, with a first  
        collection of detectably labeled nucleic acids,  
        said first collection of nucleic acids derived  
        from mRNA of human heart; and then  
10 measuring the label detectably bound to each probe of  
    said microarray.

23. A method of identifying exons in a eukaryotic genome,  
comprising:  
15 algorithmically predicting at least one exon from  
    genomic sequence of said eukaryote; and then  
    detecting specific hybridization of detectably labeled  
        nucleic acids to a single exon probe,  
wherein said detectably labeled nucleic acids are derived  
20 from mRNA from the heart of said eukaryote, said probe is a  
single exon probe having a fragment identical in sequence  
to, or complementary in sequence to, said predicted exon,  
said probe is included within a microarray according to  
claim 12, and said fragment is selectively hybridizable at  
25 high stringency.

24. A method of assigning exons to a single gene,  
comprising:  
    identifying a plurality of exons from genomic  
30 sequence according to the method of claim 23; and  
    then  
    measuring the expression of each of said exons in a  
        plurality of tissues and/or cell types using  
        hybridization to single exon microarrays having a  
35 probe with said exon,



wherein a common pattern of expression of said exons in said plurality of tissues and/or cell types indicates that the exons should be assigned to a single gene.

5 25. A nucleic acid sequence as set out in any of SEQ ID Nos: 1 - 10,283 which encodes a peptide.

26. A peptide encoded by a sequence as set out in any of SEQ ID Nos: 1 - 10,283.

10

27. A peptide comprising a sequence as set out in any of SEQ ID Nos: 10,284 - 15,322.

**Amendments to the claims have been filed as follows**

1. A spatially-addressable set of single exon nucleic acid probes for measuring gene expression in a sample derived from human heart comprising at least 50 single exon nucleic probes, said probes comprising any one of the nucleotide sequences set out in SEQ ID NOs: 1 - 5,202 or a complementary sequence, or a unique fragment of such a sequence wherein at least 50% of said single exon nucleic acid probes lack prokaryotic and bacteriophage vector sequence and wherein at least 50% of said single exon nucleic acid probes lack homopolymeric stretches of A & T.
2. A spatially-addressable set of single exon nucleic acid probes as claimed in claim 1 wherein each of said plurality of probes is separately and addressably amplifiable.
3. A spatially-addressable set of single exon nucleic acid probes as claimed in claim 1 wherein each of said plurality of probes is separately and addressably isolatable from said plurality.
4. A spatially-addressable set of single exon nucleic acid probes as claimed in any of claims 1 to 3 wherein said probes comprise any one of the nucleotide sequences set out in SEQ ID NOS.: 5,203 - 10,283.
5. A spatially-addressable set of single exon nucleic acid probes as claimed in any of claims 1 to 4, wherein each of said plurality of probes is amplifiable using at least one common primer.

6. A spatially-addressable set of single exon nucleic acid probes as claimed in any of claims 1 to 5 wherein the set comprises between 50 - 20,000 single exon nucleic acid probes.
7. A spatially-addressable set of single exon nucleic acid probes as claimed in any of claims 1 to 6, wherein the average length of the single exon nucleic acid probes is between 25 and 500 bp.
10. A spatially-addressable set of single exon nucleic acid probes as claimed in any of claims 1 - 9 characterised in that said set of probes is addressably disposed upon a substrate.
11. A spatially-addressable set of single exon nucleic acid probes as claimed in claim 10 wherein said substrate is selected from glass, amorphous silicon, crystalline silicon and plastic.
12. A microarray comprising a spatially addressable set of single exon nucleic acid probes as claimed in any of claims 1 - 11.
13. A method of measuring gene expression in a sample derived from human heart, comprising:
  - contacting the microarray of claim 12, with a first collection of detectably labeled nucleic acids, said first collection of nucleic acids derived from mRNA of human heart; and then
  - measuring the label detectably bound to each probe of said microarray.

14. A method of identifying exons in a eukaryotic genome, comprising:

algorithmically predicting at least one exon from genomic sequence of said eukaryote; and then detecting specific hybridization of detectably labeled nucleic acids to a single exon probe, wherein said detectably labeled nucleic acids are derived from mRNA from the heart of said eukaryote, said probe is a single exon probe having a fragment identical in sequence to, or complementary in sequence to, said predicted exon, said probe is included within a microarray according to claim 12, and said fragment is selectively hybridizable at high stringency.

15. A method of assigning exons to a single gene, comprising:

identifying a plurality of exons from genomic sequence according to the method of claim 14; and then measuring the expression of each of said exons in a plurality of tissues and/or cell types using hybridization to single exon microarrays having a probe with said exon, wherein a common pattern of expression of said exons in said plurality of tissues and/or cell types indicates that the exons should be assigned to a single gene.



Application No: GB 0024263.6  
Claims searched: 1-12 and 22-24

Examiner: L. V. Thomas  
Date of search: 15 March 2001

## Patents Act 1977 Search Report under Section 17

### Databases searched:

UK Patent Office collections, including GB, EP, WO & US patent specifications, in:  
UK CI (Ed.S):  
Int CI (Ed.7):  
Other: Online: EPODOC, WPI, BIOSIS, MEDLINE, CAS-ONLINE, SCISEARCH, EMBASE

### Documents considered to be relevant:

Category	Identity of document and relevant passage	Relevant to claims
E, A	EP 1043405 A2 (AFFYMETRIX, INC.) see col.3 l.21 - col.4 l.23 and col.10 l.42 - col.11 l.38	1,22
E, A	WO 01/09369 A2 (AFFYMETRIX, INC.) see p.3 l.30 - p.4 l.24 and p.10 l.16 - p.11 l.19	1,22

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|---|--|
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